

247	84.4	87	2	US-08-161-965-14	Sequence 44, Appl	78.1	75	US-09-249-471-57	Sequence 41, Appl
248	84.4	87	2	US-08-634-471-11	Sequence 44, Appl	78.1	75	US-09-249-471-57	Sequence 57, Appl
249	87.1	87	2	US-09-249-471-11	Sequence 44, Appl	78.1	75	US-09-249-471-57	Sequence 6, Appl
250	84.4	87	3	US-09-249-471-11	Sequence 44, Appl	78.1	75	US-09-249-471-57	Sequence 13, Appl
251	84.4	87	3	US-09-249-471-11	Sequence 44, Appl	78.1	75	US-09-249-471-57	Sequence 17, Appl
252	84.4	87	3	US-08-809-455-41	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 6, Appl
253	84.4	87	3	US-09-249-471-11	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
254	84.4	87	3	US-09-249-471-11	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
255	84.4	88	2	US-08-465-389-43	Sequence 43, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
256	84.4	88	2	US-08-465-389-43	Sequence 43, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
257	84.4	88	2	US-08-465-389-43	Sequence 43, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
258	84.4	88	2	US-08-465-389-43	Sequence 43, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
259	84.4	88	2	US-08-465-389-43	Sequence 43, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
260	84.4	88	2	US-08-465-389-43	Sequence 43, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
261	84.4	88	2	US-08-465-389-43	Sequence 43, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
262	84.4	88	2	US-08-465-389-43	Sequence 43, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
263	84.4	88	2	US-08-465-389-43	Sequence 43, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
264	84.4	88	2	US-08-465-389-43	Sequence 43, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
265	84.4	88	2	US-08-465-389-43	Sequence 43, Appl	78.1	75	US-08-809-455-41	Sequence 57, Appl
266	84.4	199	4	US-09-249-471-11	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
267	84.4	199	4	US-09-249-471-11	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
268	84.4	199	4	US-09-249-471-11	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
269	84.4	204	2	US-08-809-455-41	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
270	84.4	241	4	US-08-161-965-14	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
271	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
272	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
273	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
274	84.4	199	4	US-09-249-471-11	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
275	84.4	204	2	US-08-809-455-41	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
276	84.4	241	4	US-08-161-965-14	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
277	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
278	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
279	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
280	84.4	199	4	US-09-249-471-11	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
281	84.4	204	2	US-08-809-455-41	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
282	84.4	241	4	US-08-161-965-14	Sequence 44, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
283	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
284	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
285	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
286	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
287	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
288	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
289	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
290	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
291	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
292	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
293	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
294	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
295	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
296	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
297	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
298	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
299	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
300	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
301	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
302	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
303	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
304	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
305	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
306	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
307	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
308	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
309	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
310	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
311	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
312	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
313	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
314	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
315	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
316	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
317	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
318	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl
319	84.4	511	3	US-08-272-247-4	Sequence 4, Appl	78.1	75	US-08-809-455-41	Sequence 41, Appl

539	24	75.0	321	4	US-09-540-014-25	Sequence 25, Appl	612	24	75.0	152	4	US-08-484-432-12	Sequence 42, Appl
540	24	75.0	321	4	US-09-146-433-15	Sequence 15, Appl	613	24	75.0	152	4	US-08-879-589-4	Sequence 4, Appl
541	24	75.0	322	5	US-09-146-433-15	Sequence 15, Appl	614	24	75.0	154	4	US-08-879-589-4	Sequence 4, Appl
542	24	75.0	324	1	US-08-017-413-11	Sequence 11, Appl	615	24	75.0	154	4	US-08-879-589-4	Sequence 4, Appl
543	24	75.0	324	2	US-08-017-413-11	Sequence 11, Appl	616	24	75.0	155	2	US-08-878-589-18	Sequence 18, Appl
544	24	75.0	324	3	US-08-068-577-11	Sequence 11, Appl	617	24	75.0	155	2	US-08-878-589-18	Sequence 18, Appl
545	24	75.0	324	3	US-08-068-577-11	Sequence 11, Appl	618	24	75.0	155	3	US-08-878-589-18	Sequence 18, Appl
546	24	75.0	324	3	US-08-801-563-11	Sequence 11, Appl	619	24	75.0	156	4	US-09-134-001C-5301	Sequence 5301, Ap
547	24	75.0	328	3	US-08-801-563-11	Sequence 11, Appl	620	24	75.0	156	4	US-09-134-001C-5301	Sequence 5301, Ap
548	24	75.0	328	4	US-08-156-427-13	Sequence 13, Appl	621	24	75.0	157	1	US-08-821-501-4	Sequence 8, Appl
549	24	75.0	329	2	US-08-156-427-13	Sequence 13, Appl	622	24	75.0	157	1	US-08-821-501-4	Sequence 8, Appl
550	24	75.0	329	2	US-07-842-165-13	Sequence 13, Appl	623	24	75.0	158	4	US-08-156-427-13	Sequence 20, Appl
551	24	75.0	330	1	US-07-842-165-13	Sequence 13, Appl	624	24	75.0	158	4	US-08-156-427-13	Sequence 20, Appl
552	24	75.0	330	1	US-07-704-348-8	Sequence 8, Appl	625	24	75.0	159	3	US-08-542-822-27	Sequence 27, Appl
553	24	75.0	334	4	US-09-734-575-22	Sequence 8, Appl	626	24	75.0	159	3	US-08-542-822-27	Sequence 27, Appl
554	24	75.0	334	4	US-09-734-575-22	Sequence 8, Appl	627	24	75.0	159	3	US-08-542-822-27	Sequence 27, Appl
555	24	75.0	338	4	US-09-739-455-9	Sequence 9, Appl	628	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
556	24	75.0	338	4	US-09-739-455-10	Sequence 10, Appl	629	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
557	24	75.0	338	4	US-09-739-455-11	Sequence 11, Appl	630	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
558	24	75.0	338	4	US-09-739-455-19	Sequence 19, Appl	631	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
559	24	75.0	338	4	US-09-739-455-19	Sequence 19, Appl	632	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
560	24	75.0	338	4	US-09-739-455-21	Sequence 21, Appl	633	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
561	24	75.0	345	3	US-09-739-455-21	Sequence 21, Appl	634	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
562	24	75.0	345	4	US-09-442-531-5	Sequence 5, Appl	635	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
563	24	75.0	367	4	US-09-141-501C-443C	Sequence 443C, Ap	636	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
564	24	75.0	367	4	US-09-671-549-2	Sequence 2, Appl	637	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
565	24	75.0	364	4	US-09-335-549-27	Sequence 37, Appl	638	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
566	24	75.0	364	4	US-09-347-549-2	Sequence 37, Appl	639	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
567	24	75.0	364	4	US-08-902-731-2	Sequence 2, Appl	640	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
568	24	75.0	364	4	US-08-144-501C-3591	Sequence 3591, Ap	641	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
569	24	75.0	364	4	US-09-235-524-2	Sequence 2, Appl	642	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
570	24	75.0	366	4	US-08-928-219-59	Sequence 59, Appl	643	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
571	24	75.0	367	4	US-08-026-580-24	Sequence 24, Appl	644	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
572	24	75.0	367	4	US-08-473-649K-1	Sequence 1, Appl	645	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
573	24	75.0	367	4	US-09-457-649-23	Sequence 23, Appl	646	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
574	24	75.0	372	4	US-09-296-904-14	Sequence 14, Appl	647	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
575	24	75.0	372	4	US-09-457-649-23	Sequence 23, Appl	648	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
576	24	75.0	372	4	US-09-640-101-24	Sequence 24, Appl	649	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
577	24	75.0	375	4	US-09-323-972A-33	Sequence 33, Appl	650	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
578	24	75.0	392	4	US-09-416-050A-2	Sequence 2, Appl	651	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
579	24	75.0	392	4	US-09-644-990-2	Sequence 2, Appl	652	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
580	24	75.0	392	4	US-09-645-303-2	Sequence 2, Appl	653	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
581	24	75.0	392	4	US-08-661-569-2	Sequence 2, Appl	654	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
582	24	75.0	393	1	US-08-036-404-2	Sequence 2, Appl	655	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
583	24	75.0	393	3	US-08-459-393A-2	Sequence 2, Appl	656	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
584	24	75.0	396	4	US-09-046-992-4	Sequence 4, Appl	657	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
585	24	75.0	397	1	US-08-476-000-63	Sequence 63, Appl	658	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
586	24	75.0	397	1	US-08-472-840-63	Sequence 63, Appl	659	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
587	24	75.0	397	4	US-08-476-976-63	Sequence 63, Appl	660	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
588	24	75.0	397	3	US-08-474-418-62	Sequence 63, Appl	661	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
589	24	75.0	404	3	US-08-459-393A-7	Sequence 7, Appl	662	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
590	24	75.0	410	1	US-07-945-293-1	Sequence 1, Appl	663	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
591	24	75.0	416	4	US-08-565-049-4	Sequence 4, Appl	664	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
592	24	75.0	419	4	US-09-134-001C-3441	Sequence 3441, Ap	665	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
593	24	75.0	420	1	US-08-391-253-7	Sequence 7, Appl	666	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
594	24	75.0	420	1	US-08-391-253-7	Sequence 7, Appl	667	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
595	24	75.0	420	1	US-08-391-253-7	Sequence 7, Appl	668	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
596	24	75.0	429	1	US-08-839-425-11	Sequence 11, Appl	669	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
597	24	75.0	429	2	US-08-839-425-11	Sequence 11, Appl	670	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
598	24	75.0	429	2	US-08-839-425-17	Sequence 17, Appl	671	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
599	24	75.0	429	2	US-08-839-425-10	Sequence 10, Appl	672	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
600	24	75.0	429	2	US-08-839-425-11	Sequence 11, Appl	673	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
601	24	75.0	428	1	US-08-966-959-2	Sequence 2, Appl	674	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
602	24	75.0	428	2	US-08-966-959-2	Sequence 2, Appl	675	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
603	24	75.0	428	4	US-08-884-680-2	Sequence 2, Appl	676	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
604	24	75.0	433	1	US-08-417-492-2	Sequence 2, Appl	677	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
605	24	75.0	436	4	US-09-534-849-2	Sequence 2, Appl	678	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
606	24	75.0	436	4	US-09-534-849-2	Sequence 2, Appl	679	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
607	24	75.0	453	1	US-08-374-155A-8	Sequence 8, Appl	680	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
608	24	75.0	463	2	US-08-765-396-9	Sequence 9, Appl	681	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
609	24	75.0	456	1	US-08-671-671-1	Sequence 1, Appl	682	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
610	24	75.0	456	1	US-08-092-849-6	Sequence 6, Appl	683	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl
611	24	75.0	456	5	US-094-01642A-5	Sequence 5, Appl	684	24	75.0	160	4	US-08-434-831A-19	Sequence 44, Appl

685	24	75.0	637	2	US-08-155-173B-14	Sequence 14, Appl	258	24	75.0	922	3	US-08-945-086A-14	Sequence 14, Appl
686	24	75.0	637	2	US-08-465-473B-16	Sequence 16, Appl	759	24	75.0	922	3	US-08-945-086A-20	Sequence 20, Appl
687	24	75.0	638	3	US-09-047-118-2	Sequence 2, Appl	760	24	75.0	922	4	US-09-141-286-6	Sequence 6, Appl
688	24	75.0	638	3	US-08-961-082-2	Sequence 2, Appl	761	24	75.0	922	4	US-09-141-286-11	Sequence 11, Appl
689	24	75.0	668	4	US-09-173-151A-26	Sequence 35, Appl	762	24	75.0	922	4	US-08-940-056A-20	Sequence 20, Appl
690	24	75.0	686	4	US-08-947-565-27	Sequence 37, Appl	763	24	75.0	922	4	US-08-945-105A-14	Sequence 14, Appl
691	24	75.0	682	3	US-08-481-415-6	Sequence 6, Appl	764	24	75.0	922	4	US-08-945-105A-20	Sequence 20, Appl
692	24	75.0	682	3	US-08-947-565-27	Sequence 37, Appl	765	24	75.0	922	4	US-09-648-797-14	Sequence 14, Appl
693	24	75.0	686	4	US-09-224-524-21	Sequence 2, Appl	766	24	75.0	922	4	US-09-648-797-20	Sequence 20, Appl
694	24	75.0	686	4	US-09-224-524-21	Sequence 2, Appl	767	24	75.0	922	4	US-08-241-194A-40	Sequence 40, Appl
695	24	75.0	713	2	US-08-849-212-4	Sequence 1, Appl	768	24	75.0	929	2	US-08-195-276A-12	Sequence 12, Appl
696	24	75.0	727	4	US-09-134-001C-4067	Sequence 1067, Ap	769	24	75.0	929	3	US-08-195-276A-12	Sequence 12, Appl
697	24	75.0	766	4	US-09-134-001C-4065	Sequence 1065, Ap	770	24	75.0	929	3	US-08-940-086A-40	Sequence 40, Appl
698	24	75.0	777	2	US-08-221-193A-16	Sequence 16, Appl	771	24	75.0	929	4	US-08-940-086A-40	Sequence 40, Appl
699	24	75.0	777	2	US-08-465-473A-16	Sequence 16, Appl	772	24	75.0	929	4	US-08-945-115A-12	Sequence 12, Appl
700	24	75.0	777	2	US-08-480-474-16	Sequence 16, Appl	773	24	75.0	929	4	US-09-648-797-14	Sequence 14, Appl
701	24	75.0	777	3	US-08-940-086A-16	Sequence 16, Appl	774	24	75.0	922	3	US-08-968-762A-6	Sequence 6, Appl
702	24	75.0	777	4	US-08-940-086A-16	Sequence 16, Appl	775	24	75.0	922	4	US-09-648-797-14	Sequence 14, Appl
703	24	75.0	777	4	US-09-648-797-16	Sequence 16, Appl	776	24	75.0	922	4	US-08-945-105A-14	Sequence 14, Appl
704	24	75.0	777	4	US-09-648-797-16	Sequence 16, Appl	777	24	75.0	922	4	US-08-945-105A-20	Sequence 20, Appl
705	24	75.0	785	1	US-07-941-067A-1	Sequence 1, Appl	778	24	75.0	922	4	US-09-648-797-14	Sequence 14, Appl
706	24	75.0	785	1	US-07-941-067A-1	Sequence 1, Appl	779	24	75.0	922	4	US-09-648-797-14	Sequence 14, Appl
707	24	75.0	785	4	US-09-513-648-1	Sequence 4, Appl	780	24	75.0	922	4	US-08-231-194A-2	Sequence 2, Appl
708	24	75.0	849	3	US-08-804-489A-17	Sequence 17, Appl	781	24	75.0	922	4	US-08-480-474-2	Sequence 2, Appl
709	24	75.0	849	3	US-08-804-489A-17	Sequence 17, Appl	782	24	75.0	922	4	US-08-480-474-2	Sequence 2, Appl
710	24	75.0	854	2	US-09-231-193A-12	Sequence 32, Appl	783	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
711	24	75.0	854	2	US-09-231-193A-12	Sequence 32, Appl	784	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
712	24	75.0	854	3	US-08-480-474-32	Sequence 32, Appl	785	24	75.0	922	4	US-08-945-105A-2	Sequence 2, Appl
713	24	75.0	854	3	US-08-940-086A-32	Sequence 32, Appl	786	24	75.0	922	4	US-08-945-105A-2	Sequence 2, Appl
714	24	75.0	854	4	US-08-940-086A-32	Sequence 32, Appl	787	24	75.0	922	4	US-08-945-105A-2	Sequence 2, Appl
715	24	75.0	854	4	US-08-935-105A-32	Sequence 32, Appl	788	24	75.0	922	4	US-08-480-474-36	Sequence 36, Appl
716	24	75.0	854	4	US-08-940-086A-32	Sequence 32, Appl	789	24	75.0	922	4	US-08-480-474-36	Sequence 36, Appl
717	24	75.0	863	3	US-09-436-328B-2	Sequence 2, Appl	790	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
718	24	75.0	866	2	US-09-483-181-1	Sequence 2, Appl	791	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
719	24	75.0	870	2	US-08-231-193A-30	Sequence 30, Appl	792	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
720	24	75.0	870	2	US-08-231-193A-30	Sequence 30, Appl	793	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
721	24	75.0	873	3	US-08-480-474-36	Sequence 36, Appl	794	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
722	24	75.0	873	3	US-08-480-474-36	Sequence 36, Appl	795	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
723	24	75.0	870	4	US-08-940-086A-30	Sequence 30, Appl	796	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
724	24	75.0	870	4	US-08-935-105A-30	Sequence 30, Appl	797	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
725	24	75.0	870	4	US-09-648-797-36	Sequence 36, Appl	798	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
726	24	75.0	875	2	US-08-231-193A-28	Sequence 28, Appl	799	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
727	24	75.0	875	2	US-08-480-474-28	Sequence 28, Appl	800	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
728	24	75.0	875	3	US-08-480-474-28	Sequence 28, Appl	801	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
729	24	75.0	875	4	US-08-940-086A-28	Sequence 28, Appl	802	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
730	24	75.0	875	4	US-08-940-086A-28	Sequence 28, Appl	803	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
731	24	75.0	875	4	US-09-648-797-28	Sequence 28, Appl	804	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
732	24	75.0	875	4	US-09-648-797-28	Sequence 28, Appl	805	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
733	24	75.0	885	4	US-08-264-578-31	Sequence 31, Appl	806	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
734	24	75.0	891	2	US-08-231-193A-26	Sequence 26, Appl	807	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
735	24	75.0	891	2	US-08-231-193A-26	Sequence 26, Appl	808	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
736	24	75.0	891	3	US-08-480-474-26	Sequence 26, Appl	809	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
737	24	75.0	891	3	US-08-940-086A-26	Sequence 26, Appl	810	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
738	24	75.0	891	4	US-09-648-797-26	Sequence 26, Appl	811	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
739	24	75.0	891	4	US-08-945-086A-26	Sequence 26, Appl	812	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
740	24	75.0	891	4	US-09-648-797-26	Sequence 26, Appl	813	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
741	24	75.0	905	4	US-09-134-001C-4782	Sequence 3782, Ap	814	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
742	24	75.0	908	2	US-08-231-193A-31	Sequence 31, Appl	815	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
743	24	75.0	908	2	US-08-480-474-31	Sequence 31, Appl	816	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
744	24	75.0	908	3	US-08-480-474-31	Sequence 31, Appl	817	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
745	24	75.0	908	4	US-08-940-086A-31	Sequence 31, Appl	818	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
746	24	75.0	908	4	US-08-940-086A-31	Sequence 31, Appl	819	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
747	24	75.0	908	4	US-08-940-086A-31	Sequence 31, Appl	820	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
748	24	75.0	908	4	US-08-940-086A-31	Sequence 31, Appl	821	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
749	24	75.0	911	1	US-08-596-995-2	Sequence 2, Appl	822	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
750	24	75.0	920	1	US-08-026-148E-9	Sequence 9, Appl	823	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
751	24	75.0	920	1	US-08-026-148E-10	Sequence 10, Appl	824	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
752	24	75.0	922	2	US-08-231-193A-14	Sequence 14, Appl	825	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
753	24	75.0	922	2	US-08-231-193A-14	Sequence 14, Appl	826	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
754	24	75.0	922	2	US-08-195-276A-14	Sequence 14, Appl	827	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
755	24	75.0	922	3	US-08-480-474-14	Sequence 14, Appl	828	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
756	24	75.0	922	3	US-08-480-474-14	Sequence 14, Appl	829	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl
757	24	75.0	922	3	US-08-480-474-20	Sequence 20, Appl	830	24	75.0	922	4	US-08-945-086A-2	Sequence 2, Appl

831	24	75.0	1902	4	US-09-320-479-19	Sequence 18, Appl	984	23	58.8	5	3	US-08-809-455-21	Sequence 71, Appl
832	24	75.0	1810	5	PCT US95511621-1	Sequence 1, Appl	985	23	58.8	5	3	US-09-219-161-71	Sequence 71, Appl
833	24	75.0	2544	2	US-08-726-626A-2	Sequence 32, Appl	986	23	58.8	5	3	US-09-219-161-71	Sequence 71, Appl
834	24	75.0	3111	2	US-08-460-169-4	Sequence 4, Appl	987	22	58.8	7	2	US-08-460-169-4	Sequence 80, Appl
835	24	75.0	3111	2	US-08-125-077-4	Sequence 4, Appl	988	22	58.8	7	2	US-08-486-197-80	Sequence 80, Appl
836	24	75.0	3420	2	US-08-477-151-8	Sequence 8, Appl	989	22	58.8	7	2	US-08-486-197-80	Sequence 80, Appl
837	23	71.9	12	2	US-08-936-561-36	Sequence 26, Appl	990	22	58.8	7	2	US-08-486-197-80	Sequence 80, Appl
838	23	71.9	34	2	US-08-936-561-36	Sequence 26, Appl	991	22	58.8	7	2	US-08-486-197-80	Sequence 80, Appl
839	23	71.9	36	4	US-09-149-476-430	Sequence 402, App	992	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
840	23	71.9	56	4	US-08-974-549A-127	Sequence 127, App	993	22	58.8	7	2	US-09-219-172-80	Sequence 80, Appl
841	23	71.9	60	4	US-08-791-115B-19	Sequence 19, Appl	994	22	58.8	7	2	US-09-219-172-80	Sequence 80, Appl
842	23	71.9	60	4	US-08-791-115B-20	Sequence 20, Appl	995	22	58.8	7	2	US-09-219-172-80	Sequence 80, Appl
843	23	71.9	60	4	US-08-791-115B-21	Sequence 21, Appl	996	22	58.8	7	2	US-09-219-172-80	Sequence 80, Appl
844	23	71.9	129	6	US-08-791-115B-21	Sequence 21, Appl	997	22	58.8	7	2	US-09-219-172-80	Sequence 80, Appl
845	23	71.9	140	3	US-08-936-561-36	Sequence 26, Appl	998	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
846	23	71.9	161	4	US-08-188-930-276	Sequence 276, App	999	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
847	23	71.9	160	4	US-08-134-930-276	Sequence 276, App	1000	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
848	23	71.9	179	4	US-08-826-500A-4	Sequence 4854, App	1001	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
849	23	71.9	181	2	US-08-640-977-3	Sequence 3, Appl	1002	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
850	23	71.9	194	1	US-08-118-465A-7	Sequence 7, Appl	1003	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
851	23	71.9	194	1	US-08-118-465A-7	Sequence 7, Appl	1004	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
852	23	71.9	208	2	US-09-906-119-7	Sequence 7, Appl	1005	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
853	23	71.9	208	2	US-09-906-119-7	Sequence 7, Appl	1006	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
854	23	71.9	209	3	US-09-134-506-2	Sequence 3, Appl	1007	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
855	23	71.9	219	2	US-09-134-506-2	Sequence 3, Appl	1008	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
856	23	71.9	246	2	US-08-640-977-3	Sequence 3, Appl	1009	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
857	23	71.9	287	1	US-08-365-981-9	Sequence 9, Appl	1010	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
858	23	71.9	296	2	US-08-640-977-3	Sequence 3, Appl	1011	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
859	23	71.9	325	4	US-08-836-500A-4	Sequence 4, Appl	1012	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
860	23	71.9	378	4	US-09-199-637A-367	Sequence 367, App	1013	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
861	23	71.9	429	4	US-09-134-506-2	Sequence 3, Appl	1014	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
862	23	71.9	391	4	US-08-791-115B-27	Sequence 27, Appl	1015	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
863	24	71.9	403	4	US-08-791-115B-23	Sequence 23, Appl	1016	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
864	24	71.9	403	4	US-08-791-115B-23	Sequence 23, Appl	1017	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
865	23	71.9	403	4	US-08-791-115B-23	Sequence 23, Appl	1018	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
866	23	71.9	430	4	US-08-791-115B-23	Sequence 23, Appl	1019	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
867	23	71.9	431	4	US-08-791-115B-23	Sequence 23, Appl	1020	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
868	23	71.9	431	4	US-08-791-115B-23	Sequence 23, Appl	1021	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
869	23	71.9	431	4	US-08-791-115B-23	Sequence 23, Appl	1022	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
870	23	71.9	431	4	US-08-791-115B-23	Sequence 23, Appl	1023	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
871	23	71.9	450	3	US-09-071-434-1	Sequence 1, Appl	1024	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
872	23	71.9	461	4	US-08-457-042B-61	Sequence 61, Appl	1025	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
873	23	71.9	480	4	US-08-965-902A-4	Sequence 4, Appl	1026	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
874	23	71.9	480	4	US-08-965-902A-4	Sequence 4, Appl	1027	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
875	23	71.9	552	3	US-08-851-843A-4	Sequence 4, Appl	1028	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
876	23	71.9	552	3	US-08-851-843A-4	Sequence 4, Appl	1029	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
877	23	71.9	552	4	US-09-420-323-4	Sequence 4, Appl	1030	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
878	23	71.9	565	4	US-08-906-152A-12	Sequence 12, Appl	1031	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
879	23	71.9	615	4	US-08-965-902A-4	Sequence 4, Appl	1032	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
880	23	71.9	617	1	US-07-879-617A-11	Sequence 11, Appl	1033	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
881	23	71.9	617	1	US-08-301-722A-3	Sequence 3, Appl	1034	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
882	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1035	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
883	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1036	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
884	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1037	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
885	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1038	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
886	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1039	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
887	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1040	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
888	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1041	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
889	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1042	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
890	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1043	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
891	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1044	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
892	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1045	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
893	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1046	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
894	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1047	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
895	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1048	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
896	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1049	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
897	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1050	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
898	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1051	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
899	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1052	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
900	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1053	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
901	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1054	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
902	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1055	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl
903	23	71.9	617	1	US-08-240-783B-3	Sequence 3, Appl	1056	22	58.8	7	2	US-08-634-641-80	Sequence 80, Appl

972 22 68.8 78 2 US-08-167-611C-47
976 22 68.8 78 4 US-08-466-071A-47
979 22 68.8 78 4 US-08-462-043-47
980 22 68.8 83 1 US-07-947-035-18
981 22 68.8 83 1 US-08-321-695A-12
982 22 68.8 94 1 US-07-989-845-28
983 22 68.8 94 1 US-07-989-844-12
984 22 68.8 94 1 US-08-161-044-12
985 22 68.8 94 1 US-08-246-121-12
986 22 68.8 94 1 US-08-451-111-11
987 22 68.8 94 5 PCT-US93-11297-12
988 22 68.8 94 5 PCT-US93-11298-28
989 22 68.8 105 3 US-08-407-165-3
990 22 68.8 118 4 US-08-545-809A-108
991 22 68.8 119 3 US-09-029-267-14
992 22 68.8 119 1 US-08-360-125-5
993 22 68.8 119 2 US-08-450-578-5
994 22 68.8 119 2 US-09-017-628-5
995 22 68.8 119 2 US-09-014-899-5
996 22 68.8 119 4 US-08-450-463-5
997 22 68.8 119 6 5425942-1
998 22 68.8 121 4 US-09-142-583A-4
999 22 68.8 121 2 US-09-462-529A-5
1000 22 68.8 132 4 US-09-134-801C-4894

ALIGNMENTS

RESULT 1
US-08-465-480-70
Sequence 70, Application US/08465380
Patent No. 5864894
GENERAL INFORMATION:
APPLICANT: George P. Vlasak, Patrick H. Stanssens,
APPLICANT: Joris H.L. Meusens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansseman, Matthew Moyle,
APPLICANT: Peter W. Berquam
TITLE OF INVENTION: NEMATOQUE-EXTRACTED ANTICOGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 456
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C., DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465-480
FILING DATE: June 5, 1995
CLASSIFICATION: 540
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BUGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 489-0440
FILING DATE: June 5, 1995
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
US-08-486-397-70

LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
US-08-465-380-70

Query Match 93.8% Score 30; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 20*05;
Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
|||||
DB 1 GYRN 5

RESULT 2
US-08-486-397-70
Sequence 70, Application US/08466397
Patent No. 5866542

GENERAL INFORMATION:
APPLICANT: George P. Vlasak, Patrick H. Stanssens,
APPLICANT: Joris H.L. Meusens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansseman, Matthew Moyle,
APPLICANT: Peter W. Berquam
TITLE OF INVENTION: NEMATOQUE-EXTRACTED ANTICOGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 457
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C., DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486-397
FILING DATE: June 5, 1995
CLASSIFICATION: 540
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BUGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
FILING DATE: June 5, 1995
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
US-08-486-397-70

Query Match 93.8% Score 30; DB 2; Length 5;
Best Local Similarity 100.0%; Pred. No. 20*05;
Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
|||||

1b 1 GFYRN 5

RESULT 3
 US-08-486-399-70
 : Sequence 70, Application US/08486399
 : Patent No. 5866543
 : GENERAL INFORMATION:
 : APPLICANT: George P. Vlasuk, Patrick H. Stanssens,
 : APPLICANT: Joris H.L. Menssens, Marc J. Lauwereys,
 : APPLICANT: Yves P. Laroche, Laurent S. Jespers,
 : APPLICANT: Yannick G.J. Gaussemans, Matthew Moyle,
 : APPLICANT: Peter W. Bergum
 : TITLE OF INVENTION: NEMATOIDE-EXTRACTED ANTICOLLAGULANT
 : NUMBER OF SEQUENCES: 356
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lyon & Lyon
 : STREET: 633 West Fifth Street
 : CITY: Los Angeles
 : STATE: California
 : COUNTRY: U.S.A.
 : ZIP: 90071

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/486,399
 FILING DATE: June 5, 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 213/270
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510

INFORMATION FOR SEQ ID NO: 70:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal fragment
 US-08-486-399-70

Query Match 93.8% Score 30; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 3 GFYRN 7
1b 1 GFYRN 5

RESULT 4
 US-08-461-965-70
 : Sequence 70, Application US/08461965
 : Patent No. 5872068
 : GENERAL INFORMATION:
 : APPLICANT: George P. Vlasuk, Patrick H. Stanssens,
 : APPLICANT: Joris H.L. Menssens, Marc J. Lauwereys,
 : APPLICANT: Yves P. Laroche, Laurent S. Jespers,
 : APPLICANT: Yannick G.J. Gaussemans, Matthew Moyle,
 : APPLICANT: Peter W. Bergum

TITLE OF INVENTION: NEMATOIDE-EXTRACTED ANTICOLLAGULANT
 TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/461,965
 FILING DATE: June 5, 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/426,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 30,158
 REFERENCE/DOCKET NUMBER: 213/270
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 70:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal fragment
 US-08-461-965-70

Query Match 93.8% Score 40; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 3 GFYRN 7
1b 1 GFYRN 5

RESULT 5
 US-08-634-611
 : Sequence 70, Application US/080634611
 : Patent No. 5901214
 : GENERAL INFORMATION:
 : APPLICANT: Vlasuk, George P. Vlasuk
 : APPLICANT: Stanssens, Patrick Eric Hugo
 : APPLICANT: Menssens, Joris Hilda Hoven
 : APPLICANT: Lauwereys, Marc Josef
 : APPLICANT: Laroche, Yves Rene
 : APPLICANT: Jespers, Laurent Stephane
 : APPLICANT: Gaussemans, Yannick Georges Jozei
 : APPLICANT: Moy G, Matthew
 : APPLICANT: Bergum, Peter W.
 : TITLE OF INVENTION: NEMATOIDE-EXTRACTED ANTICOLLAGULANT
 : TITLE OF INVENTION: PROTEIN
 : NUMBER OF SEQUENCES: 356
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Lyon & Lyon
 : STREET: 633 West Fifth Street
 : CITY: Los Angeles
 : STATE: California

1 COUNTRY: U.S.A.
 2 ZIP: 90071
 3 COMPUTER READABLE FORM:
 4 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 5 MEDIUM TYPE: Storage
 6 COMPUTER: IBM Compatible
 7 OPERATING SYSTEM: IBM P.C. DOS 5.0
 8 SOFTWARE: Word Perfect 5.1
 9 CURRENT APPLICATION DATA:
 10 APPLICATION NUMBER: US/09/64,641
 11 FILING DATE: April 19, 1996
 12 PRIOR APPLICATION DATA:
 13 APPLICATION NUMBER: PCT/US95/011
 14 FILING DATE: October 17, 1995
 15 APPLICATION NUMBER: 08/486,499
 16 FILING DATE: June 5, 1995
 17 APPLICATION NUMBER: 08/486,497
 18 FILING DATE: June 5, 1995
 19 APPLICATION NUMBER: 08/461,965
 20 FILING DATE: June 5, 1995
 21 APPLICATION NUMBER: 08/426,110
 22 FILING DATE: October 18, 1994
 23 ATTORNEY/AGENT INFORMATION:
 24 NAME: BIGGS, SUZANNE L.
 25 REGISTRATION NUMBER: 30,158
 26 REFERENCE: "BRIEF" 2:5, 1:6
 27 TELECOMMUNICATION INFORMATION:
 28 TELEPHONE: (214) 489-1600
 29 TELEFAX: (214) 489-1600
 30 TELEX: 67-4510
 31 INFORMATION FOR SEQ ID NO: 70:
 32 SEQUENCE CHARACTERISTICS:
 33 LENGTH: 5 amino acids
 34 TYPE: amino acid
 35 TOPOLOGY: linear
 36 MOLECULE TYPE: peptide
 37 FRAGMENT TYPE: internal fragment
 38 US-09 644-641-70

Query Match 93.8%; Score 40; DB 2; Length 5;
 Best Local Similarity 100.0%; Pred. No. 20+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 DB 1 GYRN 5

RESULT 6
 US 09 249-471-70
 Sequence 70, Application US/09/49471
 Patent No. 6040441

1 GENERAL INFORMATION:
 2 APPLICANT: Vlasuk, George Phillip
 3 APPLICANT: Stanssens, Patrick Eric Hugo
 4 APPLICANT: Messens, Joris Hilda Lieven
 5 APPLICANT: Lauwereys, Marc Joset
 6 APPLICANT: Laroché, Yves Rene
 7 APPLICANT: Jespers, Laurent Stephane
 8 APPLICANT: Ganssmans, Yvanick Georges Jozet
 9 APPLICANT: Moyle, Matthew
 10 APPLICANT: Berquam, Peter W.
 11 TITLE OF INVENTION: NEURALGIC EXTRACTED SERINE PROTEASE
 12 TITLE OF INVENTION: INHIBITORS AND ANTIDOTULANT
 13 NUMBER OF SEQUENCES: 456
 14 CORRESPONDENCE ADDRESS:
 15 ADDRESSEE: Lyon & Lyon
 16 STREET: 633 West Fifth Street
 17 STREET: Suite 4700
 18 CITY: Los Angeles

1 STATE: California
 2 COUNTRY: U.S.A.
 3 ZIP: 90071
 4 COMPUTER READABLE FORM:
 5 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 6 MEDIUM TYPE: Storage
 7 COMPUTER: IBM Compatible
 8 OPERATING SYSTEM: IBM P.C. DOS 5.0
 9 SOFTWARE: Word Perfect 5.1
 10 CURRENT APPLICATION DATA:
 11 APPLICATION NUMBER: 08/486,499
 12 FILING DATE: April 17, 1997
 13 APPLICATION NUMBER: PCT/US96/14241
 14 FILING DATE: October 17, 1995
 15 APPLICATION NUMBER: 08/486,499
 16 FILING DATE: June 5, 1995
 17 APPLICATION NUMBER: 08/486,497
 18 FILING DATE: June 5, 1995
 19 APPLICATION NUMBER: 08/461,965
 20 FILING DATE: June 5, 1995
 21 APPLICATION NUMBER: 08/426,110
 22 FILING DATE: October 18, 1994
 23 ATTORNEY/AGENT INFORMATION:
 24 NAME: BIGGS, SUZANNE L.
 25 REGISTRATION NUMBER: 30,158
 26 REFERENCE: "BRIEF" 2:5, 1:6
 27 TELECOMMUNICATION INFORMATION:
 28 TELEPHONE: (214) 489-1600
 29 TELEFAX: (214) 489-1600
 30 TELEX: 67-4510
 31 INFORMATION FOR SEQ ID NO: 70:
 32 SEQUENCE CHARACTERISTICS:
 33 LENGTH: 5 amino acids
 34 TYPE: amino acid
 35 TOPOLOGY: linear
 36 MOLECULE TYPE: peptide
 37 FRAGMENT TYPE: internal fragment
 38 US-09-249-471-70

Query Match 93.8%; Score 40; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 20+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 DB 1 GYRN 5

RESULT 7
 US 09 249-472-70
 Sequence 70, Application US/09/249472
 Patent No. 6040418

1 GENERAL INFORMATION:
 2 APPLICANT: Vlasuk, George Phillip
 3 APPLICANT: Stanssens, Patrick Eric Hugo
 4 APPLICANT: Messens, Joris Hilda Lieven
 5 APPLICANT: Lauwereys, Marc Joset
 6 APPLICANT: Laroché, Yves Rene
 7 APPLICANT: Jespers, Laurent Stephane
 8 APPLICANT: Ganssmans, Yvanick Georges Jozet
 9 APPLICANT: Moyle, Matthew
 10 APPLICANT: Berquam, Peter W.
 11 TITLE OF INVENTION: NEURALGIC EXTRACTED SERINE PROTEASE
 12 TITLE OF INVENTION: INHIBITORS AND ANTIDOTULANT
 13 NUMBER OF SEQUENCES: 456
 14 CORRESPONDENCE ADDRESS:
 15 ADDRESSEE: Lyon & Lyon

```

1 STREET: 633 West Fifth Street
2 STREET: Suite 4700
3 CITY: Los Angeles
4 STATE: California
5 COUNTRY: U.S.A.
6 ZIP: 90071
7
8 COMPUTER READABLE FORM:
9 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
10 MEDIUM TYPE: storage
11 COMPUTER: IBM Compatible
12 OPERATING SYSTEM: IBM P.C. DOS 5.0
13 SOFTWARE: Word Perfect 5.1
14 CURRENT APPLICATION DATA:
15 APPLICATION NUMBER: US/09/249,472
16 FILING DATE:
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 08/409,455
19 FILING DATE: April 17, 1997
20 APPLICATION NUMBER: 08/409,455
21 FILING DATE: October 17, 1995
22 APPLICATION NUMBER: 08/486,399
23 FILING DATE: June 5, 1995
24 APPLICATION NUMBER: 08/445,380
25 FILING DATE: June 5, 1995
26 APPLICATION NUMBER: 08/461,965
27 FILING DATE: June 5, 1995
28 APPLICATION NUMBER: 08/426,110
29 FILING DATE: October 18, 1994
30 ATTORNEY/AGENT INFORMATION:
31 NAME: BIGGS, SUZANNE L.
32 REGISTRATION NUMBER: 30,158
33 REFERENCE/POCKET NUMBER: 216,270
34 TELECOMMUNICATION INFORMATION:
35 TELEPHONE: (213) 489-1600
36 TELEFAX: (213) 955-0440
37 TELEX: 67-3510
38 INFORMATION FOR SEQ ID NO: 70:
39 SEQUENCE CHARACTERISTICS:
40 LENGTH: 5 amino acids
41 TYPE: amino acid
42 TOPOLOGY: linear
43 MOLECULE TYPE: peptide
44 FRAGMENT TYPE: internal fragment
45 US-09-249-472-70

```

```

Query Match 93.8%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GYRN 7
DB 1 GYRN 5

```

```

RESULT 8
US-09-249-451-70
Sequence 70, Application US/09/249451
Patent No. 6087487
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansmans, Yannick Georges Jozet
APPLICANT: Moyle, Peter W.
TITLE OF INVENTION: NPWATOF-EXTRACTED SERINE PROTEASE
TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT

```

```

1 NUMBER OF SEQUENCES: 456
2 CORRESPONDENCE ADDRESS:
3 ADDRESSEE: Lyon & Lyon
4 STREET: 633 West Fifth Street
5 CITY: Los Angeles
6 STATE: California
7 COUNTRY: U.S.A.
8 ZIP: 90071
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
12 MEDIUM TYPE: storage
13 COMPUTER: IBM Compatible
14 OPERATING SYSTEM: IBM P.C. DOS 5.0
15 SOFTWARE: Word Perfect 5.1
16 CURRENT APPLICATION DATA:
17 APPLICATION NUMBER: US/09/249,451
18 FILING DATE:
19 PRIOR APPLICATION DATA:
20 APPLICATION NUMBER: 08/409,455
21 FILING DATE: April 17, 1997
22 APPLICATION NUMBER: 08/409,455
23 FILING DATE: October 17, 1995
24 APPLICATION NUMBER: 08/486,399
25 FILING DATE: June 5, 1995
26 APPLICATION NUMBER: 08/445,380
27 FILING DATE: June 5, 1995
28 APPLICATION NUMBER: 08/461,965
29 FILING DATE: June 5, 1995
30 APPLICATION NUMBER: 08/426,110
31 FILING DATE: October 18, 1994
32 ATTORNEY/AGENT INFORMATION:
33 NAME: BIGGS, SUZANNE L.
34 REGISTRATION NUMBER: 30,158
35 REFERENCE/POCKET NUMBER: 216,270
36 TELECOMMUNICATION INFORMATION:
37 TELEPHONE: (213) 489-1600
38 TELEFAX: (213) 955-0440
39 TELEX: 67-3510
40 INFORMATION FOR SEQ ID NO: 70:
41 SEQUENCE CHARACTERISTICS:
42 LENGTH: 5 amino acids
43 TYPE: amino acid
44 TOPOLOGY: linear
45 MOLECULE TYPE: peptide
46 FRAGMENT TYPE: internal fragment
47 US-09-249-451-70

```

```

Query Match 93.8%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GYRN 7
DB 1 GYRN 5

```

```

RESULT 9
US-08-809-455-70
Sequence 70, Application US/08809455
Patent No. 6090916
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansmans, Yannick Georges Jozet
APPLICANT: Moyle, Peter W.
APPLICANT: Berqum, Peter W.

```

? TITLE OF INVENTION: REMEDIATION-EXTRACTING SURFING PROLEASE
 ? TITLE OF INVENTION: TRIHIBITORS AND ANTICONGESTANT
 ? TITLE OF INVENTION: PROTEIN
 ? NUMBER OF SEQUENCES: 456
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: LYON & LYON
 ? STREET: 644 West Fifth Street
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 4.5" Diskette, 1.44 Mb
 ? MEDIUM TYPE: Storage
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C., DOS 5.0
 ? SOFTWARE: Word Perfect 5.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/08/409,455
 ? FILING DATE: April 17, 1997
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/409,455
 ? FILING DATE: April 17, 1997
 ? APPLICATION NUMBER: 08/486,399
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,397
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/465,380
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/461,965
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/426,110
 ? FILING DATE: October 18, 1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BIGGS, SUZANNE L.
 ? REGISTRATION NUMBER: 30,158
 ? TELEPHONE: (214) 489-1600
 ? TELEFAX: (214) 955-0440
 ? TELEX: 67-4510
 ? INFORMATION FOR SEQ ID NO: 70:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 5 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: Linear
 ? MOLECULE TYPE: Peptide
 ? FRAGMENT TYPE: Internal Fragment
 ? US-08 409-455-70

Query Match 93.8%; Score 40; DB 3; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 4 GFYRN 7
 Db 1 GFYRN 5

RESULT 10
 US 09-249-461-70
 ? Sequence 70, Application US/05244451
 ? Patent No. 6096877
 ? GENERAL INFORMATION:
 ? APPLICANT: Vlasak, George Phillip
 ? APPLICANT: Stanssens, Patrick Eric Hugo
 ? APPLICANT: Messons, Joris Hilda Lieven
 ? APPLICANT: Lauwereys, Marc Josef
 ? APPLICANT: Laroche, Yves Rene
 ? APPLICANT: Jaspers, Laurent Stephane
 ? APPLICANT: Ganssmans, Yvanick Georges Jozef
 ? APPLICANT: Moyle, Matthew

? APPLICANT: Borgum, Peter W.
 ? TITLE OF INVENTION: REMEDIATION-EXTRACTING SURFING PROLEASE
 ? TITLE OF INVENTION: INHIBITORS AND ANTICONGESTANT
 ? TITLE OF INVENTION: PROTEIN
 ? NUMBER OF SEQUENCES: 456
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: LYON & LYON
 ? STREET: 644 West Fifth Street
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 4.5" Diskette, 1.44 Mb
 ? MEDIUM TYPE: Storage
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C., DOS 5.0
 ? SOFTWARE: Word Perfect 5.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/249,461
 ? FILING DATE:
 ? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/409,455
 ? FILING DATE: April 17, 1997
 ? APPLICATION NUMBER: 08/486,399
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/486,397
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/465,380
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/461,965
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/426,110
 ? FILING DATE: October 18, 1994
 ? NAME: BIGGS, SUZANNE L.
 ? REGISTRATION NUMBER: 30,158
 ? TELEPHONE: (214) 489-1600
 ? TELEFAX: (214) 955-0440
 ? TELEX: 67-4510
 ? INFORMATION FOR SEQ ID NO: 70:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 5 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: Linear
 ? MOLECULE TYPE: Peptide
 ? FRAGMENT TYPE: Internal Fragment
 ? US-09-249-461-70

Query Match 93.8%; Score 40; DB 4; Length 5;
 Best Local Similarity 100.0%; Pred. No. 2e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0;

QY 4 GFYRN 7
 Db 1 GFYRN 5

RESULT 11
 US 09-249-448-70
 ? Sequence 70, Application US/05244448
 ? Patent No. 6121445
 ? GENERAL INFORMATION:
 ? APPLICANT: Vlasak, George Phillip
 ? APPLICANT: Stanssens, Patrick Eric Hugo
 ? APPLICANT: Messons, Joris Hilda Lieven
 ? APPLICANT: Lauwereys, Marc Josef
 ? APPLICANT: Laroche, Yves Rene


```

: APPLICANT: Jespers Laurent Strophane
: APPLICANT: Gaussemans, Yannick Georges Marcel
: APPLICANT: Moyle, Matthew
: APPLICANT: Beatum, Peter W.
: TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
: TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE
: TITLE OF INVENTION: PROTEIN
: NUMBER OF SEQUENCES: 356
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: MEDIUM TYPE: storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US-09-249,448
: FILING DATE:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/809,455
: FILING DATE: April 17, 1997
: APPLICATION NUMBER: 08/496,994
: FILING DATE: June 5, 1995
: APPLICATION NUMBER: 08/486,397
: FILING DATE: June 5, 1995
: APPLICATION NUMBER: 08/465,380
: FILING DATE: June 5, 1995
: APPLICATION NUMBER: 08/461,965
: FILING DATE: June 5, 1995
: APPLICATION NUMBER: 08/326,110
: FILING DATE: October 18, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: BUGS, SUZANNE L.
: REGISTRATION NUMBER: 30,158
: REFERENCE NUMBER: 21,276
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 499-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 70:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal fragment
: US-09-249-448-70

```

```

Query Match 93.8%; Score 30; DB 3; Length 5;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

```

```

QY 4 GFYFN 7
Db 1 GFYFN 5

```

RESULT 12

```

US-08-465-380-79
: Sequence 74, Application US/08465380
: Patent No. 5863894
: GENERAL INFORMATION:
: APPLICANT: George F. Vlasak, Patricia H. Stanssens,
: APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,

```

```

: APPLICANT: Yves R. Laroche, Laurent St. Jespers,
: APPLICANT: Yannick G.J. Gaussemans, Matthew Moyle,
: APPLICANT: Peter W. Beatum
: TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
: TITLE OF INVENTION: PROTEIN
: NUMBER OF SEQUENCES: 356
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon
: STREET: 633 West Fifth Street
: STREET: Suite 4700
: CITY: Los Angeles
: STATE: California
: COUNTRY: U.S.A.
: ZIP: 90071
: COMPUTER READABLE FORM:
: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
: MEDIUM TYPE: storage
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: IBM P.C. DOS 5.0
: SOFTWARE: Word Perfect 5.1
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: 08/326,110
: FILING DATE: June 5, 1995
: CLASSIFICATION: 530
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/326,110
: FILING DATE: October 18, 1994
: ATTORNEY/AGENT INFORMATION:
: NAME: BUGS, SUZANNE L.
: REGISTRATION NUMBER: 30,158
: REFERENCE NUMBER: 21,276
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (213) 489-1600
: TELEFAX: (213) 955-0440
: TELEX: 67-3510
: INFORMATION FOR SEQ ID NO: 79:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 7 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal fragment
: PEPTIDE:
: OTHER INFORMATION: Xaa is local variable and
: OTHER INFORMATION: is an amino acid, provided
: OTHER INFORMATION: that at least one Xaa is Gly, or
: OTHER INFORMATION: Asp.
: US-08-465-380-79

```

```

Query Match 93.8%; Score 30; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2e+05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

```

```

QY 3 GFYFN 7
Db 3 GFYFN 7

```

RESULT 13

```

US-09-196-997-79
: Sequence 79, Application US/08486497
: Patent No. 5866542
: GENERAL INFORMATION:

```

```

: APPLICANT: George F. Vlasak, Patricia H. Stanssens,
: APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
: APPLICANT: Yves R. Laroche, Laurent St. Jespers,
: APPLICANT: Yannick G.J. Gaussemans, Matthew Moyle,
: APPLICANT: Peter W. Beatum
: TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT
: TITLE OF INVENTION: PROTEIN
: NUMBER OF SEQUENCES: 357
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Lyon & Lyon

```

```

1 STREET: 633 West Fifth Street
2 STREET: Suite 4700
3 CITY: Los Angeles
4 STATE: California
5 COUNTRY: U.S.A.
6 ZIP: 90071
7 COMPUTER READABLE FORM:
8 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
9 MEDIUM TYPE: Storage
10 COMPUTER: IBM Compatible
11 OPERATING SYSTEM: IBM P.C. DOS 5.0
12 SOFTWARE: Word Perfect 5.1
13 CURRENT APPLICATION DATA:
14 FILING DATE: June 5, 1995
15 APPLICATION NUMBER: US/08/486,397
16 CLASSIFICATION: 530
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: 08/426,110
19 FILING DATE: October 18, 1994
20 ATTORNEY/AGENT INFORMATION:
21 NAME: BIGGS, SUZANNE L.
22 REGISTRATION NUMBER: 40,158
23 REFERENCE/EXCERPT NUMBER: 23,270
24 TELECOMMUNICATION INFORMATION:
25 TELEPHONE: (213) 489-1600
26 TELEFAX: (213) 955-0440
27 TELEX: 67-3510
28 INFORMATION FOR SEQ ID NO: 79:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 7 amino acids
31 TYPE: amino acid
32 TOPOLOGY: linear
33 MOLECULE TYPE: peptide
34 FRAGMENT TYPE: internal fragment
35 FEATURE:
36 OTHER INFORMATION: Xaa in locations 1 and 2
37 OTHER INFORMATION: Is an amino acid, provided
38 OTHER INFORMATION: that at least one Xaa is Glu or
39 OTHER INFORMATION: Asp.
40 US 08-486-397-79

```

```

Query Match 93.8%; Score 40; DB 2; Length 7;
Best Local Similarity 100.0%; Prod. No. 20-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 3 GYRN 7

RESULT 14
US-08-486-397-79
Sequence 79, Application US/08/486,397
Patent No. 5866543
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patrick H. Stanssens,
APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssems, Matthew Moyle,
APPLICANT: Peter W. Berquim
TITLE OF INVENTION: NEMAZOLE EXTRACTED ANTICARCIN
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: June 5, 1995
APPLICATION NUMBER: US/08/486,397
CLASSIFICATION: 530

```

```

1 MEDIUM TYPE: Storage
2 COMPUTER: IBM Compatible
3 OPERATING SYSTEM: IBM P.C. DOS 5.0
4 SOFTWARE: Word Perfect 5.1
5 CURRENT APPLICATION DATA:
6 FILING DATE: June 5, 1995
7 APPLICATION NUMBER: US/08/486,399
8 CLASSIFICATION: 530
9 PRIOR APPLICATION DATA:
10 APPLICATION NUMBER: 08/426,110
11 FILING DATE: October 18, 1994
12 ATTORNEY/AGENT INFORMATION:
13 NAME: BIGGS, SUZANNE L.
14 REGISTRATION NUMBER: 40,158
15 REFERENCE/EXCERPT NUMBER: 23,270
16 TELECOMMUNICATION INFORMATION:
17 TELEPHONE: (213) 489-1600
18 TELEFAX: (213) 955-0440
19 TELEX: 67-3510
20 INFORMATION FOR SEQ ID NO: 79:
21 SEQUENCE CHARACTERISTICS:
22 LENGTH: 7 amino acids
23 TYPE: amino acid
24 TOPOLOGY: linear
25 MOLECULE TYPE: peptide
26 FRAGMENT TYPE: internal fragment
27 FEATURE:
28 OTHER INFORMATION: Xaa in locations 1 and 2
29 OTHER INFORMATION: Is an amino acid, provided
30 OTHER INFORMATION: that at least one Xaa is Glu or
31 OTHER INFORMATION: Asp.
32 US-08-486-399-79

```

```

Query Match 93.8%; Score 40; DB 2; Length 7;
Best Local Similarity 100.0%; Prod. No. 20-05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 3 GYRN 7

```

```

RESULT 15
US-08-461-465-79
Sequence 79, Application US/08461965
Patent No. 5872098
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patrick H. Stanssens,
APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssems, Matthew Moyle,
APPLICANT: Peter W. Berquim
TITLE OF INVENTION: NEMAZOLE EXTRACTED ANTICARCIN
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: June 5, 1995
APPLICATION NUMBER: US/08/461,965
CLASSIFICATION: 530

```

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 40,158
 REFERENCE/ATTORNEY NUMBER: 01/024
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 489-1600
 TELEFAX: (212) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 79
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal fragment
 FEATURE:
 OTHER INFORMATION: Xaa in locations 1 and 2
 OTHER INFORMATION: is an amino acid, provided
 OTHER INFORMATION: that at least one Xaa is Glu or
 OTHER INFORMATION: Asp.
 US-08-461-965-79

Query Match 93.8% Score 30; Dg 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 20-05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 Db 3 GYRN 7

RESULT 16

US-08-634-641-79
 Sequence 79, Application US/08634641
 Patent No. 5955294

GENERAL INFORMATION:
 APPLICANT: Vlasak, George P.; Vlasak
 APPLICANT: Stanssens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwereys, Marc Josef
 APPLICANT: Laroche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Gansmans, Yannick Georges Rene
 APPLICANT: Moyle, Matthew W.
 APPLICANT: Berquim, Peter W.
 TITLE OF INVENTION: NEMATODE EXTRACTED ANTICOAGULANT
 TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/486,399
 FILING DATE: April 19, 1996
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 17, 1995
 APPLICATION NUMBER: 08/486,399
 FILING DATE: March 5, 1996

APPLICATION NUMBER: 08/486,397
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/465,380
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/461,965
 FILING DATE: June 5, 1995
 APPLICATION NUMBER: 08/466,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 40,158
 REFERENCE/ATTORNEY NUMBER: 01/0136
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (212) 489-1600
 TELEFAX: (212) 955-0440
 TELEX: 67-3510
 INFORMATION FOR SEQ ID NO: 79
 SEQUENCE CHARACTERISTICS:
 LENGTH: 7 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: internal fragment
 FEATURE:
 OTHER INFORMATION: Xaa in locations 1 and 2
 OTHER INFORMATION: is an amino acid, provided
 OTHER INFORMATION: that at least one Xaa is Glu or
 OTHER INFORMATION: Asp.
 US-08-634-641-79

Query Match 93.8% Score 30; Dg 2; Length 7;
 Best Local Similarity 100.0%; Pred. No. 20-05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 Db 3 GYRN 7

RESULT 17

US-09-249-471-79
 Sequence 79, Application us/09249471
 Patent No. 6040441
 GENERAL INFORMATION:
 APPLICANT: Vlasak, George Phillip
 APPLICANT: Stanssens, Patrick Eric Hugo
 APPLICANT: Messens, Joris Hilda Lieven
 APPLICANT: Lauwereys, Marc Josef
 APPLICANT: Laroche, Yves Rene
 APPLICANT: Jespers, Laurent Stephane
 APPLICANT: Gansmans, Yannick Georges Rene
 APPLICANT: Moyle, Matthew W.
 APPLICANT: Berquim, Peter W.
 TITLE OF INVENTION: NEMATODE EXTRACTED SERINE PROTEASE
 TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT
 TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 356
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: 633 West Fifth Street
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 09/249,471

```

1 FILING DATE:
2 PRIOR APPLICATION DATA:
3 APPLICATION NUMBER: 08/486,495
4 FILING DATE: April 17, 1997
5 APPLICATION NUMBER: 08/486,497
6 FILING DATE: October 17, 1995
7 APPLICATION NUMBER: 08/486,499
8 FILING DATE: June 5, 1995
9 APPLICATION NUMBER: 08/486,497
10 FILING DATE: June 5, 1995
11 APPLICATION NUMBER: 08/486,495
12 FILING DATE: June 5, 1995
13 APPLICATION NUMBER: 08/426,110
14 FILING DATE: October 18, 1994
15 ATTORNEY/AGENT INFORMATION:
16 NAME: BIGGS, SUZANNE L.
17 REGISTRATION NUMBER: 30,158
18 REFERENCE/WORK NUMBER: 216/270
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: (213) 489-1600
21 TELEX: 67-3510
22 INFORMATION FOR SEQ ID NO: 79:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 7 amino acids
25 TYPE: amino acid
26 TOPOLOGY: linear
27 MOLECULE TYPE: peptide
28 FRAGMENT TYPE: internal fragment
29 FEATURE:
30 OTHER INFORMATION: Xaa in locations 1 and 2
31 OTHER INFORMATION: is an amino acid, provided
32 OTHER INFORMATION: that at least one Xaa is Glu or
33 OTHER INFORMATION: Asp.
34 US-09-249-471-79

```

```

Query Match 93.8% Score 40; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 20+05;
Matches 5; Conservatize 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 3 GYRN 7

DB 3 GYRN 7

```

RESULT 18
US-09-249-472-79
Sequence 79, Application US/0249472
Patent No. 6046318
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gausmants, Yvanick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Berqum, Peter W.
TITLE OF INVENTION: NEMATOSE EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESS: 1500 S. Lynn
STREET: 634 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071

```

```

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: IBM compatible
COMPUTER: IBM compatible
OPERATING SYSTEM: IBM PC, DOS 5.0
SOFTWARE: Word Perfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0249472
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/409,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: 08/409,453
FILING DATE: October 17, 1995
APPLICATION NUMBER: 08/486,499
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/486,497
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/465,480
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/461,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/WORK NUMBER: 216/270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
FEATURE:
OTHER INFORMATION: Xaa in locations 1 and 2
OTHER INFORMATION: is an amino acid, provided
OTHER INFORMATION: that at least one Xaa is Glu or
OTHER INFORMATION: Asp.
US-09-249-472-79

```

```

Query Match 93.8% Score 40; DB 4; Length 7;
Best Local Similarity 100.0%; Pred. No. 20+05;
Matches 5; Conservatize 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 3 GYRN 7

DB 3 GYRN 7

```

RESULT 19
US-09-249-451-79
Sequence 79, Application US/009249451
Patent No. 6067487
GENERAL INFORMATION:
APPLICANT: Vlasuk, George Phillip
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Messens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gausmants, Yvanick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Berqum, Peter W.
TITLE OF INVENTION: NEMATOSE EXTRACTED SERINE PROTEASE
INHIBITORS AND ANTICOAGULANT
TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356

```


OTHER INFORMATION: Asp.

US-09-249-448-79

Query Match 93.8%; Score 30; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 20; 05;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIIII
Db 3 GYRN 7

RESULT 23
US-08-465-380-47
Sequence 47, Application US/08465380
Patent No. 5863894
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssems, Matthew Moyle,
APPLICANT: Peter W. Berquim
TITLE OF INVENTION: NEMATODE EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/465,380
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE TO EFFECTIVE DATE: 01/01/98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-4510
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-465-380-47

Query Match 93.8%; Score 30; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9; 4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIIII
Db 54 GYRN 58

RESULT 24
US-08-486-397-47
Sequence 47, Application US/08486397
Patent No. 5866542
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssems, Matthew Moyle,
APPLICANT: Peter W. Berquim
TITLE OF INVENTION: NEMATODE EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,497
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE TO EFFECTIVE DATE: 01/01/98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-4510
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-486-397-47

Query Match 93.8%; Score 30; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9; 4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIIII
Db 54 GYRN 58

RESULT 25
US-08-486-399-47
Sequence 47, Application US/08486399
Patent No. 5866543
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssems, Matthew Moyle,
APPLICANT: Peter W. Berquim
TITLE OF INVENTION: NEMATODE EXTRACTED ANTICOAGULANT
NUMBER OF SEQUENCES: 357
CORRESPONDENCE ADDRESS:
ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,497
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE TO EFFECTIVE DATE: 01/01/98
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-4510
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 78 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma caninum
US-08-486-399-47

Query Match 93.8%; Score 30; DB 2; Length 78;
Best Local Similarity 100.0%; Pred. No. 9; 4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIIII
Db 54 GYRN 58

```

1  NUMBER OF SEQUENCES: 356
2  CORRESPONDENCE ADDRESS:
3  ADDRESSEE: Lyon & Lyon
4  STREET: 633 West Fifth Street
5  CITY: Los Angeles
6  STATE: California
7  COUNTRY: U.S.A.
8  ZIP: 90071
9
10 COMPUTER READABLE FORM:
11 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
12 MEDIUM TYPE: storage
13 COMPUTER: IBM Compatible
14 OPERATING SYSTEM: IBM PC, DOS 5.0
15 SOFTWARE: Word Perfect 5.1
16
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US/08/486,499
19 FILING DATE: June 5, 1995
20 CLASSIFICATION: 530
21
22 PRIOR APPLICATION DATA:
23 APPLICATION NUMBER: 08/426,110
24 FILING DATE: October 18, 1994
25 ATTORNEY/AGENT INFORMATION:
26 NAME: REGIS, SUZANNE L.
27 REGISTRATION NUMBER: 40,158
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (213) 489-1600
30 TELEFAX: (213) 955-0440
31
32 INFORMATION FOR SEQ ID NO: 47:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 78 amino acids
35 TYPE: amino acid
36 TOPOLOGY: linear
37 MOLECULE TYPE: peptide
38 ORIGINAL SOURCE:
39 ORGANISM: Ancylostoma caninum
40
41 US 08-486-499-47

```

Query Match 93.88% Score 40; DB 2; Length 78;

Best Local Similarity 100.00%; Pred. No. 9, 4;

Matches 5; Conservatvie 0; Mismatches 0; Indels 0; Gaps 3;

QY 3 GYRN 7

DB 54 GYRN 58

RESULT 26

US-08-461-965-47

Sequence 47, Application US/08461965

Patent No. 5872098

GENERAL INFORMATION:

```

1  APPLICANT: George P. Vlasuk, Patrick H. Stanssens,
2  APPLICANT: Joris H.L. Meuniers, Marc J. Lemaireys,
3  APPLICANT: Yves R. Laroche, Laurence S. Jespers,
4  APPLICANT: Yannick G.J. Gansomans, Matthew Moyle,
5  APPLICANT: Peter W. Berquq
6  TITLE OF INVENTION: REMARK-EXTRACTED ANTICOAGULANT
7  TITLE OF INVENTION: PROTEIN
8  NUMBER OF SEQUENCES: 456
9  CORRESPONDENCE ADDRESS:
10 ADDRESSEE: Lyon & Lyon
11 STREET: 633 West Fifth Street
12 CITY: Los Angeles
13 STATE: California
14 COUNTRY: U.S.A.
15 ZIP: 90071

```

```

16 COMPUTER READABLE FORM:
17 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
18 MEDIUM TYPE: storage

```

```

1  COMPUTER: IBM Compatible
2  OPERATING SYSTEM: IBM PC, DOS 5.0
3  SOFTWARE: Word Perfect 5.1
4  CURRENT APPLICATION DATA:
5  APPLICATION NUMBER: 08/426,110
6  FILING DATE: October 18, 1994
7  ATTORNEY/AGENT INFORMATION:
8  NAME: REGIS, SUZANNE L.
9  REGISTRATION NUMBER: 40,158
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (213) 489-1600
12 TELEFAX: (213) 955-0440
13
14 INFORMATION FOR SEQ ID NO: 47:
15 SEQUENCE CHARACTERISTICS:
16 LENGTH: 78 amino acids
17 TYPE: amino acid
18 TOPOLOGY: linear
19 MOLECULE TYPE: peptide
20 ORIGINAL SOURCE:
21 ORGANISM: Ancylostoma caninum
22
23 US-08-461-965-47

```

Query Match 93.88% Score 40; DB 2; Length 78;

Best Local Similarity 100.00%; Pred. No. 9, 4;

Matches 5; Conservatvie 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

DB 54 GYRN 58

RESULT 27

US-08-634-641-47

Sequence 47, Application US/08634641

Patent No. 5955294

GENERAL INFORMATION:

```

1  APPLICANT: Vlasuk, George P. Vlasuk
2  APPLICANT: Stanssens, Patrick Eric Budd
3  APPLICANT: Meuniers, Joris Hilda Lieveb
4  APPLICANT: Lemaireys, Marc Joset
5  APPLICANT: Laroche, Yves Rene
6  APPLICANT: Jespers, Laurent Stephane
7  APPLICANT: Gansomans, Yannick Georges Jozef
8  APPLICANT: Moyle, Matthew
9  APPLICANT: Berquq, Peter W.
10 TITLE OF INVENTION: REMARK-EXTRACTED ANTICOAGULANT
11 TITLE OF INVENTION: PROTEIN
12 NUMBER OF SEQUENCES: 356
13 CORRESPONDENCE ADDRESS:
14 ADDRESSEE: Lyon & Lyon
15 STREET: 633 West Fifth Street
16 CITY: Los Angeles
17 STATE: California
18 COUNTRY: U.S.A.
19 ZIP: 90071

```

```

20 COMPUTER READABLE FORM:
21 MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
22 MEDIUM TYPE: storage
23 COMPUTER: IBM Compatible
24 OPERATING SYSTEM: IBM PC, DOS 5.0
25 SOFTWARE: Word Perfect 5.1
26 CURRENT APPLICATION DATA:
27 APPLICATION NUMBER: 08/426,110
28 FILING DATE: April 19, 1996
29 PRIOR APPLICATION DATA:
30 APPLICATION NUMBER: 08/400,712

```


? FILING DATE: October 17, 1995
 ? APPLICATION NUMBER: 08/446,400
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/446,407
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/446,480
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/441,965
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/426,110
 ? FILING DATE: October 18, 1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BIGGS, SUZANNE L.
 ? REGISTRATION NUMBER: 30,158
 ? REFERENCE CHECK NUMBER: 319/136
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (213) 489-1600
 ? TELEFAX: (213) 955-0440
 ? TELEX: 67-3510
 ? INFORMATION FOR SEQ ID NO: 47:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 78 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? ORIGINAL SOURCE:
 ? ORGANISM: Ancylostoma caninum
 ? US-08-634-641-47

Query Match 93.8% Score 30; DB 2; Length 78;
 Best Local Similarity 100.0%; Pred. No. 6;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 3 GYPN 7
 Db 54 GYPN 58

RESULT 28
 US-09-249-471-47
 ? Sequence 47, Application US/09249471
 ? Patent No. 6040441
 ? GENERAL INFORMATION:
 ? APPLICANT: Vlasuk, George Phillip
 ? APPLICANT: Stanssens, Patrick Eric Hugo
 ? APPLICANT: Messers, Joris Hilda Lieven
 ? APPLICANT: Lauwereys, Marc Josef
 ? APPLICANT: Laroche, Yves Rene
 ? APPLICANT: Jespers, Laurent Stephane
 ? APPLICANT: Gasmans, Yvanick Georges Joost
 ? APPLICANT: Moyle, Matthew
 ? APPLICANT: Berqum, Peter W.
 ? TITLE OF INVENTION: REMARKS-EXTENDED SERINE PEPTASE
 ? TITLE OF INVENTION: INHIBITORS AND ANTICOGULANT
 ? TITLE OF INVENTION: PROTEIN
 ? NUMBER OF SEQUENCES: 356
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: 1905 5 Lyle
 ? STREET: 634 West Fifth Street
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? MEDIUM TYPE: Storage
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C. DOS 5.0
 ? SOFTWARE: Word Perfect 5.1
 ? CURRENT APPLICATION DATA:
 ? APPLICATION NUMBER: US/09/249,471
 ? FILING DATE:

? PRIOR APPLICATION DATA:
 ? APPLICATION NUMBER: 08/809,455
 ? FILING DATE: April 17, 1997
 ? APPLICATION NUMBER: 08/246,432-41
 ? FILING DATE: October 17, 1995
 ? APPLICATION NUMBER: 08/486,499
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/436,497
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/465,480
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/441,965
 ? FILING DATE: June 5, 1995
 ? APPLICATION NUMBER: 08/426,110
 ? FILING DATE: October 18, 1994
 ? ATTORNEY/AGENT INFORMATION:
 ? NAME: BIGGS, SUZANNE L.
 ? REGISTRATION NUMBER: 30,158
 ? REFERENCE CHECK NUMBER: 319/136
 ? TELECOMMUNICATION INFORMATION:
 ? TELEPHONE: (213) 489-1600
 ? TELEFAX: (213) 955-0440
 ? TELEX: 67-3510
 ? INFORMATION FOR SEQ ID NO: 47:
 ? SEQUENCE CHARACTERISTICS:
 ? LENGTH: 78 amino acids
 ? TYPE: amino acid
 ? TOPOLOGY: linear
 ? MOLECULE TYPE: peptide
 ? ORIGINAL SOURCE:
 ? ORGANISM: Ancylostoma caninum
 ? US-09-249-471-47

Query Match 93.8% Score 30; DB 3; Length 78;
 Best Local Similarity 100.0% Pred. No. 9;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;

QY 3 GYPN 7
 Db 54 GYPN 58

RESULT 29
 US-09-249-472-47
 ? Sequence 17, Application US/09249472
 ? Patent No. 6046318
 ? GENERAL INFORMATION:
 ? APPLICANT: Vlasuk, George Phillip
 ? APPLICANT: Stanssens, Patrick Eric Hugo
 ? APPLICANT: Messers, Joris Hilda Lieven
 ? APPLICANT: Lauwereys, Marc Josef
 ? APPLICANT: Laroche, Yves Rene
 ? APPLICANT: Jespers, Laurent Stephane
 ? APPLICANT: Gasmans, Yvanick Georges Joost
 ? APPLICANT: Moyle, Matthew
 ? APPLICANT: Berqum, Peter W.
 ? TITLE OF INVENTION: REMARKS-EXTENDED SERINE PEPTASE
 ? TITLE OF INVENTION: INHIBITORS AND ANTICOGULANT
 ? TITLE OF INVENTION: PROTEIN
 ? NUMBER OF SEQUENCES: 456
 ? CORRESPONDENCE ADDRESS:
 ? ADDRESSEE: 1905 5 Lyle
 ? STREET: 634 West Fifth Street
 ? CITY: Los Angeles
 ? STATE: California
 ? COUNTRY: U.S.A.
 ? ZIP: 90071
 ? COMPUTER READABLE FORM:
 ? MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
 ? MEDIUM TYPE: Storage
 ? COMPUTER: IBM Compatible
 ? OPERATING SYSTEM: IBM P.C. DOS 5.0

CITY: Los Angeles

STAFF: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/809,455
FILING DATE: April 17, 1997
PCT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/13231
FILING DATE: October 17, 1995
APPLICATION NUMBER: 06/446,369
FILING DATE: June 5, 1995
APPLICATION NUMBER: 04/187,507
FILING DATE: June 5, 1995
APPLICATION NUMBER: 04/466,386
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/461,265
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/226,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE CHECK NUMBER: 216,276
TRIE COMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67 3510

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 78 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORGANISM: Ancylostoma caninum

US-08-809-455-47

Query Match 93.8%, Score 30; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

|||||

Db 54 GFYRN 58

RESULT 32

US-09-249-461-47

Sequence 47, Application US/09249461

Patent No. 6096877

GENERAL INFORMATION:

APPLICANT: Vlasov, George Phillip

APPLICANT: Stassen, Patrick Eric Hugo

APPLICANT: Messens, Joris Hilda Lieven

APPLICANT: Lawereys, Marc Joscf

APPLICANT: Laroche, Yves Rene

APPLICANT: Jespers, Laurent Stephane

APPLICANT: Gansmans, Yannick Georges Jozef

APPLICANT: Moyle, Matthew

APPLICANT: Bergum, Peter W

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSES: Lyon & Lyon

STREET: 633 West Fifth Street

STREET: Suite 4706
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: Storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/249,461
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/809,455
FILING DATE: April 17, 1997
APPLICATION NUMBER: 07/000,121
FILING DATE: October 17, 1995
APPLICATION NUMBER: 06/486,399
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/486,397
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/463,480
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/463,965
FILING DATE: June 5, 1995
APPLICATION NUMBER: 06/429,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE CHECK NUMBER: 216,276
TRIE COMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67 3510

INFORMATION FOR SEQ ID NO: 47:

SEQUENCE CHARACTERISTICS:

LENGTH: 78 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORGANISM: Ancylostoma caninum

US-09-249-461-47

Query Match 93.8%, Score 30; DB 4; Length 78;
Best Local Similarity 100.0%; Pred. No. 9.3;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7

|||||

Db 54 GFYRN 58

RESULT 33

US-09-249-448-47

Sequence 47, Application US/09249448

Patent No. 6121435

GENERAL INFORMATION:

APPLICANT: Vlasov, George Phillip

APPLICANT: Stassen, Patrick Eric Hugo

APPLICANT: Messens, Joris Hilda Lieven

APPLICANT: Lawereys, Marc Joscf

APPLICANT: Laroche, Yves Rene

APPLICANT: Jespers, Laurent Stephane

APPLICANT: Gansmans, Yannick Georges Jozef

APPLICANT: Moyle, Matthew

APPLICANT: Bergum, Peter W

TITLE OF INVENTION: NEMATODE-EXTRACTED SERINE PROTEASE

TITLE OF INVENTION: INHIBITORS AND ANTICOAGULANT

TITLE OF INVENTION: PROTEIN

1 NUMBER OF SEQUENCES: 456
 2 CORRESPONDENCE ADDRESS:
 3 ADDRESSEE: Lyon & Lyon
 4 STREET: 644 West Fifth Street
 5 CITY: Los Angeles
 6 STATE: California
 7 COUNTRY: U.S.A.
 8 ZIP: 90071
 9 COMPUTER READABLE FORM:
 10 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 11 MEDIUM TYPE: storage
 12 COMPUTER: IBM Compatible
 13 OPERATING SYSTEM: IBM P.C. DOS 5.0
 14 SOFTWARE: Word Perfect 5.1
 15 CURRENT APPLICATION DATA:
 16 APPLICATION NUMBER: US/09/249,448
 17 FILING DATE:
 18 PRIOR APPLICATION DATA:
 19 APPLICATION NUMBER: 08/489,400
 20 FILING DATE: April 17, 1997
 21 APPLICATION NUMBER: PCT/93/21423
 22 FILING DATE: October 17, 1995
 23 APPLICATION NUMBER: 08/486,399
 24 FILING DATE: Feb 5, 1995
 25 APPLICATION NUMBER: 08/486,397
 26 FILING DATE: June 5, 1995
 27 APPLICATION NUMBER: 08/465,480
 28 FILING DATE: June 5, 1995
 29 APPLICATION NUMBER: 08/461,965
 30 FILING DATE: June 5, 1995
 31 APPLICATION NUMBER: 08/426,110
 32 FILING DATE: October 18, 1994
 33 ATTORNEY/AGENT INFORMATION:
 34 NAME: BIGGS, SUZANNE L.
 35 REGISTRATION NUMBER: 30,158
 36 REFERENCE/5-YYT NUMBER: 214,279
 37 TELECOMMUNICATION INFORMATION:
 38 TELEPHONE: (213) 489-1600
 39 TELEFAX: (213) 955-0440
 40 TELEX: 67-3510
 41 INFORMATION FOR SEQ ID NO: 47:
 42 SEQUENCE CHARACTERISTICS:
 43 LENGTH: 78 amino acids
 44 TYPE: amino acid
 45 TOPOLOGY: linear
 46 MOLECULE TYPE: peptide
 47 ORIGINAL SOURCE:
 48 ORGANISM: Ancylostoma caninum
 49 US 09 249 448 47

Query Match 93.8% Score 30; DB 3; Length 78;
 Best Local Similarity 100.0%; Prod. No. 9,4;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYRN 7
 DB 54 GYRN 58

RESULT 34
 US 09-465-480-25
 ? Sequence 25, Application US/09/249,448
 ? Patent No. 5863894
 ? GENERAL INFORMATION:
 ? APPLICANT: George P. Vlasuk, Patrick H. Stausseus,
 ? APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,
 ? APPLICANT: Yves R. Laroche, Laurent S. Jespers,
 ? APPLICANT: Yvanick G.J. Gansseus, Matthew Moyle,
 ? APPLICANT: Peter W. Berquam
 ? TITLE OF INVENTION: REMAINDER EXTRACTED ANTICAGULANT
 ? NUMBER OF SEQUENCES: 456

1 CORRESPONDENCE ADDRESS:
 2 ADDRESSEE: Lyon & Lyon
 3 STREET: 644 West Fifth Street
 4 CITY: Los Angeles
 5 STATE: California
 6 COUNTRY: U.S.A.
 7 ZIP: 90071
 8 COMPUTER READABLE FORM:
 9 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 10 MEDIUM TYPE: storage
 11 COMPUTER: IBM Compatible
 12 OPERATING SYSTEM: IBM P.C. DOS 5.0
 13 SOFTWARE: Word Perfect 5.1
 14 CURRENT APPLICATION DATA:
 15 APPLICATION NUMBER: 08/465,480
 16 FILING DATE: June 5, 1995
 17 CLASSIFICATION:
 18 PRIOR APPLICATION DATA:
 19 APPLICATION NUMBER: 08/426,110
 20 FILING DATE: October 18, 1994
 21 ATTORNEY/AGENT INFORMATION:
 22 NAME: BIGGS, SUZANNE L.
 23 REGISTRATION NUMBER: 30,158
 24 REFERENCE/5-YYT NUMBER: 214,279
 25 TELECOMMUNICATION INFORMATION:
 26 TELEPHONE: (213) 489-1600
 27 TELEFAX: (213) 955-0440
 28 TELEX: 67-3510
 29 INFORMATION FOR SEQ ID NO: 25:
 30 SEQUENCE CHARACTERISTICS:
 31 LENGTH: 82 amino acids
 32 TYPE: amino acid
 33 TOPOLOGY: linear
 34 MOLECULE TYPE: peptide
 35 ORIGINAL SOURCE:
 36 ORGANISM: Ancylostoma caninum
 37 US 08-465-380-25

Query Match 93.8% Score 40; DB 2; Length 82;
 Best Local Similarity 100.0%; Prod. No. 9,8;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYRN 7
 DB 51 GYRN 55

RESULT 35
 US 08-465-380-49
 ? Sequence 49, Application US/08/465,480
 ? Patent No. 5863894
 ? GENERAL INFORMATION:
 ? APPLICANT: George P. Vlasuk, Patrick H. Stausseus,
 ? APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,
 ? APPLICANT: Yves R. Laroche, Laurent S. Jespers,
 ? APPLICANT: Yvanick G.J. Gansseus, Matthew Moyle,
 ? APPLICANT: Peter W. Berquam
 ? TITLE OF INVENTION: REMAINDER EXTRACTED ANTICAGULANT
 ? NUMBER OF SEQUENCES: 456

1 CORRESPONDENCE ADDRESS:
 2 ADDRESSEE: Lyon & Lyon
 3 STREET: 644 West Fifth Street
 4 CITY: Los Angeles
 5 STATE: California
 6 COUNTRY: U.S.A.
 7 ZIP: 90071
 8 COMPUTER READABLE FORM:
 9 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 10 MEDIUM TYPE: storage
 11 COMPUTER: IBM Compatible

1 OPERATING SYSTEM: IBM P.C. DOS 5.0
 2 SOFTWARE: Word Perfect 5.1
 3 CURRENT APPLICATION DATA:
 4 APPLICATION NUMBER: 08/326,110
 5 FILING DATE: October 18, 1994
 6 ATTORNEY/AGENT INFORMATION:
 7 NAME: BIGGS, SUZANNE L.
 8 REGISTRATION NUMBER: 40,158
 9 REFERENCE/JOINT NUMBER: 213,269
 10 TELECOMMUNICATION INFORMATION:
 11 TELEPHONE: (213) 489-1600
 12 TELEFAX: (213) 955-0440
 13 INFORMATION FOR SEQ ID NO: 49:
 14 SEQUENCE CHARACTERISTICS:
 15 LENGTH: 82 amino acids
 16 TYPE: amino acid
 17 TOPOLOGY: linear
 18 MOLECULE TYPE: peptide
 19 ORIGINAL SOURCE:
 20 ORGANISM: Ancylostoma canaliculatum
 21 US-08-465-380-49

Query Match 93.8%; Score 30; DB 2; Length 82;
 Best Local Similarity: 100.0%; Prod. No. 9.8;
 Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0.
 QY 3 GYRN 7
 Db 51 GYRN 55

RESULT 36
 US-08-480-478-54
 Sequence 54, Application 05/08486478
 Patent No. 5864009
 GENERAL INFORMATION:
 APPLICANT: GEORGE P. VIASUK; PATRICK ERIC
 APPLICANT: HUGO STANSENS; JORIS HILDA
 APPLICANT: LIEVEN MESSENS; MARC JOZEF
 APPLICANT: LAURENCE; YVES RENE LAROCHE;
 APPLICANT: LAURENT STEPHANE JESPEERS, and
 APPLICANT: YANNICK GEORGES JOZEF
 APPLICANT: GANSEMAN
 TITLE OF INVENTION: NEMATODE EXTRACTED ANTI
 TITLE OF INVENTION: COAGULANT PROTEIN
 NUMBER OF SEQUENCES: 86
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: FastSeq Version 1.5
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: 06-JUN-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: 18 OCTOBER 1994
 ATTORNEY/AGENT INFORMATION:

NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 40,158
 REFERENCE/JOINT NUMBER: 213,269
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 82 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Ancylostoma canaliculatum
 US-08-498-556-79
 Query Match 93.8%; Score 49; DB 2; Length 82;
 Best Local Similarity: 100.0%; Prod. No. 9.8;
 Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0.
 QY 3 GYRN 7
 Db 51 GYRN 55

RESULT 37
 US-08-498-556-79
 Sequence 25, Application 05/08486497
 Patent No. 5866542
 GENERAL INFORMATION:
 APPLICANT: GEORGE P. VIASUK; PATRICK ERIC STANSENS;
 APPLICANT: JORIS HILDA; MESSENS; MARC JOZEF;
 APPLICANT: YVES RENE LAROCHE; LAURENT STEPHANE JESPEERS;
 APPLICANT: YANNICK GEORGES JOZEF; GANSEMAN; MATTHEW WOYLE;
 APPLICANT: PETER W. BEQUIM
 TITLE OF INVENTION: NEMATODE EXTRACTED ANTI
 TITLE OF INVENTION: PROTEIN
 NUMBER OF SEQUENCES: 357
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lyon & Lyon
 STREET: Suite 4700
 CITY: Los Angeles
 STATE: California
 COUNTRY: U.S.A.
 ZIP: 90071
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 MEDIUM TYPE: storage
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: IBM P.C. DOS 5.0
 SOFTWARE: Word Perfect 5.1
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: 08/326,486,397
 FILING DATE: June 5, 1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/326,110
 FILING DATE: October 18, 1994
 ATTORNEY/AGENT INFORMATION:
 NAME: BIGGS, SUZANNE L.
 REGISTRATION NUMBER: 40,158
 REFERENCE/JOINT NUMBER: 213,269
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (213) 489-1600
 TELEFAX: (213) 955-0440
 INFORMATION FOR SEQ ID NO: 25:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 82 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 ORIGINAL SOURCE:
 ORGANISM: Ancylostoma canaliculatum

US-08-486-499-25

Query Match 94.8% Score 40; DB 2; Length 82;
 Best Local Similarity 100.0%; Prod. No. 9.8;
 Matches 5; Conservatv 0; Mismatches 0; Gaps 0;

QY 4 GYRN 7
 1111
 51 GYRN 55

RESULT 48

US-08-486-497-49
 : Sequence 49; Application US/08486497

: Patent No. 5866542

: GENERAL INFORMATION:

: APPLICANT: George P. Vlasek, Patric H. Stanssens,

: APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,

: APPLICANT: Yves R. Laroche, Laurent S. Jespers,

: APPLICANT: Yvanick G.J. Ganssems, Matthew Mayle,

: APPLICANT: Peter W. Berquim

: TITLE OF INVENTION: NEMAPHIL EXTRACTED ANTICAGULANT

: NUMBER OF SEQUENCES: 457

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Lyon & Lyon

: STREET: 643 West Fifth Street

: CITY: Los Angeles

: STATE: California

: COUNTRY: U.S.A.

: ZIP: 90071

: COMPUTER READABLE FORM:

: MEDIUM TYPE: 3.5" Diskette, 1.44 MB

: COMPUTER: IBM Compatible

: OPERATING SYSTEM: IBM P.C. DOS 5.0

: SOFTWARE: Word Perfect 5.1

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: 08/426,110

: FILING DATE: June 5, 1995

: CLASSIFICATION: 530

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 08/426,110

: FILING DATE: October 18, 1994

: ATTORNEY/AGENT INFORMATION:

: NAME: BIGGS, SUZANNE L.

: REGISTRATION NUMBER: 40,158

: REFERENCE/AGENT NUMBER: 219,266

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (213) 489-1600

: TELEFAX: (213) 955-0440

: TELEX: 67-3510

: INFORMATION FOR SEQ ID NO: 49:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 82 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: peptide

: ORIGINAL SOURCE:

: ORGANISM: Anryclostoma ceylanicum

US-08-486-497-49

Query Match 94.8% Score 40; DB 2; Length 82;
 Best Local Similarity 100.0%; Prod. No. 9.8;
 Matches 5; Conservatv 0; Mismatches 0; Indels 0;

QY 4 GYRN 7
 1111
 51 GYRN 55

RESULT 49

US-08-486-499-25

: Sequence 25; Application US/08486499

: Patent No. 5866543

: GENERAL INFORMATION:

: APPLICANT: George P. Vlasek, Patric H. Stanssens,

: APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,

: APPLICANT: Yves R. Laroche, Laurent S. Jespers,

: APPLICANT: Yvanick G.J. Ganssems, Matthew Mayle,

: APPLICANT: Peter W. Berquim

: TITLE OF INVENTION: NEMAPHIL EXTRACTED ANTICAGULANT

: NUMBER OF SEQUENCES: 456

: CORRESPONDENCE ADDRESS:

: ADDRESSEE: Lyon & Lyon

: STREET: 643 West Fifth Street

: CITY: Los Angeles

: STATE: California

: COUNTRY: U.S.A.

: ZIP: 90071

: COMPUTER READABLE FORM:

: MEDIUM TYPE: 3.5" Diskette, 1.44 MB

: COMPUTER: IBM Compatible

: OPERATING SYSTEM: IBM P.C. DOS 5.0

: SOFTWARE: Word Perfect 5.1

: CURRENT APPLICATION DATA:

: APPLICATION NUMBER: 08/426,110

: FILING DATE: June 5, 1995

: CLASSIFICATION: 530

: PRIOR APPLICATION DATA:

: APPLICATION NUMBER: 08/426,110

: FILING DATE: October 18, 1994

: ATTORNEY/AGENT INFORMATION:

: NAME: BIGGS, SUZANNE L.

: REGISTRATION NUMBER: 40,158

: REFERENCE/AGENT NUMBER: 219,270

: TELECOMMUNICATION INFORMATION:

: TELEPHONE: (213) 489-1600

: TELEFAX: (213) 955-0440

: TELEX: 67-3510

: INFORMATION FOR SEQ ID NO: 25:

: SEQUENCE CHARACTERISTICS:

: LENGTH: 82 amino acids

: TYPE: amino acid

: TOPOLOGY: linear

: MOLECULE TYPE: peptide

: ORIGINAL SOURCE:

: ORGANISM: Anryclostoma ceylanicum

US-08-486-499-25

Query Match 92.8% Score 40; DB 2; Length 82;
 Best Local Similarity 100.0%; Prod. No. 9.8;
 Matches 5; Conservatv 0; Mismatches 0; Indels 0;

QY 4 GYRN 7
 1111
 51 GYRN 55

RESULT 40

US-08-486-499-49
 : Sequence 49; Application US/08486499

: Patent No. 5866543

: GENERAL INFORMATION:

: APPLICANT: George P. Vlasek, Patric H. Stanssens,

: APPLICANT: Joris H.L. Meuseus, Marc J. Lauwereys,

: APPLICANT: Yves R. Laroche, Laurent S. Jespers,

: APPLICANT: Yvanick G.J. Ganssems, Matthew Mayle,

: APPLICANT: Peter W. Berquim

: TITLE OF INVENTION: NEMAPHIL EXTRACTED ANTICAGULANT

: NUMBER OF SEQUENCES: 356

```

CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
MEDIUM TYPE: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,399
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/AGENT NUMBER: 213,273
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO. 49:
SEQUENCE CHARACTERISTICS:
LENGTH: 82 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma ceylanicum
US-08-486-399-49

```

```

Query Match 93.8% Score 40; DB 2; Length 82;
Best Local Similarity 100.0% Pref. No. 9.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GYRN 7
DB 51 GYRN 55

```

```

RESULT 41
US-08-461-965-25
Sequence 25, Application US/08/461965
Patent No. 5872098
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mousens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssemaans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE EXTRACTED ANTICOGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
MEDIUM TYPE: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158

```

```

OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/AGENT NUMBER: 213,243
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 92 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Ancylostoma ceylanicum
US-08-461-965-25

```

```

Query Match 93.8% Score 40; DB 2; Length 82;
Best Local Similarity 100.0% Pref. No. 9.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 3 GYRN 7
DB 51 GYRN 55

```

```

RESULT 42
US-08-461-965-49
Sequence 49, Application US/08/461965
Patent No. 5872098
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mousens, Marc J. Lauwereys,
APPLICANT: Yves R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Ganssemaans, Matthew Moyle,
APPLICANT: Peter W. Bergum
TITLE OF INVENTION: NEMATODE EXTRACTED ANTICOGULANT
NUMBER OF SEQUENCES: 356
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon
STREET: 633 West Fifth Street
SUITE: Suite 4700
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" diskette, 1.44 Mb
MEDIUM TYPE: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/426,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158

```

1 REFERENCE: 214 89644 250719
2 TELECOMMUNICATION INFORMATION:
3 TELEPHONE: (214) 489 1600
4 TELEFAX: (214) 955-0440
5 TELEX: 67-4510
6 INFORMATION FOR SEQ ID NO: 49:
7 SEQUENCE CHARACTERISTICS:
8 LENGTH: 82 amino acids
9 TYPE: amino acid
10 TOPOLOGY: linear
11 MOLECULE TYPE: peptide
12 ORIGINAL SOURCE:
13 ORGANISM: Anacyclostoma coplanicum
14 US 08-461-965-45

Query Match 94.8%; Score 30; DB 2; Length 82;
Best Local Similarity 100.0%; Prod. No. 9.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYRN 7
11111
DB 51 GYRN 55

RESULT 44

US-08-426-110A-54

1 Sequence 54; Application US/08/426110A
2 Patent No. 5945275
3 GENERAL INFORMATION:
4 APPLICANT: GEORGE P. VLASAK; PATRICK ERIC
5 APPLICANT: HUGO STANSENS; JORIS HILDA
6 APPLICANT: LIEVEN MESSERS; MARC JOYEF
7 APPLICANT: LAURENCE YVES BENE LAKECHIE
8 APPLICANT: LAURENT STEPHANE JESPERES; and
9 APPLICANT: YANNICK GEORGES WITTE
10 APPLICANT: GANSMANS
11 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
12 TITLE OF INVENTION: COAGULANT PROTEIN
13 NUMBER OF SEQUENCES: 86
14 CORRESPONDENCE ADDRESS:
15 ADDRESSEE: LYON 8 LYON
16 STREET: 633 West Fifth Street
17 CITY: Los Angeles
18 STATE: California
19 COUNTRY: U.S.A.
20 ZIP: 90071
21 COMPUTER READABLE FORM:
22 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
23 MEDIUM TYPE: storage
24 COMPUTER: IBM Compatible
25 OPERATING SYSTEM: IBM P.C. DOS 5.0
26 SOFTWARE: FastSeq Version 1.5
27 CURRENT APPLICATION DATA:
28 APPLICATION NUMBER: US/08/426,110A
29 FILING DATE: 18 October 1994
30 CLASSIFICATION: 530
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER:
33 FILING DATE:
34 ATTORNEY/AGENT INFORMATION:
35 NAME: ROSEN, ROBERT L.
36 REGISTRATION NUMBER: 39,159
37 REFERENCE TO PARENT APPLICATION:
38 REFERENCE TO PARENT NUMBER: 2507290
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: (214) 489-1600
41 TELEFAX: (214) 955-0440
42 TELEX: 67-4510
43 INFORMATION FOR SEQ ID NO: 54:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 82 amino acids
46 TYPE: amino acid
47 TOPOLOGY: linear

US-08-426-110A-54

Query Match 94.8%; Score 30; DB 2; Length 82;
Best Local Similarity 100.0%; Prod. No. 9.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYRN 7
11111
DB 51 GYRN 55

RESULT 44

1 Sequence 25; Application US/08/434641
2 Patent No. 5955294
3 GENERAL INFORMATION:
4 APPLICANT: VLASAK, George P. Vlasak
5 APPLICANT: STANSENS, Patrick Eric Hugo
6 APPLICANT: MESSERS, Joris Hilda Lieve
7 APPLICANT: LAURENCE, Yves Rene
8 APPLICANT: JESPERES, Laurent Stephane
9 APPLICANT: GANSMANS, Yannick Georges Jozef
10 APPLICANT: WITTE, Matthew
11 APPLICANT: BERGMAN, Peter W.
12 TITLE OF INVENTION: NEMATODE-EXTRACTED ANTI-
13 TITLE OF INVENTION: PROTEIN
14 NUMBER OF SEQUENCES: 356
15 CORRESPONDENCE ADDRESS:
16 ADDRESSEE: LYON 8 LYON
17 STREET: 633 West Fifth Street
18 CITY: Los Angeles
19 STATE: California
20 COUNTRY: U.S.A.
21 ZIP: 90071
22 COMPUTER READABLE FORM:
23 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
24 MEDIUM TYPE: storage
25 COMPUTER: IBM Compatible
26 OPERATING SYSTEM: IBM P.C. DOS 5.0
27 SOFTWARE: Word Perfect 5.1
28 CURRENT APPLICATION DATA:
29 APPLICATION NUMBER: US/08/434,641
30 FILING DATE: April 19, 1996
31 PRIOR APPLICATION DATA:
32 APPLICATION NUMBER: 157,735/5,142A1
33 FILING DATE: October 17, 1995
34 ATTORNEY/AGENT INFORMATION:
35 NAME: ROSEN, ROBERT L.
36 REGISTRATION NUMBER: 39,159
37 REFERENCE TO PARENT APPLICATION:
38 REFERENCE TO PARENT NUMBER: 2507290
39 TELECOMMUNICATION INFORMATION:
40 TELEPHONE: (214) 489 1600
41 TELEFAX: (214) 955-0440
42 TELEX: 67-4510
43 INFORMATION FOR SEQ ID NO: 25:
44 SEQUENCE CHARACTERISTICS:
45 LENGTH: 82 amino acids
46 TYPE: amino acid
47 TOPOLOGY: linear
48 MOLECULE TYPE: peptide
49 ORIGINAL SOURCE:

ORGANISM: Ancylostoma ceylanicum
US-08-634-641-25

Query Match 93.8% Score 30; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 6.4;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIII
Db 51 GYRN 55

RESULT 45

US-08-634-641-49
Sequence 45 Application US:08634541
Patent No. 5955294

GENERAL INFORMATION:

APPLICANT: Vlasuk, George P. Vlasuk
APPLICANT: Stanssens, Patrick Eric Hugo
APPLICANT: Menssens, Joris Hilda Lieven
APPLICANT: Lauwereys, Marc Josef
APPLICANT: Laroche, Yves Rene
APPLICANT: Jespers, Laurent Stephane
APPLICANT: Gansseman, Yannick Georges Jozef
APPLICANT: Moyle, Matthew
APPLICANT: Bergum, Peter W.

TITLE OF INVENTION: NEMATODE-EXTRACTED ANTICOAGULANT

NUMBER OF SEQUENCES: 356

CORRESPONDENCE ADDRESS:

ADDRESSER: Lyon & Lyon

STREET: 633 West Fifth Street

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90071

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM Compatible

OPERATING SYSTEM: IBM P.C. DOS 5.0

SOFTWARE: Word Perfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: 59, 64, 641

FILING DATE: April 19, 1996

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FCT/9395/13231

FILING DATE: October 17, 1995

APPLICATION NUMBER: 08/486,399

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/486,397

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/465,380

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/461,965

FILING DATE: June 5, 1995

APPLICATION NUMBER: 08/426,110

FILING DATE: October 18, 1994

ATTORNEY/AGENT INFORMATION:

NAME: HIGGS, SUZANNE L.

REGISTRATION NUMBER: 30,158

REFERENCE/DOCKET NUMBER: 219/146

TELECOMMUNICATION INFORMATION:

TELEPHONE: (213) 489-1600

TELEFAX: (213) 955-0440

TELEX: 67-3510

INFORMATION FOR SEQ ID NO. 45:

SEQUENCE CHARACTERISTICS:

LENGTH: 82 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

ORIGINAL SOURCE:
ORGANISM: Ancylostoma ceylanicum
US-08-634-641-49

Query Match 93.8% Score 30; DB 2; Length 82;
Best Local Similarity 100.0%; Pred. No. 9.8;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIII
Db 51 GYRN 55

Search completed: April 30, 2003, 14:37:17
Job time : 27.3727 secs



GeneCore version 5.1.4.155-1578
Copyright (c) 1993 - 2003 Compton Ltd.

OM protein - protein search, using sw model

Run on: April 29, 2003, 13:07:03, Search time: 6.272 Seconds
(without alignments)
16.652 Million cell updates/sec

Title: US-09-498-556c-79

Perfect score: 32

Sequence: 1 XGCPVN 7

Scoring table: BLOSUM62
Gap: 10.0, Gapext 0.5

Searched: 328255 seqs, 8628685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum hit seq length: 0

Maximum hit seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database: Published Applications AA:
1: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-1
2: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-2
3: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-3
4: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-4
5: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-5
6: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-6
7: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-7
8: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-8
9: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-9
10: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-10
11: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-11
12: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-12
13: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-13
14: /seqs/6/1/pubdata/1/pubseq/US09-498-556c-79-14

Prod No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARY

Result No.	Score	Query Match Length	IP	Description
1	30	93.8	128	US-09-764-877-1944
2	30	93.8	269	US-09-798-626-3929
3	30	93.8	1564	US-09-804-896-43
4	30	93.8	168	US-09-801-368-244
5	27	84.4	73	US-09-854-761-4509
6	27	84.4	173	US-09-925-302-855
7	27	84.4	260	US-09-858-546-5
8	27	84.4	392	US-09-813-718-16
9	27	84.4	415	US-09-813-718-14
10	27	84.4	437	US-09-813-718-12
11	27	84.4	471	US-09-813-718-10
12	27	84.4	475	US-09-925-302-855
13	27	84.4	484	US-09-813-718-10
14	27	84.4	530	US-09-813-718-10
15	27	84.4	530	US-09-858-546-2
16	27	84.4	2711	US-09-808-602-82
17	25	78.1	60	US-09-854-761-39057
18	25	78.1	57	US-09-764-877-1944
19	25	78.1	67	US-09-764-877-1944

20	25	78.1	74	US-09-148-164-42
21	25	78.1	74	US-09-148-164-42
22	25	78.1	139	US-09-949-482-109
23	25	78.1	155	US-09-981-876-178
24	25	78.1	155	US-09-148-164-42
25	25	78.1	259	US-09-813-718-12
26	25	78.1	263	US-09-813-718-12
27	25	78.1	332	US-09-925-302-855
28	25	78.1	406	US-09-949-482-109
29	25	78.1	413	US-09-949-482-109
30	25	78.1	413	US-09-949-482-109
31	25	78.1	418	US-09-925-302-855
32	25	78.1	439	US-09-925-302-855
33	25	78.1	472	US-09-925-302-855
34	25	78.1	485	US-09-925-302-855
35	25	78.1	485	US-09-925-302-855
36	25	78.1	411	US-09-925-302-855
37	25	78.1	411	US-09-925-302-855
38	25	78.1	411	US-09-925-302-855
39	25	78.1	416	US-09-925-302-855
40	25	78.1	416	US-09-925-302-855
41	25	78.1	416	US-09-925-302-855
42	25	78.1	416	US-09-925-302-855
43	25	78.1	416	US-09-925-302-855
44	25	78.1	416	US-09-925-302-855
45	25	78.1	416	US-09-925-302-855
46	25	78.1	416	US-09-925-302-855
47	25	78.1	416	US-09-925-302-855
48	25	78.1	416	US-09-925-302-855
49	25	78.1	416	US-09-925-302-855
50	25	78.1	416	US-09-925-302-855
51	25	78.1	416	US-09-925-302-855
52	25	78.1	416	US-09-925-302-855
53	25	78.1	416	US-09-925-302-855
54	25	78.1	416	US-09-925-302-855
55	25	78.1	416	US-09-925-302-855
56	25	78.1	416	US-09-925-302-855
57	25	78.1	416	US-09-925-302-855
58	25	78.1	416	US-09-925-302-855
59	25	78.1	416	US-09-925-302-855
60	25	78.1	416	US-09-925-302-855
61	25	78.1	416	US-09-925-302-855
62	25	78.1	416	US-09-925-302-855
63	25	78.1	416	US-09-925-302-855
64	25	78.1	416	US-09-925-302-855
65	25	78.1	416	US-09-925-302-855
66	25	78.1	416	US-09-925-302-855
67	25	78.1	416	US-09-925-302-855
68	25	78.1	416	US-09-925-302-855
69	25	78.1	416	US-09-925-302-855
70	25	78.1	416	US-09-925-302-855
71	25	78.1	416	US-09-925-302-855
72	25	78.1	416	US-09-925-302-855
73	25	78.1	416	US-09-925-302-855
74	25	78.1	416	US-09-925-302-855
75	25	78.1	416	US-09-925-302-855
76	25	78.1	416	US-09-925-302-855
77	25	78.1	416	US-09-925-302-855
78	25	78.1	416	US-09-925-302-855
79	25	78.1	416	US-09-925-302-855
80	25	78.1	416	US-09-925-302-855
81	25	78.1	416	US-09-925-302-855
82	25	78.1	416	US-09-925-302-855
83	25	78.1	416	US-09-925-302-855
84	25	78.1	416	US-09-925-302-855
85	25	78.1	416	US-09-925-302-855
86	25	78.1	416	US-09-925-302-855
87	25	78.1	416	US-09-925-302-855
88	25	78.1	416	US-09-925-302-855
89	25	78.1	416	US-09-925-302-855
90	25	78.1	416	US-09-925-302-855
91	25	78.1	416	US-09-925-302-855
92	25	78.1	416	US-09-925-302-855

Wed Apr 30 14:03:41 2003

677	25	78.1	692	9	08-10-199	461	560	App	Sequence 560, App	750	25	78.1	692	9	08-10-199	461	560	App	Sequence 560, App
678	25	78.1	692	9	08-10-199	462	560	App	Sequence 560, App	751	25	78.1	692	9	08-10-199	463	560	App	Sequence 560, App
679	25	78.1	692	9	08-10-199	463	560	App	Sequence 560, App	752	25	78.1	692	9	08-10-199	464	560	App	Sequence 560, App
680	25	78.1	692	9	08-10-199	464	560	App	Sequence 560, App	753	25	78.1	692	9	08-10-199	465	560	App	Sequence 560, App
681	25	78.1	692	9	08-10-199	465	560	App	Sequence 560, App	754	25	78.1	692	9	08-10-199	466	560	App	Sequence 560, App
682	25	78.1	692	9	08-10-199	466	560	App	Sequence 560, App	755	25	78.1	692	9	08-10-199	467	560	App	Sequence 560, App
683	25	78.1	692	9	08-10-199	467	560	App	Sequence 560, App	756	25	78.1	692	9	08-10-199	468	560	App	Sequence 560, App
684	25	78.1	692	9	08-10-199	468	560	App	Sequence 560, App	757	25	78.1	692	9	08-10-199	469	560	App	Sequence 560, App
685	25	78.1	692	9	08-10-199	469	560	App	Sequence 560, App	758	25	78.1	692	9	08-10-199	470	560	App	Sequence 560, App
686	25	78.1	692	9	08-10-199	470	560	App	Sequence 560, App	759	25	78.1	692	9	08-10-199	471	560	App	Sequence 560, App
687	25	78.1	692	9	08-10-199	471	560	App	Sequence 560, App	760	25	78.1	692	9	08-10-199	472	560	App	Sequence 560, App
688	25	78.1	692	9	08-10-199	472	560	App	Sequence 560, App	761	25	78.1	692	9	08-10-199	473	560	App	Sequence 560, App
689	25	78.1	692	9	08-10-199	473	560	App	Sequence 560, App	762	25	78.1	692	9	08-10-199	474	560	App	Sequence 560, App
690	25	78.1	692	9	08-10-199	474	560	App	Sequence 560, App	763	25	78.1	692	9	08-10-199	475	560	App	Sequence 560, App
691	25	78.1	692	9	08-10-199	475	560	App	Sequence 560, App	764	25	78.1	692	9	08-10-199	476	560	App	Sequence 560, App
692	25	78.1	692	9	08-10-199	476	560	App	Sequence 560, App	765	25	78.1	692	9	08-10-199	477	560	App	Sequence 560, App
693	25	78.1	692	9	08-10-199	477	560	App	Sequence 560, App	766	25	78.1	692	9	08-10-199	478	560	App	Sequence 560, App
694	25	78.1	692	9	08-10-199	478	560	App	Sequence 560, App	767	25	78.1	692	9	08-10-199	479	560	App	Sequence 560, App
695	25	78.1	692	9	08-10-199	479	560	App	Sequence 560, App	768	25	78.1	692	9	08-10-199	480	560	App	Sequence 560, App
696	25	78.1	692	9	08-10-199	480	560	App	Sequence 560, App	769	25	78.1	692	9	08-10-199	481	560	App	Sequence 560, App
697	25	78.1	692	9	08-10-199	481	560	App	Sequence 560, App	770	25	78.1	692	9	08-10-199	482	560	App	Sequence 560, App
698	25	78.1	692	9	08-10-199	482	560	App	Sequence 560, App	771	25	78.1	692	9	08-10-199	483	560	App	Sequence 560, App
699	25	78.1	692	9	08-10-199	483	560	App	Sequence 560, App	772	25	78.1	692	9	08-10-199	484	560	App	Sequence 560, App
700	25	78.1	692	9	08-1														

834	25	78.1	692	12	US-10-176-596-590	Sequence 590, Aff	699	25	78.1	692	9	US-10-176-596-590
835	25	78.1	742	9	US-10-176-596-590	Sequence 591, Aff	749	25	78.1	742	6	US-10-176-596-590
836	25	78.1	792	6	US-10-176-596-590	Sequence 592, Aff	799	25	78.1	792	3	US-10-176-596-590
837	25	78.1	842	3	US-10-176-596-590	Sequence 593, Aff	849	25	78.1	842	0	US-10-176-596-590
838	25	78.1	892	0	US-10-176-596-590	Sequence 594, Aff	899	25	78.1	892	9	US-10-176-596-590
839	25	78.1	942	3	US-10-176-596-590	Sequence 595, Aff	949	25	78.1	942	6	US-10-176-596-590
840	25	78.1	992	0	US-10-176-596-590	Sequence 596, Aff	999	25	78.1	992	3	US-10-176-596-590
841	25	78.1	1042	3	US-10-176-596-590	Sequence 597, Aff	1049	25	78.1	1042	0	US-10-176-596-590
842	25	78.1	1092	0	US-10-176-596-590	Sequence 598, Aff	1099	25	78.1	1092	9	US-10-176-596-590
843	25	78.1	1142	3	US-10-176-596-590	Sequence 599, Aff	1149	25	78.1	1142	6	US-10-176-596-590
844	25	78.1	1192	0	US-10-176-596-590	Sequence 600, Aff	1199	25	78.1	1192	3	US-10-176-596-590
845	25	78.1	1242	3	US-10-176-596-590	Sequence 601, Aff	1249	25	78.1	1242	0	US-10-176-596-590
846	25	78.1	1292	0	US-10-176-596-590	Sequence 602, Aff	1299	25	78.1	1292	9	US-10-176-596-590
847	25	78.1	1342	3	US-10-176-596-590	Sequence 603, Aff	1349	25	78.1	1342	6	US-10-176-596-590
848	25	78.1	1392	0	US-10-176-596-590	Sequence 604, Aff	1399	25	78.1	1392	3	US-10-176-596-590
849	25	78.1	1442	3	US-10-176-596-590	Sequence 605, Aff	1449	25	78.1	1442	0	US-10-176-596-590
850	25	78.1	1492	0	US-10-176-596-590	Sequence 606, Aff	1499	25	78.1	1492	9	US-10-176-596-590
851	25	78.1	1542	3	US-10-176-596-590	Sequence 607, Aff	1549	25	78.1	1542	6	US-10-176-596-590
852	25	78.1	1592	0	US-10-176-596-590	Sequence 608, Aff	1599	25	78.1	1592	3	US-10-176-596-590
853	25	78.1	1642	3	US-10-176-596-590	Sequence 609, Aff	1649	25	78.1	1642	0	US-10-176-596-590
854	25	78.1	1692	0	US-10-176-596-590	Sequence 610, Aff	1699	25	78.1	1692	9	US-10-176-596-590
855	25	78.1	1742	3	US-10-176-596-590	Sequence 611, Aff	1749	25	78.1	1742	6	US-10-176-596-590
856	25	78.1	1792	0	US-10-176-596-590	Sequence 612, Aff	1799	25	78.1	1792	3	US-10-176-596-590
857	25	78.1	1842	3	US-10-176-596-590	Sequence 613, Aff	1849	25	78.1	1842	0	US-10-176-596-590
858	25	78.1	1892	0	US-10-176-596-590	Sequence 614, Aff	1899	25	78.1	1892	9	US-10-176-596-590
859	25	78.1	1942	3	US-10-176-596-590	Sequence 615, Aff	1949	25	78.1	1942	6	US-10-176-596-590
860	25	78.1	1992	0	US-10-176-596-590	Sequence 616, Aff	1999	25	78.1	1992	3	US-10-176-596-590
861	25	78.1	2042	3	US-10-176-596-590	Sequence 617, Aff	2049	25	78.1	2042	0	US-10-176-596-590
862	25	78.1	2092	0	US-10-176-596-590	Sequence 618, Aff	2099	25	78.1	2092	9	US-10-176-596-590
863	25	78.1	2142	3	US-10-176-596-590	Sequence 619, Aff	2149	25	78.1	2142	6	US-10-176-596-590
864	25	78.1	2192	0	US-10-176-596-590	Sequence 620, Aff	2199	25	78.1	2192	3	US-10-176-596-590
865	25	78.1	2242	3	US-10-176-596-590	Sequence 621, Aff	2249	25	78.1	2242	0	US-10-176-596-590
866	25	78.1	2292	0	US-10-176-596-590	Sequence 622, Aff	2299	25	78.1	2292	9	US-10-176-596-590
867	25	78.1	2342	3	US-10-176-596-590	Sequence 623, Aff	2349	25	78.1	2342	6	US-10-176-596-590
868	25	78.1	2392	0	US-10-176-596-590	Sequence 624, Aff	2399	25	78.1	2392	3	US-10-176-596-590
869	25	78.1	2442	3	US-10-176-596-590	Sequence 625, Aff	2449	25	78.1	2442	0	US-10-176-596-590
870	25	78.1	2492	0	US-10-176-596-590	Sequence 626, Aff	2499	25	78.1	2492	9	US-10-176-596-590
871	25	78.1	2542	3	US-10-176-596-590	Sequence 627, Aff	2549	25	78.1	2542	6	US-10-176-596-590
872	25	78.1	2592	0	US-10-176-596-590	Sequence 628, Aff	2599	25	78.1	2592	3	US-10-176-596-590
873	25	78.1	2642	3	US-10-176-596-590	Sequence 629, Aff	2649	25	78.1	2642	0	US-10-176-596-590
874	25	78.1	2692	0	US-10-176-596-590	Sequence 630, Aff	2699	25	78.1	2692	9	US-10-176-596-590
875	25	78.1	2742	3	US-10-176-596-590	Sequence 631, Aff	2749	25	78.1	2742	6	US-10-176-596-590
876	25	78.1	2792	0	US-10-176-596-590	Sequence 632, Aff	2799	25	78.1	2792	3	US-10-176-596-590
877	25	78.1	2842	3	US-10-176-596-590	Sequence 633, Aff	2849	25	78.1	2842	0	US-10-176-596-590
878	25	78.1	2892	0	US-10-176-596-590	Sequence 634, Aff	2899	25	78.1	2892	9	US-10-176-596-590
879	25	78.1	2942	3	US-10-176-596-590	Sequence 635, Aff	2949	25	78.1	2942	6	US-10-176-596-590
880	25	78.1	2992	0	US-10-176-596-590	Sequence 636, Aff	2999	25	78.1	2992	3	US-10-176-596-590
881	25	78.1	3042	3	US-10-176-596-590	Sequence 637, Aff	3049	25	78.1	3042	0	US-10-176-596-590
882	25	78.1	3092	0	US-10-176-596-590	Sequence 638, Aff	3099	25	78.1	3092	9	US-10-176-596-590
883	25	78.1	3142	3	US-10-176-596-590	Sequence 639, Aff	3149	25	78.1	3142	6	US-10-176-596-590
884	25	78.1	3192	0	US-10-176-596-590	Sequence 640, Aff	3199	25	78.1	3192	3	US-10-176-596-590
885	25	78.1	3242	3	US-10-176-596-590	Sequence 641, Aff	3249	25	78.1	3242	0	US-10-176-596-590
886	25	78.1	3292	0	US-10-176-596-590	Sequence 642, Aff	3299	25	78.1	3292	9	US-10-176-596-590
887	25	78.1	3342	3	US-10-176-596-590	Sequence 643, Aff	3349	25	78.1	3342	6	US-10-176-596-590
888	25	78.1	3392	0	US-10-176-596-590	Sequence 644, Aff	3399	25	78.1	3392	3	US-10-176-596-590
889	25	78.1	3442	3	US-10-176-596-590	Sequence 645, Aff	3449	25	78.1	3442	0	US-10-176-596-590
890	25	78.1	3492	0	US-10-176-596-590	Sequence 646, Aff	3499	25	78.1	3492	9	US-10-176-596-590
891	25	78.1	3542	3	US-10-176-596-590	Sequence 647, Aff	3549	25	78.1	3542	6	US-10-176-596-590
892	25	78.1	3592	0	US-10-176-596-590	Sequence 648, Aff	3599	25	78.1	3592	3	US-10-176-596-590
893	25	78.1	3642	3	US-10-176-596-590	Sequence 649, Aff	3649	25	78.1	3642	0	US-10-176-596-590
894	25	78.1	3692	0	US-10-176-596-590	Sequence 650, Aff	3699	25	78.1	3692	9	US-10-176-596-590
895	25	78.1	3742	3	US-10-176-596-590	Sequence 651, Aff	3749	25	78.1	3742	6	US-10-176-596-590
896	25	78.1	3792	0	US-10-176-596-590	Sequence 652, Aff	3799	25	78.1	3792	3	US-10-176-596-590
897	25	78.1	3842	3	US-10-176-596-590	Sequence 653, Aff	3849	25	78.1	3842	0	US-10-176-596-590
898	25	78.1	3892	0	US-10-176-596-590	Sequence 654, Aff	3899	25	78.1	3892	9	US-10-176-596-590
899	25	78.1	3942	3	US-10-176-596-590	Sequence 655, Aff	3949	25	78.1	3942	6	US-10-176-596-590
900	25	78.1	3992	0	US-10-176-596-590	Sequence 656, Aff	3999	25	78.1	3992	3	US-10-176-596-590

```

969      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
970      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
971      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
972      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
973      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
974      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
975      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
976      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
977      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
978      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
979      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
980      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
981      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
982      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
983      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
984      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
985      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
986      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
987      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
988      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
989      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
990      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
991      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
992      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
993      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
994      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
995      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
996      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
997      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
998      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
999      25 78.1 802 9 05-10-194-745-412 Sequence 312, App
1000     25 78.1 802 9 05-10-194-745-412 Sequence 312, App

```

ALIGNMENTS

```

RESULT 1
US-09-764-877-1934
? Sequence 1934, Application US/09764877
? Patent No. US20020147140A1
? GENERAL INFORMATION:
? APPLICANT: Rosen et al.
? TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
? FILE REFERENCE: none
? CURRENT APPLICATION NUMBER: 09/0764877
? PRIOR APPLICATION DATE: 2001-01-17
? NUMBER OF SEQ ID NOS: 4031
? SOFTWARE: Patent In Ver. 2.0
? SEQ ID NO: 1934
? LENGTH: 148
? TYPE: PRI
? ORGANISM: Homo sapiens
US-09-764-877-1934

```

```

Query Match 93.8% Score 40; DB 10; Length 148;
Best local Similarity 100.0%, Pred. No. 42;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GYRN 7
DB 62 GYRN 66

```

```

RESULT 2
US-09-764-877-1934
? Sequence 1934, Application US/09764877
? Patent No. US20020147140A1
? GENERAL INFORMATION:
? APPLICANT: NAKAGAWA, SAPOSHI
? APPLICANT: MIZOGUCHI, HIROSHI
? APPLICANT: ANDO, SEIKO

```

```

? APPLICANT: HAYASHI, MIKIRO
? APPLICANT: CHAI, RIKO
? APPLICANT: YOKOI, HARUHIRO
? APPLICANT: IATOH, NAOKO
? APPLICANT: SUMIH, AKIHIRO
? APPLICANT: KIKU, MASAO
? APPLICANT: CHAI, ZHIG
? TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
? FILE REFERENCE: 249-125
? CURRENT APPLICATION NUMBER: 09/0764877
? PRIOR APPLICATION DATE: 2000-12-18
? PRIOR FILING DATE: 1999-12-16
? FILE REFERENCE: 249-125
? PRIOR APPLICATION NUMBER: 09/0764877
? PRIOR FILING DATE: 2000-04-07
? NUMBER OF SEQ ID NOS: 7059
? SOFTWARE: Patent In Ver. 3.0
? SEQ ID NO: 3828
? LENGTH: 260
? TYPE: PRI
? ORGANISM: Corynebacterium glutamicum
US-09-764-877-1934

```

```

Query Match 93.8% Score 40; DB 9; Length 260;
Best local Similarity 100.0%, Pred. No. 78;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GYRN 7
DB 105 GYRN 105

```

```

RESULT 3
US-09-864-866-43
? Sequence 43, Application US/09864866
? Patent No. US20020127656A1
? GENERAL INFORMATION:
? APPLICANT: Lloyd, K. Stephen
? APPLICANT: McCulloch, Amanda K.
? TITLE OF INVENTION: DNA REPAIR POLYPEPTIDES AND METHODS OF USE
? FILE REFERENCE: 265,00170101
? CURRENT APPLICATION NUMBER: 09/0864866
? PRIOR FILING DATE: 2000-05-24
? PRIOR APPLICATION NUMBER: 09/0864866
? NUMBER OF SEQ ID NOS: 49
? SOFTWARE: Patent In Ver. 3.0
? SEQ ID NO: 43
? LENGTH: 268
? TYPE: PRI
? ORGANISM: Micrococcus luteus
US-09-864-866-43

```

```

Query Match 93.8% Score 40; DB 10; Length 268;
Best local Similarity 100.0%, Pred. No. 80;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GYRN 7
DB 95 GYRN 94

```

```

RESULT 4
US-09-864-866-43
? Sequence 43, Application US/09864866
? Patent No. US20020127656A1
? GENERAL INFORMATION:
? APPLICANT: Busby, Robert
? APPLICANT: Call, Brian
? APPLICANT: Hecht, Peter

```

APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Wray
APPLICANT: Milne, Todd
APPLICANT: RO. US2002012850A1M1: 01-30
APPLICANT: Royer, John
APPLICANT: Salama, Sofia
APPLICANT: Sherman, Amir
APPLICANT: Silva, Jeff
APPLICANT: Summers, Eric
TITLE OF INVENTION: Methods for Improving Secondary Metabolite Production in Fungi
FILE REFERENCE: 109272.147
CURRENT APPLICATION NUMBER: US2002012850A1
CURRENT FILING DATE: 2001-03-07
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/487,558
PRIOR FILING DATE: 2000-01-19
PRIOR APPLICATION NUMBER: US 60/160,587
PRIOR FILING DATE: 1999-10-20
NUMBER OF SEQ ID NOS: 440
SOFTWARE: PatentIn version 3.0
SEQ ID NO: 244
LENGTH: 1564
TYPE: PRI
ORGANISM: *Sporobolomyces cerevisiae*
US-09-801-468-244

Query Match 93.99; Score 60; DP 10; Length 1564;
Best local similarity 100.0%; Prod. No. 1363-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYEN 7
Db 1363 GYEN 1367

RESULT 5
US-09-864-761-45609
Sequence 45609, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharron G.
APPLICANT: Rack, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GINGIVAE DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: A60004-X1
CURRENT APPLICATION NUMBER: US 60/344,761
CURRENT FILING DATE: 2001-05-29
PRIOR APPLICATION NUMBER: US 56/488,312
PRIOR FILING DATE: 2000-09-04
PRIOR APPLICATION NUMBER: US 60/207,477
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/532,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24283.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,459
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/006656
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006657
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006658
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006659
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006660
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006662
PRIOR FILING DATE: 2001-01-30

PRIOR APPLICATION NUMBER: PCT/US01/006662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/006660
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/244,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 60/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 60/224,204
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 45117
SOFTWARE: Automatic Sequence List and Enzyme vers. 1.1
SEQ ID NO: 45609
LENGTH: 79
TYPE: PRI
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC014644.3
OTHER INFORMATION: EXPRESSED IN LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
OTHER INFORMATION: HUMAN H11: 6174247.1, EVALUATE 2.50e-01
OTHER INFORMATION: SWISSPROT H11: 134133, EVALUATE 3.10e-01
US-09-864-761-45609

Query Match 84.4%; Score 27; DP 10; Length 79;
Best local similarity 80.0%; Prod. No. 14402;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYEN 7
Db 72 GYEN 76

RESULT 6
US-09-925-402-855
Sequence 455, Application 09/0925402
Patent No. US20020044941A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA104
CURRENT APPLICATION NUMBER: US 60/425,409
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: PCT/US01/006619
PRIOR FILING DATE: 2000-04-08
PRIOR APPLICATION NUMBER: PCT/US01/006620
PRIOR FILING DATE: 1999-04-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn ver. 2.0
SEQ ID NO: 855
LENGTH: 173
TYPE: PRI
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (159)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (168)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-402-855
Query Match 84.4%; Score 27; DP 10; Length 173;
Best local similarity 80.0%; Prod. No. 214002;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYEN 7

```

111:1
Db 70 GYKN 74

RESULT 7
US-09-858 546-5
Sequence 5, Application US/09858546
Patent No. US2002017295A1
GENERAL INFORMATION:
APPLICANT: SHAO, Wei et al
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
FILE REFERENCE: CL001242
CURRENT APPLICATION NUMBER: US/09/858,546
CURRENT FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 260
TYPE: PRT
ORGANISM: Human
US-09-858 546-5

Query Match 84.4%; Score 27; DB 9; Length 260;
Best Local Similarity 80.0%; Pred. No. 4.6e-02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKN 7
111:1
Db 121 GYKN 125

RESULT 8
US-09-813-718-16
Sequence 16, Application US/09813718
Publication No. US2002019256A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Antinucyl tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Anticodonism
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-04-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 16
LENGTH: 392
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human minor
OTHER INFORMATION: TrpRS treatment in PET20B
US-09-813-718-16

Query Match 84.4%; Score 27; DB 9; Length 392;
Best Local Similarity 80.0%; Pred. No. 4.6e-02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKN 7
111:1
Db 154 GYKN 159

RESULT 9
US-09-813-718-14
Sequence 14, Application US/09813718
Publication No. US2002018266A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Antinucyl tRNA Synthetase Polypeptides Useful For

```

```

TITLE OF INVENTION: The Regulation of Anticodonism
FILE REFERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-04-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 14
LENGTH: 415
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human
OTHER INFORMATION: Supermini TrpRS in PET20B
US-09-813-718-14

Query Match 84.4%; Score 27; DB 9; Length 415;
Best Local Similarity 80.0%; Pred. No. 4.3e-02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKN 7
111:1
Db 177 GYKN 181

RESULT 10
US-09-813-718-12
Sequence 12, Application US/09813718
Publication No. US2002018266A1
GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Keisuke
TITLE OF INVENTION: Human Antinucyl-tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: the Regulation of Anticodonism
FILE REFERENCE: 00-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-04-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: Patent In Ver. 2.0
SEQ ID NO 12
LENGTH: 437
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human minor
OTHER INFORMATION: TrpRS in PET20B
US-09-813-718-12

Query Match 84.4%; Score 27; DB 9; Length 437;
Best Local Similarity 80.0%; Pred. No. 5.1e-02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYKN 7
111:1
Db 199 GYKN 204

RESULT 11
US-10-126-467B-2
Sequence 2, Application US/10126467B
Publication No. US20030059797A1
GENERAL INFORMATION:
APPLICANT: POLY, Elona
TITLE OF INVENTION: ANIMAL MODEL OF AND TEST FOR ALZHEIMER'S DISEASE
FILE REFERENCE: PALL-111
CURRENT APPLICATION NUMBER: US/10/126,467B
CURRENT FILING DATE: 2002-11-19
PRIORITY APPLICATION NUMBER: 63/284,980
PRIORITY FILING DATE: 2001-04-19
PRIORITY APPLICATION NUMBER: 09/514,895
PRIORITY FILING DATE: 2000-02-28
PRIORITY APPLICATION NUMBER: 09/484,869
PRIORITY FILING DATE: 1999-08-27
NUMBER OF SEQ ID NOS: 6

```

SOFTWARE: PatentIn version 3.1

SEQ ID NO 2
LENGTH: 471
TYPE: PPT
ORGANISM: Homo sapiens
US-10-126-467B-2

Query Match 84.4%; Score 27; DB 9; Length 471;
Best Local Similarity 80.0%; Pred. No. 5,5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
DB 246 GFYRN 250

RESULT 12

US-09-525-302-558
Sequence 16, Application US/000813718
Patent No. US20020182656A1

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: P104
CURRENT APPLICATION NUMBER: US/000813718
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: P1/US00/05918
PRIOR FILING DATE: 2000-04-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1998-04-12
NUMBER OF SEQ ID NOS: 896
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 558
LENGTH: 475
TYPE: PPT
ORGANISM: Homo sapiens
US-09-525-302-558

Query Match 84.4%; Score 27; DB 10; Length 475;
Best Local Similarity 80.0%; Pred. No. 5,5e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
DB 250 GFYRN 254

RESULT 13

US-09-813-718-10
Sequence 16, Application US/000813718
Publication No. US20020182656A1

GENERAL INFORMATION:
APPLICANT: Schimmel, Paul
APPLICANT: Wakasugi, Koisuke
TITLE OF INVENTION: Human Aminoacyl tRNA Synthetase Polypeptides Useful For
TITLE OF INVENTION: The Regulation of Angiogenesis
FILE REFERENCE: 60-221
CURRENT APPLICATION NUMBER: US/09/813,718
CURRENT FILING DATE: 2001-03-21
NUMBER OF SEQ ID NOS: 58
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 10
LENGTH: 484
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: human

OTHER INFORMATION: full-length types in pR120H
US-09-813-718-10

Query Match 84.4%; Score 27; DB 9; Length 484;
Best Local Similarity 80.0%; Pred. No. 5,6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
DB 246 GFYRN 250

RESULT 14

US-10-108-605-171
Sequence 17, Application US/01018905
Patent No. US20020160944A1

GENERAL INFORMATION:
APPLICANT: Broadus, Julie
APPLICANT: Stam, Lynn
APPLICANT: Bachmann, Jane
APPLICANT: Kambar, Kim
TITLE OF INVENTION: Nucleic Acid Sequences From Crossophila melanogaster That Encode
TITLE OF INVENTION: PROTEINS ESSENTIAL FOR LARVAL VIABILITY AND USES THEREOF
FILE REFERENCE: 11138
CURRENT FILING DATE: 2002-03-27
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US/00/761,142
PRIOR FILING DATE: 2001-01-16
PRIOR APPLICATION NUMBER: US/00/761,142
PRIOR FILING DATE: 2000-01-14
NUMBER OF SEQ ID NOS: 361
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 171
LENGTH: 530
TYPE: PPT
ORGANISM: Crossophila melanogaster
US-10-108-605-171

Query Match 84.4%; Score 27; DB 9; Length 530;
Best Local Similarity 80.0%; Pred. No. 6,1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
DB 122 GFYRN 186

RESULT 15

US-09-858-546-2
Sequence 2, Application US/99058546
Patent No. US20020172955A1

GENERAL INFORMATION:
APPLICANT: Shao, Wei et al.
TITLE OF INVENTION: ISOLATED HUMAN SECRETED PROTEINS,
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING HUMAN SECRETED PROTEINS, AND
TITLE OF INVENTION: USES THEREOF
FILE REFERENCE: 02001242
CURRENT APPLICATION NUMBER: US/00/858,546
CURRENT FILING DATE: 2001-05-17
NUMBER OF SEQ ID NOS: 5
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 2
LENGTH: 530
TYPE: PPT
ORGANISM: Human
US-09-858-546-2

Query Match 84.4%; Score 27; DB 9; Length 530;
Best Local Similarity 80.0%; Pred. No. 6,1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
DB 491 GFYRN 495

RESULT 16

US-09-808-602-82
Sequence 82, Application US/99098902


```

: APPLICANT: Rosen et al.
: TITLE OF INVENTION: Nucleic Acids, Proteins, and Antipeptides
: FILE REFERENCE: DALIO
: CURRENT APPLICATION NUMBER: US/09/498-556c
: CURRENT FILING DATE: 2001-01-17
: Prior application data removed - consult PALM or file wrapper
: NUMBER OF SEQ ID NOS: 334
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 130
: LENGTH: 67
: TYPE: PRT
: ORGANISM: Homo sapiens
US-09-764-855-130

```

```

Query Match      78.1% Score 25; DB 10; Length 67;
Best Local Similarity 80.0% Pred. No. 2,4e-02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GYNN 7
III I
DB 44 GYNN 48

```

```

RESULT 20
US-10-140-164-32
: Sequence 32, Application US/10/140164
: Publication No. US20030072736A1
: GENERAL INFORMATION:
: APPLICANT: Baker et al.
: TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor Tr16
: FILE REFERENCE: PF51401
: CURRENT APPLICATION NUMBER: US/10/140164
: CURRENT FILING DATE: 2002-05-08
: PRIOR APPLICATION NUMBER: 09/637,956
: PRIOR FILING DATE: 2000-08-10
: PRIOR APPLICATION NUMBER: 60/148,348
: PRIOR FILING DATE: 1999-08-12
: PRIOR APPLICATION NUMBER: 60/148,683
: PRIOR FILING DATE: 1999-08-13
: PRIOR APPLICATION NUMBER: 60/148,870
: PRIOR FILING DATE: 1999-08-13
: PRIOR APPLICATION NUMBER: 60/148,758
: PRIOR FILING DATE: 1999-08-16
: PRIOR APPLICATION NUMBER: 60/149,181
: PRIOR FILING DATE: 1999-08-17
: PRIOR APPLICATION NUMBER: 60/149,453
: PRIOR FILING DATE: 1999-08-18
: PRIOR APPLICATION NUMBER: 60/149,458
: PRIOR FILING DATE: 1999-08-19
: NUMBER OF SEQ ID NOS: 76
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 32
: LENGTH: 74
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-140-164-32

```

```

Query Match      78.1% Score 25; DB 9; Length 74;
Best Local Similarity 80.0% Pred. No. 2,4e-02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 3 GYNN 7
III I
DB 62 GYNN 66

```

```

RESULT 21
US-10-140-164-61
: Sequence 51, Application US/10/140164
: Publication No. US20030072736A1
: GENERAL INFORMATION:
: APPLICANT: Baker et al.
: TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor Tr16

```

```

: FILE REFERENCE: PF51401
: CURRENT APPLICATION NUMBER: US/10/140164
: CURRENT FILING DATE: 2002-05-08
: PRIOR APPLICATION NUMBER: 09/637,956
: PRIOR FILING DATE: 2000-08-10
: PRIOR APPLICATION NUMBER: 60/148,348
: PRIOR FILING DATE: 1999-08-12
: PRIOR APPLICATION NUMBER: 60/148,683
: PRIOR FILING DATE: 1999-08-13
: PRIOR APPLICATION NUMBER: 60/149,181
: PRIOR FILING DATE: 1999-08-13
: PRIOR APPLICATION NUMBER: 60/149,453
: PRIOR FILING DATE: 1999-08-16
: PRIOR APPLICATION NUMBER: 60/149,458
: PRIOR FILING DATE: 1999-08-17
: PRIOR APPLICATION NUMBER: 60/149,453
: PRIOR FILING DATE: 1999-08-18
: PRIOR APPLICATION NUMBER: 60/149,453
: PRIOR FILING DATE: 1999-08-19
: NUMBER OF SEQ ID NOS: 76
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 61
: LENGTH: 74
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-140-164-61

```

```

Query Match      78.1% Score 25; DB 9; Length 74;
Best Local Similarity 80.0% Pred. No. 2,4e-02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 3 GYNN 7
III I
DB 62 GYNN 66

```

```

RESULT 22
US-09-939-980-409
: Sequence 409, Application US/09/939980
: Patent No. US200302233A1
: GENERAL INFORMATION:
: APPLICANT: Black, Richard
: Burnham, Martin
: Hedason, John
: Knowles, David
: Konetty, Michael
: Nicholas, Richard
: Pratt, Julie
: Reickard, Richard
: Rosenberq, Martin
: Ward, Judith
: TITLE OF INVENTION: Novel Prokaryotic Polypeptides,
: and their Uses
: NUMBER OF SEQUENCES: 534
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: SmithKline Beecham Corporation
: STREET: 709 Swedeland Road
: CITY: King of Prussia
: STATE: PA
: COUNTRY: USA
: ZIP: 19406-0949
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: us/09/939,980
: FILING DATE: 27 Apr 2001
: CLASSIFICATION: unknown
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: us/96,165
: FILING DATE: unknown

```

```

1 ATTORNEY/CLIENT INFORMATION
2 NAME: Glomti, Edward R
3 PUBLICATION NUMBER: 36,991
4 REFERENCE/FILE NUMBER: 199519
5 TELECOMMUNICATION INFORMATION:
6 TELEPHONE: 610-270-4478
7 TELEFAX: 610-270-5093
8 TELEX: Unknown
9
10 INFORMATION FOR SEQ ID NO: 409:
11     SEQUENCE CHARACTERISTICS:
12         LENGTH: 139 amino acids
13         TYPE: amino acid
14         STRANDEDNESS: single
15         TOPOLOGY: linear
16
17     MOLECULE TYPE: Protein
18
19     SEQUENCE DESCRIPTION: SEQ ID NO: 409:
20 US-09 948-980-409
21
22     Query Match      78.1% Score 25.38 BB 10. Length 139.
23     Best Local Similarity 89.0% Prod. No. 436-92
24     Matches 4: Conservative 0, Mismatches 1, Indels 0, Gaps 0.
25
26 4 GYPER 7
27 1111
28 55 GIVEN 59
29
30 RESULT 23
31 US-09 981-876-178
32     Sequence 178: Application US/09/981876
33     Patent No. 5,520,994 A1
34     GENERAL INFORMATION:
35     APPLICANT: Kossel et al
36     TITLE OF INVENTION: 70 Human Secreted Proteins
37     FILE REFERENCE: P260191
38     CURRENT APPLICATION NUMBER: US/09/981876
39     CURRENT FILING DATE: 2001-10-16
40     PRIOR APPLICATION NUMBER: 09/148,545
41     PRIOR FILING DATE: 1998-07-04
42     PRIOR APPLICATION NUMBER: 60/040,162
43     PRIOR FILING DATE: 1997-03-07
44     PRIOR APPLICATION NUMBER: 60/040,343
45     PRIOR FILING DATE: 1997-03-07
46     PRIOR APPLICATION NUMBER: 60/048,621
47     PRIOR FILING DATE: 1997-03-07
48     PRIOR APPLICATION NUMBER: 60/040,161
49     PRIOR FILING DATE: 1997-03-07
50     PRIOR APPLICATION NUMBER: 60/040,626
51     PRIOR FILING DATE: 1997-03-07
52     PRIOR APPLICATION NUMBER: 60/040,644
53     PRIOR FILING DATE: 1997-03-07
54     PRIOR APPLICATION NUMBER: 60/040,436
55     PRIOR FILING DATE: 1997-03-07
56     PRIOR APPLICATION NUMBER: 60/043,163
57     PRIOR FILING DATE: 1997-03-07
58     PRIOR APPLICATION NUMBER: 60/047,615
59     PRIOR FILING DATE: 1997-05-24
60     PRIOR APPLICATION NUMBER: 60/047,633
61     PRIOR FILING DATE: 1997-05-24
62     PRIOR APPLICATION NUMBER: 60/047,694
63     PRIOR FILING DATE: 1997-05-24
64     PRIOR APPLICATION NUMBER: 60/047,597
65     PRIOR FILING DATE: 1997-05-24
66     PRIOR APPLICATION NUMBER: 60/047,502
67     PRIOR FILING DATE: 1997-05-24
68     PRIOR APPLICATION NUMBER: 60/047,643
69     PRIOR FILING DATE: 1997-05-24
70     PRIOR APPLICATION NUMBER: 60/047,694
71     PRIOR FILING DATE: 1997-05-24
72     PRIOR APPLICATION NUMBER: 60/047,617
73     PRIOR FILING DATE: 1997-05-24
74     PRIOR APPLICATION NUMBER: 60/047,618
75     PRIOR FILING DATE: 1997-05-24
76     PRIOR APPLICATION NUMBER: 60/047,593
77     PRIOR FILING DATE: 1997-05-24
78
79     PRIOR APPLICATION NUMBER: 60/047,592
80     PRIOR FILING DATE: 1997-05-24
81     PRIOR APPLICATION NUMBER: 60/047,591
82     PRIOR FILING DATE: 1997-05-24
83     PRIOR APPLICATION NUMBER: 60/047,594
84     PRIOR FILING DATE: 1997-05-24
85     PRIOR APPLICATION NUMBER: 60/047,595
86     PRIOR FILING DATE: 1997-05-24
87     PRIOR APPLICATION NUMBER: 60/047,596
88     PRIOR FILING DATE: 1997-05-24
89     PRIOR APPLICATION NUMBER: 60/047,597
90     PRIOR FILING DATE: 1997-05-24
91     PRIOR APPLICATION NUMBER: 60/047,598
92     PRIOR FILING DATE: 1997-05-24
93     PRIOR APPLICATION NUMBER: 60/047,613
94     PRIOR FILING DATE: 1997-05-24
95     PRIOR APPLICATION NUMBER: 60/047,582
96     PRIOR FILING DATE: 1997-05-24
97     PRIOR APPLICATION NUMBER: 60/047,596
98     PRIOR FILING DATE: 1997-05-24
99     PRIOR APPLICATION NUMBER: 60/047,612
100    PRIOR FILING DATE: 1997-05-24
101    PRIOR APPLICATION NUMBER: 60/047,632
102    PRIOR FILING DATE: 1997-05-24
103    PRIOR APPLICATION NUMBER: 60/047,601
104    PRIOR FILING DATE: 1997-05-24
105    PRIOR APPLICATION NUMBER: 60/043,580
106    PRIOR FILING DATE: 1997-04-11
107    PRIOR APPLICATION NUMBER: 60/043,568
108    PRIOR FILING DATE: 1997-04-11
109    PRIOR APPLICATION NUMBER: 60/043,414
110    PRIOR FILING DATE: 1997-04-11
111    PRIOR APPLICATION NUMBER: 60/043,569
112    PRIOR FILING DATE: 1997-04-11
113    PRIOR APPLICATION NUMBER: 60/043,411
114    PRIOR FILING DATE: 1997-04-11
115    PRIOR APPLICATION NUMBER: 60/043,671
116    PRIOR FILING DATE: 1997-04-11
117    PRIOR APPLICATION NUMBER: 60/043,674
118    PRIOR FILING DATE: 1997-04-11
119    PRIOR APPLICATION NUMBER: 60/043,669
120    PRIOR FILING DATE: 1997-04-11
121    PRIOR APPLICATION NUMBER: 60/043,412
122    PRIOR FILING DATE: 1997-04-11
123    PRIOR APPLICATION NUMBER: 60/043,413
124    PRIOR FILING DATE: 1997-04-11
125    PRIOR APPLICATION NUMBER: 60/043,672
126    PRIOR FILING DATE: 1997-04-11
127    PRIOR APPLICATION NUMBER: 60/043,415
128    PRIOR FILING DATE: 1997-04-11
129    PRIOR APPLICATION NUMBER: 60/048,974
130    PRIOR FILING DATE: 1997-06-06
131    PRIOR APPLICATION NUMBER: 60/056,886
132    PRIOR FILING DATE: 1997-06-22
133    PRIOR APPLICATION NUMBER: 60/056,889
134    PRIOR FILING DATE: 1997-08-22
135    PRIOR APPLICATION NUMBER: 60/056,893
136    PRIOR FILING DATE: 1997-08-22
137    PRIOR APPLICATION NUMBER: 60/056,600
138    PRIOR FILING DATE: 1997-08-22
139    PRIOR APPLICATION NUMBER: 60/046,878
140    PRIOR FILING DATE: 1997-08-22
141    PRIOR APPLICATION NUMBER: 60/056,562
142    PRIOR FILING DATE: 1997-08-22
143    PRIOR APPLICATION NUMBER: 60/056,872
144    PRIOR FILING DATE: 1997-08-22
145    PRIOR APPLICATION NUMBER: 60/056,882
146    PRIOR FILING DATE: 1997-08-22
147    PRIOR APPLICATION NUMBER: 60/056,837
148    PRIOR FILING DATE: 1997-08-22
149    PRIOR APPLICATION NUMBER: 60/056,503

```


1 PRIOR FILING DATE: 1997-08-22
2 PRIOR APPLICATION NUMBER: 60/056,868
3 PRIOR FILING DATE: 1997-08-22
4 PRIOR APPLICATION NUMBER: 60/056,879
5 PRIOR FILING DATE: 1997-08-22
6 PRIOR APPLICATION NUMBER: 60/056,880
7 PRIOR FILING DATE: 1997-08-22
8 PRIOR APPLICATION NUMBER: 60/056,894
9 PRIOR FILING DATE: 1997-08-22
10 PRIOR APPLICATION NUMBER: 60/056,911
11 PRIOR FILING DATE: 1997-08-22
12 PRIOR APPLICATION NUMBER: 60/056,940
13 PRIOR FILING DATE: 1997-08-22
14 PRIOR APPLICATION NUMBER: 60/056,974
15 PRIOR FILING DATE: 1997-08-22
16 PRIOR APPLICATION NUMBER: 60/056,910
17 PRIOR FILING DATE: 1997-08-22
18 PRIOR APPLICATION NUMBER: 60/056,944
19 PRIOR FILING DATE: 1997-08-22
20 PRIOR APPLICATION NUMBER: 60/056,631
21 PRIOR FILING DATE: 1997-08-22
22 PRIOR APPLICATION NUMBER: 60/056,845
23 PRIOR FILING DATE: 1997-08-22
24 PRIOR APPLICATION NUMBER: 60/047,892
25 PRIOR FILING DATE: 1997-08-22
26 PRIOR APPLICATION NUMBER: 60/047,595
27 PRIOR FILING DATE: 1997-05-23
28 PRIOR APPLICATION NUMBER: 60/057,761
29 PRIOR FILING DATE: 1997-05-23
30 PRIOR APPLICATION NUMBER: 60/047,599
31 PRIOR FILING DATE: 1997-05-23
32 PRIOR APPLICATION NUMBER: 60/047,588
33 PRIOR FILING DATE: 1997-05-23
34 PRIOR APPLICATION NUMBER: 60/047,585
35 PRIOR FILING DATE: 1997-05-23
36 PRIOR APPLICATION NUMBER: 60/047,586
37 PRIOR FILING DATE: 1997-05-23
38 PRIOR APPLICATION NUMBER: 60/047,590
39 PRIOR FILING DATE: 1997-05-23
40 PRIOR APPLICATION NUMBER: 60/047,594
41 PRIOR FILING DATE: 1997-05-23
42 PRIOR APPLICATION NUMBER: 60/047,589
43 PRIOR FILING DATE: 1997-05-23
44 PRIOR APPLICATION NUMBER: 60/047,593
45 PRIOR FILING DATE: 1997-05-23
46 PRIOR APPLICATION NUMBER: 60/047,614
47 PRIOR FILING DATE: 1997-05-23
48 PRIOR APPLICATION NUMBER: 60/043,578
49 PRIOR FILING DATE: 1997-04-11
50 PRIOR APPLICATION NUMBER: 60/043,576
51 PRIOR FILING DATE: 1997-04-11
52 PRIOR APPLICATION NUMBER: 60/047,501
53 PRIOR FILING DATE: 1997-05-23
54 PRIOR APPLICATION NUMBER: 60/043,670
55 PRIOR FILING DATE: 1997-04-11
56 PRIOR APPLICATION NUMBER: 60/043,672
57 PRIOR FILING DATE: 1997-08-22
58 PRIOR APPLICATION NUMBER: 60/056,664
59 PRIOR FILING DATE: 1997-08-22
60 PRIOR APPLICATION NUMBER: 60/056,876
61 PRIOR FILING DATE: 1997-08-22
62 PRIOR APPLICATION NUMBER: 60/056,881
63 PRIOR FILING DATE: 1997-08-22
64 PRIOR APPLICATION NUMBER: 60/056,909
65 PRIOR FILING DATE: 1997-08-22
66 PRIOR APPLICATION NUMBER: 60/056,875
67 PRIOR FILING DATE: 1997-08-22
68 PRIOR APPLICATION NUMBER: 60/056,862
69 PRIOR FILING DATE: 1997-08-22
70 PRIOR APPLICATION NUMBER: 60/056,887
71 PRIOR FILING DATE: 1997-08-22
72 PRIOR APPLICATION NUMBER: 60/056,908
73 PRIOR FILING DATE: 1997-08-22

1 PRIOR APPLICATION NUMBER: 60/048,964
2 PRIOR FILING DATE: 1997-08-06
3 PRIOR APPLICATION NUMBER: 60/057,650
4 PRIOR FILING DATE: 1997-09-05
5 PRIOR APPLICATION NUMBER: 60/056,884
6 PRIOR FILING DATE: 1997-08-22
7 NUMBER OF SEQ IN NOS: 280
8 SOFTWARE: BLASTN Ver. 2.0
9 SEQ ID NO 178
10 LENGTH: 155

Query Match 78.1% Score 25; DR 9; Length 155;
Best local Similarity 80.0%; Pos No 4 Re-02;
Matches 4; Conservative 0; Mismatches 1; Indels 0;

QY 3 GYRN 7
111 1
12 57 GYRN 71

RESULT 24
US-09-148-545-178
1 Sequence 178, Application US/09148545
2 Patent Office No. 022092027132A1
3 GENERAL INFORMATION:
4 APPLICANT: Rosen et al.
5 TITLE OF INVENTION: 70 Human Secreted Proteins
6 FILE REFERENCE: P2001P1
7 CURRENT FILING DATE: 1998-09-04
8 EARLIER APPLICATION NUMBER: 60/0398,641B2
9 EARLIER FILING DATE: 1998-04-06
10 EARLIER APPLICATION NUMBER: 60/040,152
11 EARLIER FILING DATE: 1997-04-07
12 EARLIER APPLICATION NUMBER: 60/040,433
13 EARLIER FILING DATE: 1997-03-07
14 EARLIER APPLICATION NUMBER: 60/048,621
15 EARLIER FILING DATE: 1997-03-07
16 EARLIER APPLICATION NUMBER: 60/040,161
17 EARLIER FILING DATE: 1997-03-07
18 EARLIER APPLICATION NUMBER: 60/040,626
19 EARLIER FILING DATE: 1997-04-07
20 EARLIER APPLICATION NUMBER: 60/040,434
21 EARLIER FILING DATE: 1997-03-07
22 EARLIER APPLICATION NUMBER: 60/040,336
23 EARLIER FILING DATE: 1997-03-07
24 EARLIER APPLICATION NUMBER: 60/040,153
25 EARLIER FILING DATE: 1997-04-07
26 EARLIER APPLICATION NUMBER: 60/047,615
27 EARLIER FILING DATE: 1997-05-23
28 EARLIER APPLICATION NUMBER: 60/047,600
29 EARLIER FILING DATE: 1997-05-23
30 EARLIER APPLICATION NUMBER: 60/047,557
31 EARLIER FILING DATE: 1997-05-23
32 EARLIER APPLICATION NUMBER: 60/047,582
33 EARLIER FILING DATE: 1997-05-23
34 EARLIER APPLICATION NUMBER: 60/047,633
35 EARLIER FILING DATE: 1997-05-23
36 EARLIER APPLICATION NUMBER: 60/047,584
37 EARLIER FILING DATE: 1997-05-23
38 EARLIER APPLICATION NUMBER: 60/047,617
39 EARLIER FILING DATE: 1997-05-23
40 EARLIER APPLICATION NUMBER: 60/047,618
41 EARLIER FILING DATE: 1997-05-23
42 EARLIER APPLICATION NUMBER: 60/047,503
43 EARLIER FILING DATE: 1997-05-23
44 EARLIER APPLICATION NUMBER: 60/047,562
45 EARLIER FILING DATE: 1997-05-23
46 EARLIER APPLICATION NUMBER: 60/047,581
47 EARLIER FILING DATE: 1997-05-23
48 EARLIER APPLICATION NUMBER: 60/047,584
49 EARLIER FILING DATE: 1997-05-23
50 EARLIER APPLICATION NUMBER: 60/047,500

SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 178
 LENGTH: 155

Query Match 78.1% Score 25; DB 9; Length 155;
 Best Local Similarity 80.0% Pred. No. 4 a-a-a-
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYFN 7
 ||| |
 DB 67 GYFN 71

RESULT 25

US-09-815-242 5352
 Sequence 26; Application US/09815242
 Patent No. US20020061569A1
 GENERAL INFORMATION:
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlson, Karl L.
 APPLICANT: Zyskind, Judith W.
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John D.
 APPLICANT: Carr, Grant J.
 APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 5352

LENGTH: 239

TYPE: PPT

ORGANISM: Staphylococcus aureus

US-09-815-242 5352

Query Match 78.1% Score 25; DB 10; Length 239;
 Best Local Similarity 80.0% Pred. No. 7.2e-02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYFN 7
 ||| |
 DB 92 GYFN 96

RESULT 26

US-09-815-242-12278
 Sequence 12278; Application US/09815242
 Patent No. US20020061569A1

GENERAL INFORMATION:

APPLICANT: Haselbeck, Robert

APPLICANT: Ohlson, Karl L.

APPLICANT: Zyskind, Judith W.

APPLICANT: Wall, Daniel

APPLICANT: Trawick, John D.

APPLICANT: Carr, Grant J.

APPLICANT: Yamamoto, Robert T.
 APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in

FILE REFERENCE: ELITRA.011A

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 14110

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 12278

LENGTH: 253

TYPE: PPT

ORGANISM: Staphylococcus aureus

US-09-815-242-12278

Query Match 78.1% Score 25; DB 10; Length 253;

Best Local Similarity 80.0% Pred. No. 7.2e-02;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GYFN 7

||||

DB 106 GYFN 110

RESULT 27

US-09-957-187-20

Sequence 20; Application US/09957187

Publication No. US20030054514A1

GENERAL INFORMATION:

APPLICANT: Shinkets, Richard A.

APPLICANT: Lakocheille, William

TITLE OF INVENTION: NAVIL PATHOGENICITIES AND PROTEINS ENCODED THEREBY

FILE REFERENCE: 15966-540 CIP 2003/03/27, 187

CURRENT FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 60/124,667

PRIOR FILING DATE: 1999-03-09

PRIOR APPLICATION NUMBER: 60/260,781

PRIOR FILING DATE: 2000-03-03

PRIOR APPLICATION NUMBER: 60/234,092

PRIOR FILING DATE: 2000-09-20

PRIOR APPLICATION NUMBER: 60/233,798

PRIOR FILING DATE: 2000-09-19

PRIOR APPLICATION NUMBER: 60/174,485

PRIOR FILING DATE: 2000-01-04

NUMBER OF SEQ ID NOS: 85

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 20

LENGTH: 302

TYPE: PPT

ORGANISM: Homo sapiens

US-09-957-187-20

Query Match 78.1% Score 25; DB 9; Length 402;
 Best Local Similarity 80.0% Pred. No. 9.1e-02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYFN 7

||||

1b 204 GEYIG, 268

RESULT 28

US 09-040 559-2
 ? Sequence 2: Application US/09/04059
 ? Publication No. 602047, 618
 ? GENERAL INFORMATION:
 ? APPLICANT: DANKER, CLYD
 ? APPLICANT: SOUNGJUN, JULIA CH
 ? TITLE OF INVENTION: COMPOUNDS THAT ENHANCE TUMOR LEAD
 ? FILE REFERENCE: ARD: 35105
 ? CURRENT APPLICATION NUMBER: US 09-040 559
 ? CURRENT FILING DATE: 2001-08-15
 ? PRIOR APPLICATION NUMBER: 602047, 592
 ? PRIOR FILING DATE: 2000-08-15
 ? NUMBER OF SEQ. IN SEQ. 4
 ? SOFTWARE: Patent In Ver. 2.1
 ? SEQ. ID NO. 2
 ? LENGTH: 306
 ? TYPE: PRI
 ? ORGANISM: Human
 US 09-040 559-2

Query Match 79.1% Score 25, 28 % Identity 20%
 Best local Similarity 80.0% Pred. No. 9, 20-02
 Matches 4: Conservative 1: Mismatches 0: Indels 0: Gaps 0.

97 6 GYEN 7

1111

1b 245 GEYS, 249

RESULT 29

US-09-041 876-24
 ? Sequence 246: Application US/09/041876
 ? Patent No. US2002016465A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Beson et al.
 ? TITLE OF INVENTION: 70 Human Secreted Proteins
 ? FILE REFERENCE: P20/1P1
 ? CURRENT APPLICATION NUMBER: 602047, 618
 ? CURRENT FILING DATE: 2001-10-19
 ? PRIOR APPLICATION NUMBER: 09/148,545
 ? PRIOR FILING DATE: 1998-09-04
 ? PRIOR APPLICATION NUMBER: 602047, 162
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 243
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 621
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 161
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 626
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 434
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 336
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 163
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 597
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 582
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 615
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 600
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 597
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 582
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 615
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 582
 ? PRIOR FILING DATE: 1997-03-07
 ? PRIOR APPLICATION NUMBER: 602047, 583
 ? PRIOR FILING DATE: 1997-03-07

? PRIOR APPLICATION NUMBER: 602047, 617
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 618
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 503
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 592
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 581
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 584
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 500
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 587
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 192
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 598
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 613
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 582
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 596
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 612
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 642
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 601
 ? PRIOR FILING DATE: 1997-05-23
 ? PRIOR APPLICATION NUMBER: 602047, 580
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 568
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 614
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 569
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 611
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 671
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 674
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 669
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 612
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 672
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 615
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 613
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 672
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 615
 ? PRIOR FILING DATE: 1997-04-11
 ? PRIOR APPLICATION NUMBER: 602047, 974
 ? PRIOR FILING DATE: 1997-06-06
 ? PRIOR APPLICATION NUMBER: 602056, 886
 ? PRIOR FILING DATE: 1997-08-22
 ? PRIOR APPLICATION NUMBER: 602056, 877
 ? PRIOR FILING DATE: 1997-08-22
 ? PRIOR APPLICATION NUMBER: 602056, 889
 ? PRIOR FILING DATE: 1997-08-22
 ? PRIOR APPLICATION NUMBER: 602056, 893
 ? PRIOR FILING DATE: 1997-08-22
 ? PRIOR APPLICATION NUMBER: 602056, 640
 ? PRIOR FILING DATE: 1997-08-22
 ? PRIOR APPLICATION NUMBER: 602056, 878
 ? PRIOR FILING DATE: 1997-08-22
 ? PRIOR APPLICATION NUMBER: 602056, 662
 ? PRIOR FILING DATE: 1997-08-22
 ? PRIOR APPLICATION NUMBER: 602056, 842

1 PRIOR FILING DATE: 1997-08-22
2 PRIOR APPLICATION NUMBER: 60/056,882
3 PRIOR FILING DATE: 1997-08-22
4 PRIOR APPLICATION NUMBER: 60/056,887
5 PRIOR FILING DATE: 1997-08-22
6 PRIOR APPLICATION NUMBER: 60/056,903
7 PRIOR FILING DATE: 1997-08-22
8 PRIOR APPLICATION NUMBER: 60/056,888
9 PRIOR FILING DATE: 1997-08-22
10 PRIOR APPLICATION NUMBER: 60/056,879
11 PRIOR FILING DATE: 1997-08-22
12 PRIOR APPLICATION NUMBER: 60/056,880
13 PRIOR FILING DATE: 1997-08-22
14 PRIOR APPLICATION NUMBER: 60/056,894
15 PRIOR FILING DATE: 1997-08-22
16 PRIOR APPLICATION NUMBER: 60/056,911
17 PRIOR FILING DATE: 1997-08-22
18 PRIOR APPLICATION NUMBER: 60/056,896
19 PRIOR FILING DATE: 1997-08-22
20 PRIOR APPLICATION NUMBER: 60/056,874
21 PRIOR FILING DATE: 1997-08-22
22 PRIOR APPLICATION NUMBER: 60/056,910
23 PRIOR FILING DATE: 1997-08-22
24 PRIOR APPLICATION NUMBER: 60/056,851
25 PRIOR FILING DATE: 1997-08-22
26 PRIOR APPLICATION NUMBER: 60/056,631
27 PRIOR FILING DATE: 1997-08-22
28 PRIOR APPLICATION NUMBER: 60/056,845
29 PRIOR FILING DATE: 1997-08-22
30 PRIOR APPLICATION NUMBER: 60/056,892
31 PRIOR FILING DATE: 1997-08-22
32 PRIOR APPLICATION NUMBER: 60/047,595
33 PRIOR FILING DATE: 1997-05-23
34 PRIOR APPLICATION NUMBER: 60/057,761
35 PRIOR FILING DATE: 05-Sep-1997
36 PRIOR APPLICATION NUMBER: 60/047,549
37 PRIOR FILING DATE: 1997-05-23
38 PRIOR APPLICATION NUMBER: 60/047,588
39 PRIOR FILING DATE: 1997-05-23
40 PRIOR APPLICATION NUMBER: 60/047,585
41 PRIOR FILING DATE: 1997-05-23
42 PRIOR APPLICATION NUMBER: 60/047,586
43 PRIOR FILING DATE: 1997-05-23
44 PRIOR APPLICATION NUMBER: 60/047,590
45 PRIOR FILING DATE: 1997-05-23
46 PRIOR APPLICATION NUMBER: 60/047,594
47 PRIOR FILING DATE: 1997-05-23
48 PRIOR APPLICATION NUMBER: 60/047,589
49 PRIOR FILING DATE: 1997-05-23
50 PRIOR APPLICATION NUMBER: 60/047,593
51 PRIOR FILING DATE: 1997-05-23
52 PRIOR APPLICATION NUMBER: 60/047,614
53 PRIOR FILING DATE: 1997-05-23
54 PRIOR APPLICATION NUMBER: 60/043,578
55 PRIOR FILING DATE: 1997-04-11
56 PRIOR APPLICATION NUMBER: 60/043,576
57 PRIOR FILING DATE: 1997-04-11
58 PRIOR APPLICATION NUMBER: 60/047,501
59 PRIOR FILING DATE: 1997-05-23
60 PRIOR APPLICATION NUMBER: 60/043,679
61 PRIOR FILING DATE: 1997-04-11
62 PRIOR APPLICATION NUMBER: 60/056,832
63 PRIOR FILING DATE: 1997-08-22
64 PRIOR APPLICATION NUMBER: 60/056,664
65 PRIOR FILING DATE: 1997-08-22
66 PRIOR APPLICATION NUMBER: 60/056,876
67 PRIOR FILING DATE: 1997-08-22
68 PRIOR APPLICATION NUMBER: 60/056,881
69 PRIOR FILING DATE: 1997-08-22
70 PRIOR APPLICATION NUMBER: 60/056,909
71 PRIOR FILING DATE: 1997-08-22
72 PRIOR APPLICATION NUMBER: 60/056,875
73 PRIOR FILING DATE: 1997-08-22

1 PRIOR APPLICATION NUMBER: 60/056,862
2 PRIOR FILING DATE: 1997-08-22
3 PRIOR APPLICATION NUMBER: 60/056,887
4 PRIOR FILING DATE: 1997-08-22
5 PRIOR APPLICATION NUMBER: 60/056,908
6 PRIOR FILING DATE: 1997-08-22
7 PRIOR APPLICATION NUMBER: 60/056,964
8 PRIOR FILING DATE: 1997-08-06
9 PRIOR APPLICATION NUMBER: 60/057,650
10 PRIOR FILING DATE: 1997-09-05
11 PRIOR APPLICATION NUMBER: 60/056,884
12 PRIOR FILING DATE: 1997-09-22
13 NUMBER OF SEQ ID NOS: 280
14 SOFTWARE: PatentIn Ver. 2.0
15 SEQ ID NO: 236
16 LENGTH: 314

Query Match 79.1%; Score 25; DB 9; Length 314;
Best Local Similarity 80.0%; Field No. 9.4e-02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Cv 3 GVERN 7
111 1
14 67 GVERN 71

RESULT 30
US-09-148 545-236
1 Sequence 236, Application 55/05146545
2 Publication No. 052003027172A1
3 GENERAL INFORMATION:
4 APPLICANT: Rosen et al.
5 TITLE OF INVENTION: 70 Human Secreted Proteins
6 FILE REFERENCE: P2001P1
7 CURRENT APPLICATION NUMBER: 05/056,212,545
8 CURRENT FILING DATE: 1998-09-04
9 EARLIER APPLICATION NUMBER: 72/3258/04182
10 EARLIER FILING DATE: 1998-03-06
11 EARLIER APPLICATION NUMBER: 60/040,162
12 EARLIER FILING DATE: 1997-03-07
13 EARLIER APPLICATION NUMBER: 60/040,333
14 EARLIER FILING DATE: 1997-03-07
15 EARLIER APPLICATION NUMBER: 60/036,521
16 EARLIER FILING DATE: 1997-03-07
17 EARLIER APPLICATION NUMBER: 60/040,161
18 EARLIER FILING DATE: 1997-03-07
19 EARLIER APPLICATION NUMBER: 60/040,626
20 EARLIER FILING DATE: 1997-03-07
21 EARLIER APPLICATION NUMBER: 60/040,334
22 EARLIER FILING DATE: 1997-03-07
23 EARLIER APPLICATION NUMBER: 60/040,336
24 EARLIER FILING DATE: 1997-03-07
25 EARLIER APPLICATION NUMBER: 60/040,164
26 EARLIER FILING DATE: 1997-03-07
27 EARLIER APPLICATION NUMBER: 60/047,615
28 EARLIER FILING DATE: 1997-05-23
29 EARLIER APPLICATION NUMBER: 60/047,600
30 EARLIER FILING DATE: 1997-05-24
31 EARLIER APPLICATION NUMBER: 60/047,597
32 EARLIER FILING DATE: 1997-05-24
33 EARLIER APPLICATION NUMBER: 60/047,584
34 EARLIER FILING DATE: 1997-05-24
35 EARLIER APPLICATION NUMBER: 60/047,617
36 EARLIER FILING DATE: 1997-05-24
37 EARLIER APPLICATION NUMBER: 60/047,618
38 EARLIER FILING DATE: 1997-05-24
39 EARLIER APPLICATION NUMBER: 60/047,503
40 EARLIER FILING DATE: 1997-05-23
41 EARLIER APPLICATION NUMBER: 60/047,592

; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 50/057,650
 ; EARLIER FILING DATE: 1997-06-06
 ; EARLIER APPLICATION NUMBER: 50/056,884
 ; EARLIER FILING DATE: 1997-08-22
 ; NUMBER OF SEQ ID NOS: 280
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 236
 ; LENGTH: 313

Query Match: 78.1%, Score 25; DP 9; Length 313;
 Best Local Similarity: 80.0%; Pred. No. 1; 0; 0;
 Matches: 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 3 GFYNN 7
 IIII
 Db 67 GFYNN 71

RESULT 31

; Sequence 1289, Application US/09925300
 ; Patent No. US20020151681A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Craig Rosen,
 ; APPLICANT: Steve Ruben
 ; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
 ; FILE REFERENCE: P101
 ; CURRENT APPLICATION NUMBER: US/09/925,300
 ; CURRENT FILING DATE: 2001-03-10
 ; PRIOR APPLICATION NUMBER: PCT/US00/05098
 ; PRIOR FILING DATE: 2000-03-08
 ; PRIOR APPLICATION NUMBER: 60/124,270
 ; PRIOR FILING DATE: 1999-03-12
 ; NUMBER OF SEQ ID NOS: 1890
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 1289
 ; LENGTH: 318
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-498-556c-79-1289

Query Match: 78.1%, Score 25; DP 10; Length 318;
 Best Local Similarity: 80.0%; Pred. No. 6; 0; 0;
 Matches: 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 3 GFYNN 7
 IIII
 Db 257 GFYNS 261

RESULT 32

; Sequence 2, Application US/09023771
 ; Patent No. US20010036649A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Meyers, Rachel
 ; APPLICANT: Rudolph-Owen, Laura
 ; TITLE OF INVENTION: 26934, A N. US20010036649A1 Cytidine Deaminase-Like
 ; FILE REFERENCE: 35800/213921
 ; CURRENT APPLICATION NUMBER: US/09/237,71
 ; CURRENT FILING DATE: 2001-03-09
 ; PRIOR APPLICATION NUMBER: 60/188,294
 ; PRIOR FILING DATE: 2000-03-10
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 2
 ; LENGTH: 339
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-802-371-2

Query Match: 78.1%, Score 25; DP 10; Length 372;
 Best Local Similarity: 80.0%; Pred. No. 1; 0; 0;
 Matches: 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 3 GFYNN 7
 IIII
 Db 297 GFYNS 301

RESULT 33

; Sequence 7, Application US/09971020
 ; Patent No. US20020108143A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sano, Hiroshi
 ; APPLICANT: Kusano, Tomonobu
 ; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the Gene
 ; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the Gene
 ; FILE REFERENCE: 026350-068
 ; CURRENT APPLICATION NUMBER: US/09/971,020
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: JP 2000-407,149
 ; PRIOR FILING DATE: 2000-10-06
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 372
 ; TYPE: PRT
 ; ORGANISM: Coffea arabica
 US-09-498-556c-79-020-7

Query Match: 78.1%, Score 25; DP 10; Length 372;
 Best Local Similarity: 80.0%; Pred. No. 1; 0; 0;
 Matches: 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 3 GFYNN 7
 IIII
 Db 354 GFYNN 358

RESULT 34

; Sequence 7, Application US/09971020
 ; Patent No. US20020108143A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sano, Hiroshi
 ; APPLICANT: Kusano, Tomonobu
 ; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the Gene
 ; TITLE OF INVENTION: Theobromine Synthase Polypeptide of Coffee Plant and the Gene
 ; FILE REFERENCE: 026350-068
 ; CURRENT APPLICATION NUMBER: US/09/971,020
 ; CURRENT FILING DATE: 2001-12-18
 ; PRIOR APPLICATION NUMBER: JP 2000-407,149
 ; PRIOR FILING DATE: 2000-10-06
 ; NUMBER OF SEQ ID NOS: 8
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 3
 ; LENGTH: 385
 ; TYPE: PRT
 ; ORGANISM: Coffea arabica
 US-09-498-556c-79-020-3

Query Match: 78.1%, Score 25; DP 10; Length 385;
 Best Local Similarity: 80.0%; Pred. No. 1; 0; 0;
 Matches: 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 3 GFYNN 7
 IIII
 Db 367 GFYNN 371

```

RESULT 35
US 09-071-020-5
: Sequence 5, Application US/09471020
: Patent No. US2002010814A1
: GENERAL INFORMATION:
: APPLICANT: Sano, Hiroshi
: APPLICANT: Kusano, Tomochika
: APPLICANT: Kikuzumi, Nori
: TITLE OF INVENTION: Theorizing a Synthesis Polypeptide of Coffee Plant and the Gene
: FILE REFERENCE: 026459-068
: CURRENT APPLICATION NUMBER: US/09-071-020
: PRIOR FILING DATE: 2001-12-18
: PRIOR APPLICATION NUMBER: JP 2000-307,149
: PRIOR FILING DATE: 2000-10-06
: NUMBER OF SEQ ID NOS: 8
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 5
: LENGTH: 485
: TYPE: PRT
: ORGANISM: Coffea arabica
US-09-071-020-5

Query Match 78.1% Score 25; DB 9; Length 385;
Best local Similarity 80.0% Pred. No. 1,2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GYRN 7
DB 467 GYNN 471

```

```

RESULT 36
US 10-002-050-10
: Sequence 10, Application US/2000050
: Publication No. US20030032095A1
: GENERAL INFORMATION:
: APPLICANT: Shimkets, Richard
: APPLICANT: Fernandes, Elma
: APPLICANT: Vernet, Corine
: APPLICANT: Yang, Meijia
: APPLICANT: Holdaq, Ferenc
: APPLICANT: Herrmann, John
: TITLE OF INVENTION: No. US20020151494A1 Nucleic Acid Sequences Encoding Human Semaphorin
: FILE REFERENCE: 15466-554 Data 54 GEN-514
: CURRENT APPLICATION NUMBER: US/10-002-050
: CURRENT FILING DATE: 2001-11-02
: PRIOR APPLICATION NUMBER: 09/604,286
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: 60/140,584
: PRIOR FILING DATE: 1999-06-23
: NUMBER OF SEQ ID NOS: 49
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 10
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
US 10-002-050-10

Query Match 78.1% Score 25; DB 9; Length 411;
Best local Similarity 80.0% Pred. No. 1,2e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GYRN 7
DB 234 GYNN 238

```

```

RESULT 37
US 10-002-304-10
: Sequence 10, Application US/21900204
: Publication No. US20030046185A1
: GENERAL INFORMATION:
: APPLICANT: Shimkets, Richard
: APPLICANT: Fernandes, Elma
: APPLICANT: Vernet, Corine
: APPLICANT: Yang, Meijia
: APPLICANT: Holdaq, Ferenc
: APPLICANT: Herrmann, John
: TITLE OF INVENTION: No. US20020151494A1 Amino Acid Sequences for Human Semaphorin
: FILE REFERENCE: 15466-554 Data 54 GEN-512
: CURRENT APPLICATION NUMBER: US/10-002-304
: CURRENT FILING DATE: 2001-11-02
: PRIOR APPLICATION NUMBER: 09/604,286
: PRIOR FILING DATE: 2000-06-23
: PRIOR APPLICATION NUMBER: 60/140,584
: PRIOR FILING DATE: 1999-06-23
: NUMBER OF SEQ ID NOS: 49
: SOFTWARE: Patent In Ver. 2.0
: SEQ ID NO 10
: LENGTH: 411
: TYPE: PRT
: ORGANISM: Homo sapiens
US 10-002-304-10

Query Match 78.1% Score 25; DB 12; Length 411;
Best local Similarity 80.0% Pred. No. 1,2e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 GYRN 7
DB 234 GYNN 238

```

```

RESULT 39
US-10-118-495-3
: Sequence 3, Application US/10118495
: Publication No. US20030074688A1
: GENERAL INFORMATION:
: APPLICANT: Henning, Christoph

```



```

; APPLICANT: Beckhof, Wayne
; APPLICANT: Kling, Rouven
; TITLE OF INVENTION: Compositions and Methods for the Production of Betaine Lipids
; FILE REFERENCE: US-06697
; CURRENT APPLICATION NUMBER: US/10/118,495
; PRIOR FILING DATE: 2002 04 08
; PRIOR APPLICATION NUMBER: 60/271,412
; PRIOR FILING DATE: 2001-04-13
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 3
; LENGTH: 416
; TYPE: PRT
; ORGANISM: Rhodobacter sphaeroides
US-10-118-495-3

```

```

Query Match      78.1%; Score 25; DB 9; Length 416;
Best Local Similarity 80.0%; Pred. No. 1,2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GYPRN 7
    ||||
DB 167 GYPRH 171

```

RESULT 40

```

; Sequence 81 Application US/06699615
; Patent No. US2002064856A1
; GENERAL INFORMATION:
; APPLICANT: PLOWMAN, GREGORY
; APPLICANT: WHYTE, DAVID
; APPLICANT: CAENEPEEL, SEAN
; APPLICANT: CHAPYDZAK, GLEN
; APPLICANT: MANNING, GERRARD
; APPLICANT: SUDAPSANAN, SUCHA
; TITLE OF INVENTION: NOVEL PROTEASES
; FILE REFERENCE: 038602/1214
; CURRENT APPLICATION NUMBER: US/09/888,615
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: 60/214,047
; PRIOR FILING DATE: 2000-06-26
; NUMBER OF SEQ ID NOS: 150
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 81
; LENGTH: 419
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-888-615-81

```

```

Query Match      78.1%; Score 25; DB 10; Length 419;
Best Local Similarity 80.0%; Pred. No. 1,4e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GYPRN 7
    ||||
DB 114 GYVRS 118

```

RESULT 41

```

US-10-007-271-4
; Sequence 4, Application US/10007271
; Patent No. US20020164766A1
; GENERAL INFORMATION:
; APPLICANT: Bandaru, Rajasekhar
; TITLE OF INVENTION: A NOVEL HUMAN METALLOPROTEINASE
; FILE REFERENCE: 10449-107601
; CURRENT APPLICATION NUMBER: US/10/007,271
; CURRENT FILING DATE: 2001-10-22
; PRIOR APPLICATION NUMBER: 60/242,303
; PRIOR FILING DATE: 2000 10-20
; NUMBER OF SEQ ID NOS: 4

```

```

; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 441
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Consensus sequence
US 10 007 271 4

```

```

Query Match      78.1%; Score 25; DB 9; Length 441;
Best Local Similarity 80.0%; Pred. No. 1,3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

QY 3 GYPRN 7
    ||||
DB 142 GYVRS 146

```

RESULT 42

```

US-10-002-050-20
; Sequence 29, Application US/10002050
; Publication No. US20030042095A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldot, Ferenc
; APPLICANT: Hertmann, John
; TITLE OF INVENTION: NO. US20030042095A1 Nucleic Acid Sequences Encoding Human S
; FILE REFERENCE: 15966 554 Cura 54 C98 814
; CURRENT APPLICATION NUMBER: US/10/052,050
; CURRENT FILING DATE: 2001 11-02
; PRIOR APPLICATION NUMBER: 09/660,286
; PRIOR FILING DATE: 2000-06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999 06-23
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 20
; LENGTH: 464
; TYPE: PRT
; ORGANISM: Homo sapiens
US 10 002-050 20

```

```

Query Match      78.1%; Score 25; DB 9; Length 464;
Best Local Similarity 80.0%; Pred. No. 1,4e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 3 GYPRN 7
    ||||
DB 237 GYVRS 291

```

RESULT 43

```

US 10 002-304-20
; Sequence 29, Application US/10002404
; Publication No. US20030046185A1
; GENERAL INFORMATION:
; APPLICANT: Shimkets, Richard
; APPLICANT: Fernandes, Elma
; APPLICANT: Vernet, Corine
; APPLICANT: Yang, Meijia
; APPLICANT: Boldot, Ferenc
; APPLICANT: Hertmann, John
; TITLE OF INVENTION: Polynucleotides and polypeptides encoded thereby
; FILE REFERENCE: 15966-554 Cura-51 C98-88
; CURRENT APPLICATION NUMBER: US/10/002,404
; CURRENT FILING DATE: 2001-11-02
; PRIOR APPLICATION NUMBER: 09/660,286
; PRIOR FILING DATE: 2000 06-22
; PRIOR APPLICATION NUMBER: 60/140,584
; PRIOR FILING DATE: 1999 06-23

```

: NUMBER OF SEQ ID NOS: 49
 : SOFTWARE: Patent In Ver. 2.0
 : SEQ ID NO: 20
 : LENGTH: 464
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US 10-004-152-20

Query Match 78.1% Score 25; Db 9; Length 464;
 Best Local Similarity 80.0%; Pred. Ro. 1.4e-03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GFYNN 7
 III I
 Db 287 GFYNN 291

RESULT 44
 US-10-004-152-20
 : Sequence 20, Application US/19994162
 : Patent No. US20020151494A1
 : GENERAL INFORMATION:
 : APPLICANT: Shimkets, Richard
 : APPLICANT: Fernandes, Elma
 : APPLICANT: Vernet, Corine
 : APPLICANT: Yang, Mingliu
 : APPLICANT: Boldon, Ferenc
 : APPLICANT: Bergman, John
 : TITLE OF INVENTION: No. 2520220151494A1 Amino Acid Sequences for Human Hemagglutinin

: FILE REFERENCE: 1596-554 CofA-54 CON 312
 : CURRENT APPLICATION NUMBER: 95/18/603,152
 : PRIOR FILING DATE: 2903-11-02
 : PRIOR APPLICATION NUMBER: 69/664,286
 : PRIOR FILING DATE: 2000-06-22
 : PRIOR APPLICATION NUMBER: 60/140,584
 : PRIOR FILING DATE: 1999-06-23
 : NUMBER OF SEQ ID NOS: 49
 : SOFTWARE: Patent In Ver. 2.0
 : SEQ ID NO: 20
 : LENGTH: 464
 : TYPE: PRT
 : ORGANISM: Homo sapiens
 US-10-004-152-20

Query Match 78.1% Score 25; Db 9; Length 464;
 Best Local Similarity 80.0%; Pred. Ro. 1.4e-03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 GFYNN 7
 III I
 Db 287 GFYNN 291

RESULT 45
 US-09-498-29FA-114
 : Sequence 114, Application US/19994162
 : Patent No. US20020156096A1
 : GENERAL INFORMATION:
 : APPLICANT: Ashkenazi, Avi
 : APPLICANT: Parker, Kevin L.
 : APPLICANT: Botstein, David
 : APPLICANT: Desnovers, Luc
 : APPLICANT: Eaton, Dan
 : APPLICANT: Ferrara, Napoleon
 : APPLICANT: Filvaroff, Ellen
 : APPLICANT: Fong, Sherman
 : APPLICANT: Gao, Weigang
 : APPLICANT: Gerber, Hanspeter
 : APPLICANT: Gerritsen, Mary B.
 : APPLICANT: Goddard, Audrey
 : APPLICANT: Godowski, Paul J.
 : APPLICANT: Grimaldi, J. Christopher
 : APPLICANT: Gurney, Austin L.

: APPLICANT: Billam, Kenneth J.
 : APPLICANT: Klijver, Ivar J.
 : APPLICANT: Kuo, Sophia S.
 : APPLICANT: Napier, Mary A.
 : APPLICANT: Pan, James
 : APPLICANT: Pao, Nicholas F.
 : APPLICANT: Roy, Margaret Ann
 : APPLICANT: Shelton, David L.
 : APPLICANT: Stewart, Timothy A.
 : APPLICANT: Tumas, Daniel
 : APPLICANT: Williams, P. Mickey
 : APPLICANT: Wood, William L.
 : TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 : FILE REFERENCE: P2640PLC11 63/067,479,245A
 : CURRENT APPLICATION NUMBER: 09/077641
 : PRIOR FILING DATE: 2001-10-15
 : PRIOR APPLICATION NUMBER: 09/918585
 : PRIOR FILING DATE: 2001-07-30
 : PRIOR APPLICATION NUMBER: 69/966,250
 : PRIOR FILING DATE: 1997-10-17
 : PRIOR APPLICATION NUMBER: 69/964,249
 : PRIOR FILING DATE: 1997-11-04
 : PRIOR APPLICATION NUMBER: 69/065,411
 : PRIOR FILING DATE: 1997-11-14
 : PRIOR APPLICATION NUMBER: 69/066,464
 : PRIOR FILING DATE: 1997-11-21
 : PRIOR APPLICATION NUMBER: 69/077,649
 : PRIOR FILING DATE: 1998-04-11
 : PRIOR APPLICATION NUMBER: 69/077,791
 : PRIOR FILING DATE: 1998-04-12
 : PRIOR APPLICATION NUMBER: 69/078,004
 : PRIOR FILING DATE: 1998-04-14
 : PRIOR APPLICATION NUMBER: 69/078,886
 : PRIOR FILING DATE: 1998-04-20
 : PRIOR APPLICATION NUMBER: 69/078,946
 : PRIOR FILING DATE: 1998-04-20
 : PRIOR APPLICATION NUMBER: 69/078,910
 : PRIOR FILING DATE: 1998-04-20
 : PRIOR APPLICATION NUMBER: 69/078,949
 : PRIOR FILING DATE: 1998-04-20
 : PRIOR APPLICATION NUMBER: 69/079,294
 : PRIOR FILING DATE: 1998-04-25
 : PRIOR APPLICATION NUMBER: 69/079,656
 : PRIOR FILING DATE: 1998-04-26
 : PRIOR APPLICATION NUMBER: 69/079,664
 : PRIOR FILING DATE: 1998-04-27
 : PRIOR APPLICATION NUMBER: 69/079,689
 : PRIOR FILING DATE: 1998-04-27
 : PRIOR APPLICATION NUMBER: 69/079,664
 : PRIOR FILING DATE: 1998-04-27
 : PRIOR APPLICATION NUMBER: 69/079,728
 : PRIOR FILING DATE: 1998-04-27
 : PRIOR APPLICATION NUMBER: 69/079,786
 : PRIOR FILING DATE: 1998-04-27
 : PRIOR APPLICATION NUMBER: 69/079,920
 : PRIOR FILING DATE: 1998-04-30
 : PRIOR APPLICATION NUMBER: 69/079,924
 : PRIOR FILING DATE: 1998-04-30
 : PRIOR APPLICATION NUMBER: 69/080,195
 : PRIOR FILING DATE: 1998-04-31
 : PRIOR APPLICATION NUMBER: 69/080,107
 : PRIOR FILING DATE: 1998-04-31
 : PRIOR APPLICATION NUMBER: 69/080,165
 : PRIOR FILING DATE: 1998-04-31
 : PRIOR APPLICATION NUMBER: 69/080,194
 : PRIOR FILING DATE: 1998-04-31

PRIOR APPLICATION NUMBER: 60/080327
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080329
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080333
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/080334
 PRIOR FILING DATE: 1998-04-01
 PRIOR APPLICATION NUMBER: 60/081070
 PRIOR FILING DATE: 1998-04-06
 PRIOR APPLICATION NUMBER: 60/081349
 PRIOR FILING DATE: 1998-04-06
 PRIOR APPLICATION NUMBER: 60/081071
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081195
 PRIOR FILING DATE: 1998-04-08
 PRIOR APPLICATION NUMBER: 60/081203
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081329
 PRIOR FILING DATE: 1998-04-09
 PRIOR APPLICATION NUMBER: 60/081955
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081817
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081819
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081952
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/081838
 PRIOR FILING DATE: 1998-04-15
 PRIOR APPLICATION NUMBER: 60/082569
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082569
 PRIOR FILING DATE: 1998-04-21
 PRIOR APPLICATION NUMBER: 60/082704
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082804
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082700
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082797
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/082796
 PRIOR FILING DATE: 1998-04-22
 PRIOR APPLICATION NUMBER: 60/083336
 PRIOR FILING DATE: 1998-04-27
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083495
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083496
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083499
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083545
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083554
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083558
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083559
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083500
 PRIOR FILING DATE: 1998-04-29
 PRIOR APPLICATION NUMBER: 60/083742
 PRIOR FILING DATE: 1998-04-30
 PRIOR APPLICATION NUMBER: 60/084366
 PRIOR FILING DATE: 1998-05-05
 PRIOR APPLICATION NUMBER: 60/084414
 PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084441

PRIOR FILING DATE: 1998-05-06
 PRIOR APPLICATION NUMBER: 60/084637
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084639
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084640
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084598
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084627
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/084643
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/085339
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085338
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085333
 PRIOR FILING DATE: 1998-05-13
 PRIOR APPLICATION NUMBER: 60/085382
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085700
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085689
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085779
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085580
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match: 78.1%, Score 25, DB 9, Length 515;
 Best Local Similarity: 80.0%, Prod. No. 1.5e+03;
 Matches: 4, Connections: 0, Mismatches: 1, Index: 5, Gaps: 0;

0Y 3 CYRN 7
 III I
 34 415 SEVEN 319

Search completed: April 30, 2003, 13:44:59
 Job time: 51.2727 secs



395	9	81.8	52	1	RVBOMA	stable plasmid inh	468	9	81.8	55	2	A56204	hypothetical prote
396	9	81.8	52	2	SL9416	chlorophyll a/b-bi	469	9	81.8	55	1	RV0064	hypothetical OR pr
397	9	81.8	52	2	S60401	kok protein - Esch	470	9	81.8	56	2	CR0006	cytochrome bcd co
398	9	81.8	52	2	PR0481	cell division cycl	471	9	81.8	56	2	P00819	probable tropomoe
399	9	81.8	52	2	PR5124	hypothetical prote	472	9	81.8	56	2	Q20295	SMAD2 dehydrogen
400	9	81.8	52	2	P03006	hypothetical prote	473	9	81.8	56	2	P01996	protein tyrosine k
401	9	81.8	52	2	G82496	hypothetical prote	474	9	81.8	56	2	151161	protein tyrosine k
402	9	81.8	52	2	170527	cystic fibrosis tr	475	9	81.8	56	2	155300	protein tyrosine k
403	9	81.8	52	2	Q60062	hypothetical prote	476	9	81.8	56	2	P01440	concomit third d
404	9	81.8	52	2	RP9987	hypothetical prote	477	9	81.8	56	2	S46432	55 heavy chain V r
405	9	81.8	52	2	A07995	hypothetical prote	478	9	81.8	56	2	AG1135	ribosomal protein
406	9	81.8	52	2	A06078	hypothetical prote	479	9	81.8	56	2	A11493	ribosomal protein
407	9	81.8	52	2	AF0703	hypothetical prote	480	9	81.8	56	2	Q30241	52.2' 3' rns 1 - p
408	9	81.8	52	2	A01980	transposase asloep	481	9	81.8	56	2	Q63424	protein kinase A1
409	9	81.8	52	2	A02556	hypothetical prote	482	9	81.8	56	2	Q97400	hypothetical prote
410	9	81.8	52	2	A12499	hypothetical prote	483	9	81.8	56	2	B84079	hypothetical prote
411	9	81.8	52	2	S77965	ribosomal protein	484	9	81.8	56	2	Q81042	hypothetical prote
412	9	81.8	52	2	S22125	gene K protein p	485	9	81.8	56	2	Q34739	hypophthal proteol
413	9	81.8	52	2	S18013	protein-tyrosine k	486	9	81.8	56	2	Q72610	hypothetical prote
414	9	81.8	52	2	S18014	protein-tyrosine k	487	9	81.8	56	2	Q72613	hypothetical prote
415	9	81.8	52	2	Q90872	hypothetical prote	488	9	81.8	56	2	Q71256	hypothetical prote
416	9	81.8	52	2	A06462	hypothetical prote	489	9	81.8	56	2	H82647	hypothetical prote
417	9	81.8	52	2	Q42634	hypothetical prote	490	9	81.8	56	2	A07816	hypothetical prote
418	9	81.8	52	2	RP1221	hypothetical prote	491	9	81.8	56	2	Q97368	probable P11Ac fil
419	9	81.8	52	2	Q59105	hypothetical 5.8K	492	9	81.8	56	2	AB0071	hypothetical prote
420	9	81.8	52	2	Q42975	finger protein (el	493	9	81.8	56	2	AB0202	hypothetical prote
421	9	81.8	52	2	142384	cine finger protei	494	9	81.8	56	2	AF2153	hypothetical prote
422	9	81.8	52	2	149721	hypothetical prote	495	9	81.8	56	2	Q10199	protein tyrosine k
423	9	81.8	52	2	Q62813	hypothetical prote	496	9	81.8	56	2	Q16193	protein tyrosine k
424	9	81.8	52	2	RP2412	hypothetical prote	497	9	81.8	56	2	Q10187	protein tyrosine k
425	9	81.8	52	2	RP5745	unknown protein ch	498	9	81.8	56	2	Q10188	protein tyrosine k
426	9	81.8	52	2	A00095	hypothetical prote	499	9	81.8	56	2	Q42727	protein tyrosine k
427	9	81.8	52	2	AB1981	hypothetical prote	500	9	81.8	56	2	Q42724	relaxin - dnf11a
428	9	81.8	52	2	A01148	hypothetical prote	501	9	81.8	56	2	H00879	1a kappa chain V r
429	9	81.8	52	2	Q97458	hypothetical prote	502	9	81.8	56	2	Q84213	40S ribosomal prot
430	9	81.8	52	2	A02676	hypothetical prote	503	9	81.8	56	2	Q84214	40S ribosomal prot
431	9	81.8	52	2	A54777	ribM protein - Esc	504	9	81.8	56	2	Q84977	alpha-actinin-2
432	9	81.8	52	2	Q01994	protein tyrosine k	505	9	81.8	56	2	Q10198	carbon storage req
433	9	81.8	52	2	S44965	H+ transporting tw	506	9	81.8	56	2	Q10198	protein tyrosine k
434	9	81.8	52	2	RP1493	ovomacoid (PST) ty	507	9	81.8	56	2	B84366	hypothetical prote
435	9	81.8	52	2	Q03019	hemolysin Proteu	508	9	81.8	56	2	Q10380	hypothetical prote
436	9	81.8	52	2	S45255	YjIX protein homol	509	9	81.8	56	2	Q81226	hypothetical prote
437	9	81.8	52	2	Q17552	protein-tyrosine k	510	9	81.8	56	2	Q64051	hypothetical prote
438	9	81.8	52	2	Q20836	BipA-like protein	511	9	81.8	56	2	Q64052	hypothetical prote
439	9	81.8	52	2	AB1943	hypothetical prote	512	9	81.8	56	2	Q64183	hypothetical prote
440	9	81.8	52	2	140144	filamentous hemag	513	9	81.8	56	2	Q82787	hypothetical prote
441	9	81.8	52	2	Q97125	hypothetical prote	514	9	81.8	56	2	A02708	hypothetical prote
442	9	81.8	52	2	A02784	hypothetical prote	515	9	81.8	56	2	Q95869	hypothetical prote
443	9	81.8	52	2	Q10186	protein tyrosine k	516	9	81.8	56	2	Q97813	hypothetical prote
444	9	81.8	52	2	Q66426	ubiquitin/ribosoma	517	9	81.8	56	2	Q97827	(P) pppGpp-3-phosph
445	9	81.8	52	2	Q20430	calcasulin - koi	518	9	81.8	56	2	AF0934	hypothetical prote
446	9	81.8	52	2	S70224	probable membrane	519	9	81.8	56	2	Q97499	hypothetical prote
447	9	81.8	52	2	S44415	hemostatic protein z	520	9	81.8	56	2	Q22746	hypothetical prote
448	9	81.8	52	2	Q95993	hypothetical prote	521	9	81.8	56	2	Q77991	probable 4-phospho
449	9	81.8	52	2	Q91155	hypothetical prote	522	9	81.8	56	2	Q48663	pyruvate kinase (E
450	9	81.8	52	2	A09563	hypothetical prote	523	9	81.8	56	2	Q45111	histone H3 - mouse
451	9	81.8	52	2	Q67333	hypothetical prote	524	9	81.8	56	2	Q71604	ribosomal protein
452	9	81.8	52	2	Q60452	hypothetical prote	525	9	81.8	56	2	A14284	cine finger proteol
453	9	81.8	52	2	140115	filamentous hemag	526	9	81.8	56	2	Q91110	hypothetical prote
454	9	81.8	52	2	170577	amber mutation sup	527	9	81.8	56	2	Q91284	hypothetical prote
455	9	81.8	52	2	Q69993	hypothetical prote	528	9	81.8	56	2	Q97423	hypothetical prote
456	9	81.8	52	2	Q24144	hypothetical prote	529	9	81.8	56	2	Q97457	hypothetical prote
457	9	81.8	52	2	Q33915	hypothetical prote	530	9	81.8	56	2	Q86974	conserved hypethet
458	9	81.8	52	2	S44331	sox protein less	531	9	81.8	56	2	Q84389	hypothetical prote
459	9	81.8	52	2	Q41500	hypothetical prote	532	9	81.8	56	2	Q84384	hypothetical prote
460	9	81.8	52	2	Q82845	hypothetical prote	533	9	81.8	56	2	Q34575	gene 72 protein
461	9	81.8	52	2	AB2482	hypothetical prote	534	9	81.8	56	2	Q84359	hypothetical prote
462	9	81.8	52	2	Q82960	hypothetical prote	535	9	81.8	56	2	Q82970	hypothetical prote
463	9	81.8	52	2	Q82584	hypothetical prote	536	9	81.8	56	2	Q75890	hypothetical prote
464	9	81.8	52	2	Q86601	hypothetical prote	537	9	81.8	56	2	Q69940	hypothetical prote
465	9	81.8	52	2	AB0174	probable ribosome	538	9	81.8	56	2	Q69092	conserved hypethet
466	9	81.8	52	2	AF0178	hypothetical prote	539	9	81.8	56	2	177464	10' of 12S rRNA
467	9	81.8	52	2	AB1592	conserved hypethet	540	9	81.8	56	2	Q71299	hypothetical prote

541	9	81.8	58	58	2	A97246	hypothetical prote	614	9	81.8	61	2	D87531	carbon storage res
542	9	81.8	58	58	2	A82104	hypothetical prote	615	9	81.8	61	2	A91873	glycogen biosynth
543	9	81.8	58	58	2	A12072	hypothetical prote	616	9	81.8	61	2	A90401	carbon storage res
544	9	81.8	59	1	PCSH	pancreatic hormone	617	9	81.8	61	2	AF0843	carbon storage res	
545	9	81.8	59	1	ERRP1A	gene 1A protein	618	9	81.8	61	2	D87517	glycogen biosynth	
546	9	81.8	59	1	P92202	isoleucyl-tRNA synthetase	619	9	81.8	61	2	A22125	hypothetical prote	
547	9	81.8	59	2	C90820	50S ribosomal prot	620	9	81.8	61	2	P61524	tRNA-dependent RNA	
548	9	81.8	59	2	S30858	preprotein translo	621	9	81.8	61	2	B24780	homeotic protein 1	
549	9	81.8	59	2	P92369	homeotic protein 2	622	9	81.8	61	2	S70123	platelet kinase AK1	
550	9	81.8	59	2	P96252	hypothetical prote	623	9	81.8	61	2	P66539	hypothetical prote	
551	9	81.8	59	2	A84485	protein p28-9.16	624	9	81.8	61	2	JP0450	hypothetical prote	
552	9	81.8	59	2	B82471	hypothetical prote	625	9	81.8	61	2	S10105	ap65 protein - pha	
553	9	81.8	59	2	B82466	hypothetical prote	626	9	81.8	61	2	A91781	probable membrane	
554	9	81.8	59	2	A84161	hypothetical prote	627	9	81.8	61	2	S11642	hypothetical prote	
555	9	81.8	59	2	D81159	hypothetical prote	628	9	81.8	61	2	P75521	hypothetical prote	
556	9	81.8	59	2	H71570	hypothetical prote	629	9	81.8	61	2	S75321	hypothetical prote	
557	9	81.8	59	2	P96299	hypothetical prote	630	9	81.8	61	2	P75821	hypothetical prote	
558	9	81.8	59	2	P77115	probable transpasa	631	9	81.8	61	2	B64196	hypothetical prote	
559	9	81.8	59	2	A69520	hypothetical prote	632	9	81.8	61	2	A63470	hypothetical prote	
560	9	81.8	59	2	P97524	hypothetical prote	633	9	81.8	61	2	A27743	tRNA-binding protei	
561	9	81.8	59	2	A43218	carboxyl ester lip	634	9	81.8	61	2	S11630	hypothetical prote	
562	9	81.8	59	2	A39388	centromere specif	635	9	81.8	61	2	S21248	insulin related pe	
563	9	81.8	59	2	A81751	conserved hypotet	636	9	81.8	61	2	P59337	mammalian translat	
564	9	81.8	59	2	C72663	hypothetical prote	637	9	81.8	61	2	T07243	hypothetical prote	
565	9	81.8	59	2	D72674	hypothetical prote	638	9	81.8	61	2	P72084	hypothetical prote	
566	9	81.8	59	2	B87706	hypothetical prote	639	9	81.8	61	2	P82769	hypothetical prote	
567	9	81.8	59	2	D82615	hypothetical prote	640	9	81.8	61	2	T26764	hypothetical prote	
568	9	81.8	59	2	C94785	hypothetical prote	641	9	81.8	61	2	A13428	hypothetical prote	
569	9	81.8	59	2	A81250	probable transp	642	9	81.8	61	2	Q81343	hypothetical prote	
570	9	81.8	59	2	A82319	hypothetical prote	643	9	81.8	61	2	A12095	hypothetical prote	
571	9	81.8	60	1	T59P2V	short toxin 2 - wo	644	9	81.8	62	1	R5934F	ribosomal protein	
572	9	81.8	60	1	T59P2J	short toxin 2 homo	645	9	81.8	62	1	C98308	cell division inhi	
573	9	81.8	60	2	S35029	pyruvate kinase (P	646	9	81.8	62	1	C98308	cell division inhi	
574	9	81.8	60	2	S01800	pepsin (B3.4.21.	647	9	81.8	62	1	DW0P44	tRNA-binding protei	
575	9	81.8	60	2	P68870	interleukin 2 - we	648	9	81.8	62	2	T43401	interleukin 2 - mo	
576	9	81.8	60	2	P68744	integral membrane	649	9	81.8	62	2	A95922	ribosomal protein	
577	9	81.8	60	2	S65709	homeotic protein e	650	9	81.8	62	2	A95919	hypothetical prote	
578	9	81.8	60	2	P92390	actinopodia like	651	9	81.8	62	2	C93761	cell division	
579	9	81.8	60	2	P92400	actinopodia like	652	9	81.8	62	2	C93761	cell division	
580	9	81.8	60	2	S14797	homeotic protein h	653	9	81.8	62	2	P92905	inhibitor of cell	
581	9	81.8	60	2	S36771	homeotic protein h	654	9	81.8	62	2	S65944	homeotic protein e	
582	9	81.8	60	2	S36770	homeotic protein e	655	9	81.8	62	2	S65945	homeotic protein e	
583	9	81.8	60	2	S13012	homeotic protein e	656	9	81.8	62	2	S65916	homeotic protein e	
584	9	81.8	60	2	S13013	homeotic protein e	657	9	81.8	62	2	S65922	homeotic protein e	
585	9	81.8	60	2	C37290	homeotic protein h	658	9	81.8	62	2	H45186	homeotic protein g	
586	9	81.8	60	2	C37290	homeotic protein h	659	9	81.8	62	2	H45186	homeotic protein g	
587	9	81.8	60	2	S13137	homeotic protein g	660	9	81.8	62	2	A15187	homeotic protein g	
588	9	81.8	60	2	S13290	homeotic protein h	661	9	81.8	62	2	B32391	homeotic protein h	
589	9	81.8	60	2	S18301	homeotic protein e	662	9	81.8	62	2	C96925	probable DNA bindi	
590	9	81.8	60	2	S43515	tyrosine kinase	663	9	81.8	62	2	H90974	proliferative cell divi	
591	9	81.8	60	2	H97593	hypothetical prote	664	9	81.8	62	2	A98181	hypothetical prote	
592	9	81.8	60	2	P72867	Ad5-f-145 protein	665	9	81.8	62	2	C95551	ribosomal protein	
593	9	81.8	60	2	A36855	ribosomal protein	666	9	81.8	62	2	H95342	ribosomal protein	
594	9	81.8	60	2	A81061	ribosomal protein	667	9	81.8	62	2	H95342	ribosomal protein	
595	9	81.8	60	2	P94477	hypothetical prote	668	9	81.8	62	2	B84394	hypothetical prote	
596	9	81.8	60	2	P94477	hypothetical prote	669	9	81.8	62	2	E72279	hypothetical prote	
597	9	81.8	60	2	B82478	hypothetical prote	670	9	81.8	62	2	D81156	hypothetical prote	
598	9	81.8	60	2	B82465	hypothetical prote	671	9	81.8	62	2	S66174	in FM protein - Ent	
599	9	81.8	60	2	S57322	ferredoxin biosynth	672	9	81.8	62	2	S66174	hypothetical prote	
600	9	81.8	60	2	J70512	lg heavy chain V1	673	9	81.8	62	2	S71359	hypothetical prote	
601	9	81.8	60	2	P77735	hypothetical prote	674	9	81.8	62	2	A26828	cytochrome synthet	
602	9	81.8	60	2	C72247	hypothetical prote	675	9	81.8	62	2	T11140	chromosomal lysase CM	
603	9	81.8	60	2	P83515	hypothetical prote	676	9	81.8	62	2	T11140	hypothetical prote	
604	9	81.8	60	2	P97562	hypothetical prote	677	9	81.8	62	2	P92733	larger protein Kzo	
605	9	81.8	60	2	A05783	hypothetical prote	678	9	81.8	62	2	P92733	larger protein Kzo	
606	9	81.8	60	2	A03257	hypothetical prote	679	9	81.8	62	2	P92733	larger protein Kzo	
607	9	81.8	60	2	A23227	hypothetical prote	680	9	81.8	62	2	P92733	larger protein Kzo	
608	9	81.8	61	1	DW0PBF	DNA-binding protei	681	9	81.8	62	2	B72564	conserved hypotet	
609	9	81.8	61	1	P40609	glycogen biosynth	682	9	81.8	62	2	C84846	hypothetical prote	
610	9	81.8	61	2	S65438	allophycocyanin b	683	9	81.8	62	2	C84846	hypothetical prote	
611	9	81.8	61	2	S15531	serpin S615 (clon	684	9	81.8	62	2	H87634	hypothetical prote	
612	9	81.8	61	2	S39425	protamine P1 - duc	685	9	81.8	62	2	P97502	hypothetical prote	
613	9	81.8	61	2	T39834	ribosomal protein	686	9	81.8	62	2	A92840	hypothetical prote	

687	9	81.8	62	2	647674	hypothetical prote	769	9	81.8	65	2	693876	hypothetical prote
688	9	81.8	63	1	S67074	ribosomal protein	761	9	81.8	65	2	683727	hypothetical prote
689	9	81.8	63	1	R6P07F	regulatory protein	762	9	81.8	65	2	E82547	hypothetical prote
690	9	81.8	63	1	H6406s	carbon storage res	763	9	81.8	65	2	E57042	hypothetical prote
691	9	81.8	63	2	T16628	hypothetical prote	764	9	81.8	65	2	E97206	hypothetical prote
692	9	81.8	63	2	I49584	gene CD38 protein	765	9	81.8	65	2	A95405	cytochrome c bindi
693	9	81.8	63	2	I41452	probable protein t	766	9	81.8	65	2	E98316	hypothetical prote
694	9	81.8	63	2	S32731	hemectic protein t	767	9	81.8	65	2	A22666	hypothetical prote
695	9	81.8	63	2	A70896	probable f8d prot	768	9	81.8	66	1	I323	pancreatic hormone
696	9	81.8	63	2	E62945	hypothetical prote	769	9	81.8	66	1	DNVFB	DNA binding protei
697	9	81.8	63	2	I35067	hypothetical prote	770	9	81.8	66	1	C4BP1	gene c4 protein
698	9	81.8	63	2	S43041	hypothetical prote	771	9	81.8	66	2	A26550	histone H4 - beta
699	9	81.8	63	2	I29202	hypothetical prote	772	9	81.8	66	2	E97979	50S ribosomal prot
700	9	81.8	63	2	T16278	hypothetical prote	773	9	81.8	66	2	A37365	myosin heavy chain
701	9	81.8	63	2	A45194	zinc finger protei	774	9	81.8	66	2	S61083	M protein precursor
702	9	81.8	63	2	I40614	hypothetical prote	775	9	81.8	66	2	C72153	P11 protein vari
703	9	81.8	63	2	H40492	hypothetical prote	776	9	81.8	66	2	A46839	c11 protein vari
704	9	81.8	63	2	E82584	hypothetical prote	777	9	81.8	66	2	I28459	hypothetical prote
705	9	81.8	63	2	H82561	hypothetical prote	778	9	81.8	66	2	PH0946	superoxide dis M19
706	9	81.8	63	2	AF0944	probable membrane	779	9	81.8	66	2	S15542	hemectic protein H
707	9	81.8	63	2	AI3942	hypothetical prote	780	9	81.8	66	2	S15146	hemectic protein H
708	9	81.8	63	2	A22191	hypothetical prote	781	9	81.8	66	2	S45186	hemectic protein H
709	9	81.8	63	2	A22115	hypothetical prote	782	9	81.8	66	2	S15538	hemectic protein H
710	9	81.8	64	1	WW0210	p7a protein - toba	783	9	81.8	66	2	S15534	hemectic protein H
711	9	81.8	64	1	Q1BP2L	hypothetical prote	784	9	81.8	66	2	S14929	hemectic protein H
712	9	81.8	64	1	B69017	conserved hypotet	785	9	81.8	66	2	B63947	hemectic protein H
713	9	81.8	64	2	E83664	preprotein translo	786	9	81.8	66	2	C60941	hemectic protein H
714	9	81.8	64	2	F71892	1666 transposase	787	9	81.8	66	2	S14941	hemectic protein H
715	9	81.8	64	2	C95039	transcription requ	788	9	81.8	66	2	S14948	hemectic protein H
716	9	81.8	64	2	C87511	hypothetical prote	789	9	81.8	66	2	A00941	hemectic protein H
717	9	81.8	64	2	E87344	protein T20H2.14	790	9	81.8	66	2	H95110	ribosomal protein
718	9	81.8	64	2	C48555	hypothetical prote	791	9	81.8	66	2	C90793	hypothetical prote
719	9	81.8	64	2	B42456	hypothetical prote	792	9	81.8	66	2	C91120	glycogen biosynthe
720	9	81.8	64	2	H75270	transcription requ	793	9	81.8	66	2	F91253	translational requ
721	9	81.8	64	2	C92749	DNA binding protei	794	9	81.8	66	2	H67327	hypothetical prote
722	9	81.8	64	2	C92843	hypothetical prote	795	9	81.8	66	2	JT0456	hypothetical prote
723	9	81.8	64	2	E95303	conserved hypotet	796	9	81.8	66	2	I27941	hypothetical prote
724	9	81.8	64	2	E97909	transcription requ	797	9	81.8	66	2	I28327	hypothetical prote
725	9	81.8	64	2	A50919	hypothetical prote	798	9	81.8	66	2	I33559	conserved hypotet
726	9	81.8	64	2	A20427	probable exported	799	9	81.8	66	2	S44543	hypothetical prote
727	9	81.8	64	2	A72891	hypothetical prote	800	9	81.8	66	2	I27363	B22 protein - Rho
728	9	81.8	64	2	A22277	hypothetical prote	801	9	81.8	66	2	A61135	hypothetical prote
729	9	81.8	65	1	VHRV08	nucleosupid prote	802	9	81.8	66	2	I07496	hypothetical prote
730	9	81.8	65	2	H47365	myosin heavy chain	803	9	81.8	66	2	PH3695	transcription requ
731	9	81.8	65	2	S08636	core antigen (clon	804	9	81.8	66	2	E97074	probable membrane
732	9	81.8	65	2	S06078	core antigen (clon	805	9	81.8	66	2	E97733	hypothetical prote
733	9	81.8	65	2	E92798	carbon storage res	806	9	81.8	66	2	A19248	hypothetical prote
734	9	81.8	65	2	H90902	hypothetical prote	807	9	81.8	66	2	AF3493	hypothetical cytos
735	9	81.8	65	2	A87332	hypothetical prote	808	9	81.8	66	2	S45201	glycogen synthet
736	9	81.8	65	2	H84400	hypothetical prote	809	9	81.8	66	2	AF1869	hypothetical prote
737	9	81.8	65	2	G84412	hypothetical prote	810	9	81.8	67	2	A38226	cAMP dependent pro
738	9	81.8	65	2	E11721	hypothetical prote	811	9	81.8	67	2	C33341	complement c4 prot
739	9	81.8	65	2	T18040	hypothetical prote	812	9	81.8	67	2	S43442	complement c4 prot
740	9	81.8	65	2	I18170	hypothetical prote	813	9	81.8	67	2	C48716	glycine transpore
741	9	81.8	65	2	F81887	hypothetical prote	814	9	81.8	67	2	S45258	gamma protein hemol
742	9	81.8	65	2	A18900	hypothetical prote	815	9	81.8	67	2	R27471	hemectic protein k
743	9	81.8	65	2	E81123	hypothetical prote	816	9	81.8	67	2	JH0117	protein tyrosine k
744	9	81.8	65	2	A21382	hypothetical prote	817	9	81.8	67	2	I48657	alpha nsk1 protein
745	9	81.8	65	2	C82339	hypothetical prote	818	9	81.8	67	2	E70929	probable ferredoxi
746	9	81.8	65	2	C92290	hypothetical prote	819	9	81.8	67	2	A86663	hypothetical prote
747	9	81.8	65	2	A82240	hypothetical prote	820	9	81.8	67	2	C92193	hypothetical prote
748	9	81.8	65	2	A82074	hypothetical prote	821	9	81.8	67	2	A23447	hypothetical prote
749	9	81.8	65	2	S75246	hypothetical prote	822	9	81.8	67	2	C92070	conserved hypotet
750	9	81.8	65	2	C96269	conserved hypotet	823	9	81.8	67	2	PH2907	hypothetical prote
751	9	81.8	65	2	A75543	transcription requ	824	9	81.8	67	2	E63439	type III export pr
752	9	81.8	65	2	S29676	gamma protein - bac	825	9	81.8	67	2	AF1189	hypothetical prote
753	9	81.8	65	2	I40334	hypothetical prote	826	9	81.8	67	2	S70802	cell protein IV
754	9	81.8	65	2	I34636	hypothetical prote	827	9	81.8	67	2	C75497	hypothetical prote
755	9	81.8	65	2	I29346	hypothetical prote	828	9	81.8	67	2	H55008	ribosomal protein
756	9	81.8	65	2	F48279	hypothetical prote	829	9	81.8	67	2	C75544	hypothetical prote
757	9	81.8	65	2	C18671	hypothetical prote	830	9	81.8	67	2	C59098	hypothetical prote
758	9	81.8	65	2	I15856	hypothetical prote	831	9	81.8	67	2	H69946	hypothetical prote
759	9	81.8	65	2	C72558	hypothetical prote	832	9	81.8	67	2	T00991	hypothetical prote

833	9	81.8	67	2	F81618	hypothetical prote	906	9	81.8	69	2	D72645	hypothetical prote
834	9	81.8	67	2	F71150	hypothetical prote	907	9	81.8	69	2	A71363	hypothetical prote
835	9	81.8	67	2	G97724	hypothetical prote	908	9	81.8	69	2	E58726	hypothetical prote
836	9	81.8	67	2	H95905	hypothetical prote	909	9	81.8	69	2	F95914	hypothetical prote
837	9	81.8	67	2	H95419	hypothetical prote	910	9	81.8	69	2	H95925	hypothetical prote
838	9	81.8	67	2	F95772	hypothetical prote	911	9	81.8	69	2	A80255	hypothetical prote
839	9	81.8	67	2	A90891	glycogen synthetis	912	9	81.8	69	2	A15559	archaeal histone H
840	9	81.8	67	2	D98266	hypothetical prote	913	9	81.8	69	2	A15536	histone-related pr
841	9	81.8	67	2	H98133	hypothetical prote	914	9	81.8	69	2	T48848	histone Hmf1 (unp
842	9	81.8	67	2	A82154	conserved hypotet	915	9	81.8	69	2	C97581	hypothetical prote
843	9	81.8	67	2	AE3018	hypothetical prote	916	9	81.8	69	2	AC4576	hypothetical memb
844	9	81.8	67	2	AH3561	hypothetical prote	917	9	81.8	69	2	AG4377	hypothetical prote
845	9	81.8	67	2	AE2243	hypothetical prote	918	9	81.8	69	4	WH3741	hypothetical memb
846	9	81.8	68	1	O6HSNB	hypothetical prote	919	9	81.8	70	2	P04087	adenylate kinase (
847	9	81.8	68	1	R60735	PBSX prophage ORF	920	9	81.8	70	2	C96555	protein epsilon su
848	9	81.8	68	2	P01055	RNA-directed RNA p	921	9	81.8	70	2	E17493	RNA-transcripting tw
849	9	81.8	68	2	T50465	hypothetical prote	922	9	81.8	70	2	A45316	RNA-binding chara Y A
850	9	81.8	68	2	H50122	ribosomal protein	923	9	81.8	70	2	B45186	homocysteine-protein G
851	9	81.8	68	2	P46580	40S ribosomal prot	924	9	81.8	70	2	P29957	glycoprotein B9F12
852	9	81.8	68	2	H55682	keratin 16, type I	925	9	81.8	70	2	P00856	glycoprotein B9F12
853	9	81.8	68	2	S50797	RNA-protease	926	9	81.8	70	2	P00855	glycoprotein B9F12
854	9	81.8	68	2	R42677	hypothetical prote	927	9	81.8	70	2	P00858	glycoprotein B9F12
855	9	81.8	68	2	S18701	tau protein - Bact	928	9	81.8	70	2	T41375	P10 or1147 - Bomby
856	9	81.8	68	2	G97474	hypothetical prote	929	9	81.8	70	2	S02197	PK protein - Fat
857	9	81.8	68	2	T18018	hypothetical prote	930	9	81.8	70	2	T46407	hypothetical prote
858	9	81.8	68	2	J22305	hypothetical prote	931	9	81.8	70	2	E70985	hypothetical prote
859	9	81.8	68	2	G72270	hypothetical prote	932	9	81.8	70	2	S51356	TMF kinase - Therm
860	9	81.8	68	2	S33581	hypothetical prote	933	9	81.8	70	2	S48885	RNA-directed RNA p
861	9	81.8	68	2	D83137	hypothetical prote	934	9	81.8	70	2	S28932	RNA-directed RNA p
862	9	81.8	68	2	H81779	probable transcrip	935	9	81.8	70	2	E45186	homocysteine-protein G
863	9	81.8	68	2	T42852	hypothetical prote	936	9	81.8	70	2	G47186	homocysteine-protein G
864	9	81.8	68	2	H82124	heme exporter prot	937	9	81.8	70	2	E47042	homocysteine-protein H
865	9	81.8	68	2	P03158	transcription regu	938	9	81.8	70	2	G90732	hypothetical prote
866	9	81.8	68	2	H59098	hypothetical prote	939	9	81.8	70	2	G90478	hypothetical prote
867	9	81.8	68	2	T39638	probable metal hom	940	9	81.8	70	2	D84174	hypothetical prote
868	9	81.8	68	2	S78710	protein YH0850a	941	9	81.8	70	2	J20103	hypothetical RSK
869	9	81.8	68	2	R44947	filamentous repetit	942	9	81.8	70	2	E27522	hypothetical prote
870	9	81.8	68	2	S70751	MCP-1 protein spl	943	9	81.8	70	2	P61899	hypothetical prote
871	9	81.8	68	2	E82779	hypothetical prote	944	9	81.8	70	2	E47080	hypothetical prote
872	9	81.8	68	2	C85965	glycogen biosynthe	945	9	81.8	70	2	E77433	hypothetical prote
873	9	81.8	68	2	A97874	degenerate transp	946	9	81.8	70	2	E70701	hypothetical trans
874	9	81.8	68	2	P99055	hypothetical prote	947	9	81.8	70	2	G41530	hypothetical prote
875	9	81.8	68	2	A10436	insertion element	948	9	81.8	70	2	E46044	hypothetical prote
876	9	81.8	68	2	A01287	hypothetical prote	949	9	81.8	70	2	A19440	microtubule associ
877	9	81.8	68	2	E62158	hypothetical prote	950	9	81.8	70	2	E41374	protein tyrosine k
878	9	81.8	68	2	E62208	hypothetical prote	951	9	81.8	70	2	T39707	hypothetical prote
879	9	81.8	68	2	A04215	hypothetical prote	952	9	81.8	70	2	A84032	hypothetical prote
880	9	81.8	68	2	A04542	hypothetical prote	953	9	81.8	70	2	T12849	hypothetical prote
881	9	81.8	68	2	A83488	hypothetical prote	954	9	81.8	70	2	A02298	probable membrane
882	9	81.8	68	2	A83479	hypothetical prote	955	9	81.8	70	2	AH7720	conserved hypotet
883	9	81.8	68	2	A11809	phycobilisome core	956	9	81.8	70	2	AG3440	hypothetical prote
884	9	81.8	69	1	R3RT28	ribosomal protein	957	9	81.8	70	2	AH4483	hypothetical prote
885	9	81.8	69	1	M1B277	microcin B7 precu	958	9	81.8	70	2	AB1984	hypothetical prote
886	9	81.8	69	2	R33979	peptidyl-dipeptid	959	9	81.8	71	1	R48C21	ribosomal protein
887	9	81.8	69	2	S45610	januolate cyclase	960	9	81.8	71	1	R48C21	ribosomal protein
888	9	81.8	69	2	T04135	axial filament fil	961	9	81.8	71	1	H96122	kinetoplast minicr
889	9	81.8	69	2	H21078	4-oxalacetate t	962	9	81.8	71	1	DNV137	DNA-binding protel
890	9	81.8	69	2	A11084	hypothetical prote	963	9	81.8	71	2	E01211	RAH2.3 tyrosine k
891	9	81.8	69	2	S13795	hemocytin protein	964	9	81.8	71	2	A35333	glucose 6-phosphat
892	9	81.8	69	2	A45195	hemocytin protein	965	9	81.8	71	2	E62312	ribosomal protein
893	9	81.8	69	2	P90944	hypothetical prote	966	9	81.8	71	2	AH0375	40S ribosomal prot
894	9	81.8	69	2	E94305	hypothetical prote	967	9	81.8	71	2	AH0392	40S ribosomal subu
895	9	81.8	69	2	E93312	hypothetical prote	968	9	81.8	71	2	C65967	40S ribosomal subu
896	9	81.8	69	2	S66749	car-tyrosine 2 epi	969	9	81.8	71	2	E31536	40S ribosomal subu
897	9	81.8	69	2	S04566	hypothetical prote	970	9	81.8	71	2	E91132	40S ribosomal subu
898	9	81.8	69	2	G75310	hypothetical prote	971	9	81.8	71	2	E37840	hypothetical prote
899	9	81.8	69	2	G73938	hypothetical prote	972	9	81.8	71	2	A21876	vitellinogen A1
900	9	81.8	69	2	T50223	hypothetical prote	973	9	81.8	71	2	E27572	vitellinogen B1 pr
901	9	81.8	69	2	T07874	protein kinase hom	974	9	81.8	71	2	D24876	vitellinogen B2 pr
902	9	81.8	69	2	T07874	protein kinase hom	975	9	81.8	71	2	E50391	hypothetical prote
903	9	81.8	69	2	T07876	protein kinase hom	976	9	81.8	71	2	E50391	SNY-related sequen
904	9	81.8	69	2	T07878	protein kinase hom	977	9	81.8	71	2	J01161	homocysteine-protein
905	9	81.8	69	2	T02372	flaser protein B9F	978	9	81.8	71	2	A60984	homocysteine-protein

hemocytic protein B
protein F906.27
B GRP D protein
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical 8.1k
kleb protein - pla
hypothetical prote
hypothetical prote
mob protein D - Er
chemoreceptor prot
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
probable type III
hypothetical prote

ALIGNMENTS

RESULT 1
E48394
glycoprotein component 15/16 of rat fat-globule membrane protein (cattle)
C:Species: Bos primigenius taurus (cattle)
C:Date: 19-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: E48394
R:Mathier, J.H.; Bandhart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
11-like sequences.
A:Reference number: A48394; MUID:93250576; PMID:8485470
A:Accession: E48394
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 -MAT-
A:Experimental source: milk
A:Note: Sequence extracted from N26i backbone (NCBIP:131450)
C:Keywords: glycoprotein

Query Match 81.8% Score 9; DB 2; Length 7;
Best Local Similarity 66.7% Pred. No. 2; Re-06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1
1
DB 5 LAR 7

RESULT 2
E48394
major fat-globule membrane protein GP 55 - guinea pig (fragment)
C:Species: Cavia porcellus (guinea pig)
C:Date: 19-Nov-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
C:Accession: E48394
R:Mathier, J.H.; Bandhart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A:Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
11-like sequences.
A:Reference number: A48394; MUID:93250576; PMID:8485470
A:Accession: E48394
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 -MAT-
A:Experimental source: milk
A:Note: Sequence extracted from N26i backbone (NCBIP:131450)

Query Match 81.8% Score 9; DB 2; Length 7;
Best Local Similarity 66.7% Pred. No. 2; Re-06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1
1
DB 5 LAR 7

RESULT 3
P64131
hypothetical protein B (imported)
C:Species: Pseudomonas aeruginosa (fragment)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
C:Accession: P64131
P:Kawasaki, S.; Arai, H.; Igarashi, Y.; Kodama, T.
Gene 167, 87-91, 1995
A:Title: Deposition and characterization of the 4-kilobase region of the genes encoding
gamma for biosynthesis of home dL.
A:Reference number: J-155; MUID:96144254; PMID:8566817
A:Accession: P64131
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 -KAW-
A:Cross references: DDBJ:150473; EMBL:1217594
A:Note: this ORF is not annotated in GenBank entry P64131, release 114.0

Query Match 81.8% Score 9; DB 2; Length 8;
Best Local Similarity 66.7% Pred. No. 2; Re-06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1
1
DB 4 LSR 6

RESULT 4
T14818
cytochrome oxidase subunit I - Atlantic haptfish mitochondrion (fragment)
C:Species: mitochondrion Myxine glutinosa (Atlantic haptfish)
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jul-2000
C:Accession: T14818
R:Delattre, C.; Barbed, V.; Pilliet, S.; Janvier, P.; Gachelin, G.
Mol. Biol. Evol. 14, 887-814, 1997
A:Title: The main features of the craniate mitochondrial DNA between the NDI and the
A:Reference number: 217775; MUID:97398784; PMID:9254918
A:Accession: T14818
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 -DEL-
A:Cross references: DDBJ:Y09527; EMBL:244019; F08:Y09527; F08:Y09527; F08:Y09527
C:Keywords: mitochondrion

Query Match 81.8% Score 9; DB 2; Length 8;
Best Local Similarity 66.7% Pred. No. 2; Re-06;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1
1
DB 4 LSR 6

RESULT 5
T14838
cytochrome-c oxidase (E1-1-1-1-1) chain 1
C:Species: mitochondrion Bipes biporus
C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 11-May-2000
C:Accession: T14838
R:Mathier, J.H.; Bandhart, L.R.; Lane, W.S.
Mol. Biol. Evol. 14, 91-104, 1997

A:Title: Two novel gene orders and the role of light-strand replication in rearrangement
 A:Reference number: 217789; MUID:47153826; PMID:9000757

A:Accession: T14219
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1 to 284
 A:Cross-References: EMBL:071295; NID:31753232; FID:31753235; FID:AM049271.1
 C:Genetics:
 A:Genome: mitochondrion
 A:Notes: Col
 C:Keywords: mitochondrion; oxidoreductase

Query Match 81.8%; Score 9; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 Db 3 LXR 5

RESULT 6
 T14219
 Cytochrome oxidase (CO I & II) chain I - Xenosaurus grandis mitochondrion (fragment)
 C:Species: mitochondrion Xenosaurus grandis
 C:Date: 20 Sep 1996 #sequence_revision 20 Sep 1996 #text_change 21-Jul-2003
 C:Accession: T14219
 R:Macoy, J.R.; Larson, A.; Arasheva, R.B.; Faud, Z.; Papenfuss, T.J.
 Mol. Biol. Evol. 14, 91-104, 1997

A:Title: Two novel gene orders and the role of light strand replication in rearrangement
 A:Reference number: 217789; MUID:47153826; PMID:9000757
 A:Accession: T14219
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-10 cMAC
 A:Cross-References: EMBL:071293; NID:31753236; FID:AM049271.1; FID:31753275
 C:Genetics:
 A:Genome: mitochondrion
 A:Note: Col
 C:Keywords: mitochondrion; oxidoreductase

Query Match 81.8%; Score 9; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 1.4e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 Db 3 LXR 5

RESULT 7
 p00034
 dextranucrase (EC 2.4.1.5) - Streptococcus bovis (fragment)
 C:Species: Streptococcus bovis
 C:Date: 21 Feb 1994 #sequence_revision 03-Feb-1994 #text_change 16 Sep 1996
 C:Accession: P00034
 R:Dezoro, Y.; Tsumori, H.; Kakasa, H.
 submitted to JPIID, October 1994
 A:Description: Purification and properties of glycyltransferase synthesizing 1,6-alpha
 A:Reference number: P00034
 A:Accession: P00034
 A:Molecule type: protein
 A:Residues: 1-11 cEEZ
 A:Experimental source: ATCC 9809
 C:Keywords: glycyltransferase; Xenosaurus grandis

Query Match 81.8%; Score 9; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 Db 8 LXR 10

RESULT 8

A42324

cytochrome P450c27/25

C:Species: Rattus norvegicus (Norway rat)

C:Date: 21 Mar 1993 #sequence_revision 18 Mar 1993 #text_change 08 Feb-1996

C:Accession: A42324

R:Shayiq, R.M.; Azadani, N.G.

J. Biol. Chem. 267, 2121-2126, 1992

A:Title: Sequence homology between the 5' terminal regions of mRNAs for rat m

ap.

A:Reference number: A42324; MUID:02129422; PMID:1739943

A:Accession: A42324

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-12 cHAs

A:Note: Sequence extracted from RNI backbone (M0818.78404, M0818.78410)

A:Keywords: cytochrome P450c27/25

Query Match 81.8%; Score 9; DB 2; Length 12;

Best Local Similarity 66.7%; Pred. No. 1.4e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

Db 4 LXR 6

RESULT 9

P02293

heavy chain cyp19c2

C:Species: Homo sapiens (man)

C:Date: 20 Sep 1993 #sequence_revision 03-Sep-1993 #text_change 16-Aug-1996

C:Accession: P02293

R:Kishimoto, M.; Wassenaar, E.; Fairhead, B.A.; Slamon, S.; Gatalan, A.; Kovara, G.

J. Exp. Med. 171, 495-507, 1991

A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity a

A:Reference number: P02227; MUID:01168197; PMID:1879182

A:Accession: P02293

A:Molecule type: RNA

A:Residues: 1-13 cYAM

A:Experimental source: B lymphocyte

C:Keywords: heavy chain; immunoglobulin

Query Match 81.8%; Score 9; DB 2; Length 13;

Best Local Similarity 66.7%; Pred. No. 1.5e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

Db 1 LXR 3

RESULT 10

P01111

protein OAT00054 - Arabidopsis thaliana (fragment)

C:Species: Arabidopsis thaliana (mouse rat cross)

C:Date: 07 Apr 1995 #sequence_revision 26 May 1996 #text_change 05-Jun-1997

C:Accession: P01111

R:Kanno, M.; Kawakami, T.; Ishigita, A.

submitted to JPIID, March 1995

A:Reference number: P01109

A:Accession: P01111

A:Molecule type: protein

A:Residues: 1-11 cEAM

A:Experimental source: root

Query Match 81.8%; Score 9; DB 2; Length 14;

Best Local Similarity 66.7%; Pred. No. 1.6e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

Db 1 LXR 1

A:Reference number: AB0602, PMID:11677699
 A:Accession: AF0832
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-15 <EAX>
 A:Cross references: CR A:03482, BFN, CA00919, 1, PP, 4199920, 1994, 200005
 A:Genetics:
 A:Gene: STY2853a

Query Match 91.8% Score 9; DB 2; Length 15;
 Best Local Similarity 66.7% Pred. No. 1.7e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 Db 4 LTR 5

RESULT 17

C61414

chymotrypsin (EC 3.4.21.1) - slider turtle (fragment)

C:Species: Pseudemys scripta (slider)

C>Date: 06-Sep-1994 #sequence_revision 06-Sep-1994 #text_change 07-May-1999

C:Accession: C61414

R:Bhargava, A.K.; Barnard, E.A.

J. Mol. Evol. 2; 187-198, 1974

A:Title: Evolution in the fasciatic chymotrypsin families. N-terminal sequence data

A:Reference number: A61414; PMID:76146602; PMID:4807189

A:Accession: C61414

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <BHA>

C:Keywords: hydrolase; protein digestion, serine proteinase

Query Match 91.8% Score 9; DB 2; Length 15;
 Best Local Similarity 66.7% Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 Db 13 LAR 15

RESULT 18

JH0517

insulin-like growth factor-binding protein 4 - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C>Date: 21-Mar-1992 #sequence_revision 21-Mar-1992 #text_change 21-Mar-1992

C:Accession: JH0517

R:Coleman, M.E.; Pan, Y.G.E.; Etkerton, T.P.

Biochem Biophys Res Commun. 191; 1131-1136, 1991

A:Title: Identification and NH2 terminal amino acid sequence of three insulin-like growth

A:Reference number: JH0517; PMID:91109719; PMID:1722298

A:Accession: JH0517

A:Molecule type: protein

A:Residues: 1-16 <COL>

A:Experimental source: serum

Query Match 91.8% Score 9; DB 2; Length 16;
 Best Local Similarity 66.7% Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 Db 14 LAR 16

RESULT 19

B44036

collagen alpha 1(XII) chain NC3B domain - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C>Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 19-Oct-1995

C:Accession: B44036

Kobayashi, S.F.; Kobayashi, A.M.; Marikozich, E.L.; Kawai, L.K.; Morris, R.P.; Burg
 J. Biol. Chem. 267; 20087-20092, 1992
 A:Title: Identification and partial purification of a large, variant form of type XII
 A:Reference number: A44036; PMID:93015874; PMID:1400126
 A:Accession: B44036
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-16 <LIN>
 A:Experimental source: skin
 A:Remarks: sequence extracted from HEE; backbone (REFID:B15796)

Query Match 91.8% Score 9; DB 2; Length 16;
 Best Local Similarity 66.7% Pred. No. 1.8e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 Db 4 LTR 6

RESULT 20

JP0046

rifampin protein L29 Staphylococcus epidermidis (fragment)

C:Species: Staphylococcus epidermidis

C>Date: 10-Mar-1994 #sequence_revision 08-Oct-1994 #text_change 31-Oct-1997

C:Accession: JP0046

R:Chen, R.

submitted to JIPID, February 1994

A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal

A:Reference number: JP0042

A:Accession: JP0046

A:Molecule type: protein

A:Residues: 1-17 <CH>

C:Superfamily: Escherichia coli ribosomal protein L10

C:Keywords: protein biosynthesis; ribosome

Query Match 91.8% Score 9; DB 2; Length 17;
 Best Local Similarity 66.7% Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 Db 7 LTR 9

RESULT 21

A34835

C:Species: Pseudomonas aeruginosa

C>Date: 21-Mar-1992 #sequence_revision 21-Mar-1992 #text_change 23-Jul-1994

C:Accession: A34835

R:Yee, T.W.; Smith, D.W.

Proc. Natl. Acad. Sci. U.S.A. 87; 1279-1282, 1990

A:Title: Pseudomonas chromosomal replication origins: a bacterial class distinct from

A:Reference number: A34835; PMID:93169410; PMID:2105142

A:Accession: A34835

A:Molecule type: DNA

A:Residues: 1-17 <YEE>

A:Cross references: GB:M30125

C:Genetics:

A:Gene: rpmH

C:Superfamily: Escherichia coli ribosomal protein L14

C:Keywords: protein biosynthesis; ribosome

Query Match 91.8% Score 9; DB 2; Length 17;
 Best Local Similarity 66.7% Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 Db 12 LSR 14

RESULT 22

154269
 C:Species: Homo sapiens (man)
 C>Date: 01-Nov-1996 #sequence_revision 21-251 2001
 C:Accession: J02429
 R:Krahn, A.; Hochmair, R.; Muller, B.; Cloze, H.
 Hum. Genet. 90, 526-532, 1994

A:Title: Molecular evaluation of an Alu repeat including a polymorphic variable poly(A)
 A:Reference number: 154269; PMID:8481387
 A:Accession: J02429
 A>Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-17
 A:Keywords: serum albumin; serum albumin repeat; hemolysis

Query Match 81.8% Score 9; DB 2; Length 17;
 Best Local Similarity 66.7% Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 BB 5 LSR 7

RESULT 23

J02430
 C:Species: chloroplast; tomato; chloroplast (strain Tokyo)
 C>Date: 10-Mar-1994 #sequence_revision 28 Oct-1994 #text_change 23-Mar-1995
 C:Accession: J02310
 R:Kawaguchi, Y.; Kikuta, Y.
 Theor. Appl. Genet. 81, 13-20, 1991

A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).
 A:Reference number: J02306
 A:Accession: J02310
 A:Molecule type: DNA
 A:Residues: 1-17
 A:Experimental source: strain Tokyo
 C:Genetics:

A:Genome: chloroplast
 C:Keywords: chloroplast

Query Match 81.8% Score 9; DB 2; Length 17;
 Best Local Similarity 66.7% Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 BB 15 LSR 17

RESULT 24

J02420
 C:Species: chloroplast; potato; chloroplast
 C>Date: 10-Mar-1994 #sequence_revision 38-Oct-1994 #text_change 05-Nov-1994
 C:Accession: J02420; J02415
 R:Kawaguchi, Y.; Kikuta, Y.
 Theor. Appl. Genet. 81, 13-20, 1991

A:Title: Chloroplast DNA evolution in potato (Solanum tuberosum L.).
 A:Reference number: J02406
 A:Accession: J02420
 A:Molecule type: DNA
 A:Residues: 1-17
 A:Experimental source: cv. W553 4

A:Accession: J02415
 A:Molecule type: DNA
 A:Residues: 1-17
 A:Experimental source: cv. 150
 C:Genetics:

A:Genome: chloroplast

C:Keywords: chloroplast

Query Match 81.8% Score 9; DB 2; Length 17;
 Best Local Similarity 66.7% Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 BB 15 LSR 17

RESULT 25

B01414
 C:Species: painted turtle (fragment)
 C>Date: 16-Mar-1997 #sequence_revision 16 Dec 1997 #text_change 07 May 1999
 C:Accession: B01414
 R:Bhargava, A.K.; Barnard, E.A.
 J. Mol. Evol. 2, 187-198, 1973
 A:Title: Evolution in the nucleotide sequence of the cytochrome b gene
 A:Reference number: A61414; PMID:76146602; PMID:4807189
 A:Accession: B01414
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-17
 A:Keywords: hydrolase; serine protease

Query Match 81.8% Score 9; DB 2; Length 17;
 Best Local Similarity 66.7% Pred. No. 1.9e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 BB 13 LSR 15

RESULT 26

S29491
 C:Species: Torpedo marmorata (mottled electric ray)
 C>Date: 22-Nov-1993 #sequence_revision 23 Feb 1997 #text_change 19 Dec 1998
 C:Accession: S29491
 R:Vogelmeier, W.; Bennett, J.; El-Ferikh, L.A.; Pels, J.; P.R.
 FEBS Lett. 317, 53-56, 1993
 A:Title: Association of three small GTP-binding proteins with cholinergic synaptic vesicles
 A:Reference number: S29485; PMID:94154521; PMID:8428634
 A:Accession: S29491
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-18
 A:Keywords: GTP binding; lipoprotein; membrane trafficking

Query Match 81.8% Score 9; DB 2; Length 18;
 Best Local Similarity 66.7% Pred. No. 2.1e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 BB 5 LSR 7

RESULT 27

A41877
 C:Species: Yersinia pseudotuberculosis (fragment)
 C>Date: 04 Mar 1994 #sequence_revision 14 Nov 1994 #text_change 14 Nov 1994
 C:Accession: A41877
 R:Rimpilainen, M.; Forsberg, A.; Woll-Watz, H.
 J. Bacteriol. 174, 3355-3363, 1992
 A:Title: A novel protein, LerG, involved in the low calcium response of Yersinia pseudotuberculosis

RESULT 33

A60326
cholecystokinin-58 - bovine (fragment)
C:Species: Bos primigenius taurus (cat14)
C:Date: 21-Oct-1992 #sequence_revision 21 Oct 1992 #text_change 31 Dec 1993
C:Accession: A60326
R:Publ. J. Biol. Chem. 265:1519-1524, 1990
R:Publ. J. Biol. Chem. 265:1519-1524, 1990
A:Title: Purification of bovine cholecystokinin-58 and sequencing of its N-terminus.
A:Reference number: A60326; MIM:9191599; PMID:2217939
A:Accession: A60326
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-19 <EN6>
C:Keywords: neuropeptide

Query Match 81.8% Score 9; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 2.4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 17 LAR 19

RESULT 34

A60525
lysosome (EC 3.2.1.17) - cat (fragment)
C:Species: Felis silvestris catus (domestic cat)
C:Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 20-Jun 2000
C:Accession: A60525
R:Balliday, J.A.; Bell, K.; McKenzie, H.A.; Shaw, D.C.
Comp. Biochem. Physiol. B 95: 773-779, 1990
A:Title: Feline whorl proteins: identification, isolation and initial characterization of
A:Reference number: A60525; MIM:9026464; PMID:2344734
A:Accession: A60525
A:Molecule type: protein
A:Residues: 1-29 <HAI>
A:Experimental source: milk
C:Superfamily: Lysosome
C:Keywords: bacteriolytic enzyme; glycosidase; hydrolase; polysaccharide degradation

Query Match 81.8% Score 9; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 8 LAR 10

RESULT 35

JP0050
ribosomal protein L30 - bacillus megaterium (fragment)
C:Species: Bacillus megaterium
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 03 May 1996
C:Accession: JP0050
R:Kochl, K.
submitted to JPIID, February 1994
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal pr
A:Reference number: JP0050
A:Accession: JP0050
A:Molecule type: protein
A:Residues: 1-20 <ACH>
C:Superfamily: Escherichia coli ribosomal protein L30
C:Keywords: protein biosynthesis; ribosome

Query Match 81.8% Score 9; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 8 LXR 10

RESULT 36

JP0051
ribosomal protein L30 - bacillus cereus (fragment)
C:Species: Bacillus cereus
C:Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 03 May 1996
C:Accession: JP0051
R:Kochl, K.

submitted to JPIID, February 1994
A:Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal
A:Reference number: JP0051
A:Accession: JP0051
A:Molecule type: protein
A:Residues: 1-20 <ACH>
C:Superfamily: Escherichia coli ribosomal protein L30
C:Keywords: protein biosynthesis; ribosome

Query Match 81.8% Score 9; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 8 LXR 10

RESULT 37

S33001
hypothetical protein - human herpesvirus 4
C:Species: human herpesvirus 4; Epstein Barr virus
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 08-Oct 1999
C:Accession: S33001
R:Parrell, P.J.
submitted to the EMBL Data Library, March 1988
A:Reference number: S32973
A:Accession: S33001
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 <PAR>
A:Cross-references: EMBL:V01555; NID:059074; FID:0AA4847.1; FID:0164861

Query Match 81.8% Score 9; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 7 LXR 9

RESULT 38

PC2084
serine proteinase (EC 3.4.21.1) - Penicillium citrinum (strain 86-1) (fragment)
C:Species: Penicillium citrinum
C:Date: 03-May-1994 #sequence_revision 07-Oct-1994 #text_change 07 May 1999
C:Accession: PC2084
R:Watanabe, Y.; Yamashita, K.; Yamashita, Y.; Yamashita, N.; Morita, S.; Okabe, H.
Biol. Biotechnol. Biochem. 58: 747-751, 1994
A:Title: Isolation and characterization of a serine proteinase, purified and modified
A:Reference number: PC2084; MIM:94264404; PMID:7704866
A:Accession: PC2084
A:Molecule type: protein
A:Residues: 1-20 <WAI>
C:Superfamily: This protein shows selective inhibitory activity against the m subunit of
C:Keywords: hydrolase; serine proteinase

Query Match 81.8% Score 9; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.4e+04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

A:Accession: J110581
 A:Molecule type: protein
 A:Residues: 1-22 AK1
 A:Experimental source: brain
 C:Superfamily: natriuretic peptide A precursor
 C:Keywords: diuretic; hormone; natriuretic; osmoregulation

Query Match 81.8% Score 9; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 2.5e+03;
 Matches 2; Conservativeness 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 I I
 DB 2 LSK 4

RESULT 45
 F23744
 insulin-like growth factor-binding protein 4 - pit (fragment)
 C:Species: Sus scrofa domestica (domestic pig)
 C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 11-Jan-2000
 C:Accession: F23744
 R:Shimasaki, S.; Cao, L.; Shimanaka, M.; Lind, N.
 Mol. Endocrinol. 5, 938-948, 1991
 A:Title: Isolation and molecular cloning of insulin-like growth factor-binding protein-4
 A:Reference number: F23744; MIM:62049376; PMID:1719383
 A:Accession: F23744
 A>Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-22 SH1
 C:Superfamily: Insulin-like growth factor binding protein 1, thyroglobulin type 1 repeat

Query Match 81.8% Score 9; DB 2; Length 22;
 Best Local Similarity 66.7%; Pred. No. 2.5e+03;
 Matches 2; Conservativeness 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 I I
 DB 14 LAR 16

Search completed: April 30, 2003, 13:47:17
 Job time : 24.0455 secs

GenCore Version 5.1.1_p5_472
Copyright (c) 1993 - 2002 Computer Ltd.

OM protein - protein search, using sw model

Run on: April 30, 2003, 13:41:58 ; Search time 5.09091 Seconds
(without alignments)
32.589 Million cell updates/sec

Title: US-09-498-556c-357

Perfect score: 11

Sequence: 1 LXPX 4

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DR	ID	Description
1	9	81.8	11	1	PG30_GNOMY	P83328 cncorthyche
2	9	81.8	15	1	CNC1_GNOMY	P84287 cncorthyche
3	9	81.8	15	1	UC25_MAIZE	P35331 zea mays (m
4	9	81.8	16	1	IPM1_PIC	P24854 sus scrofa
5	9	81.8	18	1	YAA5_BHEA	G93905 thelouse-ide
6	9	81.8	20	1	LYC_FELCA	P37155 felis silve
7	9	81.8	20	1	REPX_APOVI	P13663 acrobacter
8	9	81.8	21	1	SYA_PAT	P50475 rattus norv
9	9	81.8	22	1	ARPF_CHICK	P23205 galus gall
10	9	81.8	23	1	CLSA_PHELP	P20479 phormidium
11	9	81.8	25	1	IPVK_PSEAN	P80898 pseudanaba
12	9	81.8	26	1	NEPV_PANTE	P33055 rana tempor
13	9	81.8	26	1	SPT3_PSEUS	P82357 pseudocauli
14	9	81.8	26	1	UBU1_BCVIN	P23356 bos taurus
15	9	81.8	26	1	NTPC_PHELP	P21502 rhizobium l
16	9	81.8	26	1	YFHA_KLEIN	P21710 klebschella
17	9	81.8	27	1	CCXP_CANFA	P58206 canis radi
18	9	81.8	27	1	SECR_CANFA	P09910 canis fami
19	9	81.8	27	1	SECR_FABIT	P32647 cyclolepus
20	9	81.8	27	1	SECR_SHEEP	P31293 ovis aries
21	9	81.8	28	1	VIG1_VACCP	G60343 vaccinia vi
22	9	81.8	29	1	H598_NEUPP	P31540 neurespora
23	9	81.8	29	1	Y51_BPT?	P30325 bacterioph
24	9	81.8	31	1	DIUX_DICVS	P82372 diptera
25	9	81.8	33	1	LYC2_HORSE	P81710 equus cabal
26	9	81.8	33	1	QPC6_PSEPP	P11227 pseudomon
27	9	81.8	34	1	FK1_PHEC1	P15101 dictyostel
28	9	81.8	34	1	PN1_PTC	P15166 sus scrofa
29	9	81.8	35	1	CRF6_MOUSE	G54261 mus muscul
30	9	81.8	36	1	F4PE_MET65	P80951 methanogeni
31	9	81.8	36	1	NEPV_PIC	P01304 sus scrofa
32	9	81.8	36	1	NEPV_SHEEP	P13765 ovis aries
33	9	81.8	36	1	PAHO_CERSI	P37999 ceratotheri

34	9	81.8	36	1	PAHO_CHICK	P41519 chinchilla
35	9	81.8	36	1	PAHO_DOGA	P13197 dromedus m
36	9	81.8	36	1	PAHO_EQUUS	P30033 equus zebra
37	9	81.8	36	1	PAHO_EKIEU	P41335 elineoccus e
38	9	81.8	36	1	PAHO_NACMO	P33684 macaca mull
39	9	81.8	36	1	PAHO_PIG	P01300 sus scrofa
40	9	81.8	36	1	PAHO_RABIT	P41166 corytolanus
41	9	81.8	36	1	PAHO_TAPPI	P39559 tapirus pin
42	9	81.8	36	1	PYY_AMDPA	P23205 ania calva
43	9	81.8	36	1	PYY_PIG	P01305 sus scrofa
44	9	81.8	37	1	CGRP_PIG	P30883 sus scrofa
45	9	81.8	37	1	CGRP_RABIT	P31888 rana ridibu
46	9	81.8	37	1	CGRP_SHEEP	P30881 ovis aries
47	9	81.8	37	1	P117_B-VIN	P21671 bos taurus
48	9	81.8	37	1	PSBY_GUITH	P74433 quillardia
49	9	81.8	37	1	Y63_BPT4	P20428 bacterioph
50	9	81.8	37	1	Y63_BPT7	P34755 bacterioph
51	9	81.8	38	1	Y139_AKCFU	P28440 archaebactob
52	9	81.8	39	1	CYL_SQIAC	P11149 squallus aca
53	9	81.8	41	1	RS26_MUSVI	P41692 mustela vis
54	9	81.8	41	1	UC21_DEVEL	P24431 equine horp
55	9	81.8	42	1	NCAP_NEVB	P39459 newcastia d
56	9	81.8	42	1	EL32_MAIZE	P51421 zea mays (m
57	9	81.8	43	1	RLFS_RAPSA	P29420 raplanus sa
58	9	81.8	43	1	Y5K_CMYV	P16445 elzevir yell
59	9	81.8	44	1	PSHK_OB-SI	P45513 odontotelia s
60	9	81.8	44	1	P3RK_SKECC	P39812 skeletaloma
61	9	81.8	44	1	RL34_HACST	P23376 bacillus st
62	9	81.8	44	1	RL34_HACSD	P05647 bacillus su
63	9	81.8	44	1	RL34_UABTH	P44370 bacophilus
64	9	81.8	44	1	RL34_PSEAF	P29436 pseudomonas
65	9	81.8	44	1	RL34_PSEPB	P16456 pseudomonas
66	9	81.8	44	1	RL34_THEMA	P58288 thermotoga
67	9	81.8	44	1	RG35_DHEKO	P18681 bacterioph
68	9	81.8	44	1	TISR_HUMAN	P99586 homo sapien
69	9	81.8	45	1	MT1B_AKATH	P38803 arabidopsis
70	9	81.8	45	1	RL34_HACHD	P99843 bacillus ha
71	9	81.8	45	1	RL34_GIHAM	G93431 staphylococ
72	9	81.8	46	1	HMB1_SHEEP	P41359 ovis aries
73	9	81.8	46	1	HXB5_SHEEP	P41357 ovis aries
74	9	81.8	46	1	RE34_CVATA	P48135 cyanophora
75	9	81.8	46	1	RL34_PSEB1	P02437 escherichia
76	9	81.8	46	1	RL34_XYLLA	P29439 xyllia pas
77	9	81.8	46	1	RL34_YHEPC	P55905 yersinia pe
78	9	81.8	47	1	EL32_SVH05	P33079 zizov-bacter
79	9	81.8	47	1	HAY_RHEJA	P60748 bioplasma
80	9	81.8	47	1	EL34_A2TAE	G66643 apifis x geo
81	9	81.8	47	1	RL34_BOPAI	P57129 bacterioph
82	9	81.8	47	1	EL34_PHECA	P24337 bacterioph
83	9	81.8	47	1	RL34_BHIVA	P91862 bacteriocus
84	9	81.8	47	1	RL34_PHEM1	P22836 proteus mir
85	9	81.8	47	1	Y556_PHEM5	P52274 proteobacteri
86	9	81.8	48	1	YTT5_TEG	P23734 apifis x geo
87	9	81.8	48	1	GS30_AZOV1	P44558 azobactater
88	9	81.8	48	1	R232_MVONB	P23392 mycoplasma
89	9	81.8	48	1	R232_MVONB	P56890 mycoplasma
90	9	81.8	48	1	EL34_MVONB	P78006 mycoplasma
91	9	81.8	48	1	EL34_PHEBA	P99905 mycoplasma
92	9	81.8	48	1	P687_PHEBA	P83616 tropozema p
93	9	81.8	49	1	HKB3_PHEB1	P77454 escherichia
94	9	81.8	49	1	HVAT_SHEEP	P26699 ovis aries
95	9	81.8	49	1	Y19W_PHEB1	P71164 escherichia
96	9	81.8	49	1	Y19W_PHEB1	P23653 pedosporea a
97	9	81.8	50	1	Y19W_PHEB1	P43967 haemophilus
98	9	81.8	51	1	HSP1_ADOSE	P35402 borrelia se
99	9	81.8	51	1	EL34_PHEB3	P16077 escherichia
100	9	81.8	52	1	FLMA_PHEB1	P13695 escherichia
101	9	81.8	52	1	FLMA_PHEB1	P92368 corytolanus
102	9	81.8	52	1	IFJA_PABIT	P26678 homo sapien
103	9	81.8	52	1	PHIA_HUMAN	P20006 mus muscul
104	9	81.8	52	1	PHIA_MOUSE	P07473 sus scrofa
105	9	81.8	52	1	PHIA_PIG	P41633 acanthamoeba
106	9	81.8	52	1	RL34_AVACA	

107	9	81.8	52	1	R140_AKATH	P15232 arabidopsis	190	9	81.8	61	1	CSKA_PSWA	P17420 arabidops
108	9	81.8	52	1	R140_BHARA	P51424 brassicaria	181	9	81.8	61	1	CSKA_PSWA	P17420 pseudomonas
109	9	81.8	52	1	R140_CHLRE	P14695 chlamydomon	182	9	81.8	61	1	CSKA_PSWA	P17420 bacterioph
110	9	81.8	52	1	R140_DICDI	P14794 dictyostell	183	9	81.8	61	1	REP1_METH	P17420 metbacteri
111	9	81.8	52	1	R140_NICZY	P15636 nicotiana s	184	9	81.8	61	1	CSKA_PSWA	P17420 schistosom
112	9	81.8	53	1	R142_MYSCA	P151415 mycoplasma s	195	9	81.8	61	1	V238_PAPV	P17420 fowlpox vir
113	9	81.8	53	1	R140_ORYSA	P152246 oryza sativ	186	9	81.8	61	1	YF73_MELIA	P17420 metbacteri
114	9	81.8	53	1	R114_CHLS6	P48645 chlorarachn	187	9	81.8	61	1	YH62_AKATH	P17420 arabidops
115	9	81.8	53	1	VUK_BPAL3	P1282 bacterioph	188	9	81.8	62	1	CSKA_PSWA	P17420 pastorella
116	9	81.8	53	1	VUK_PPPH	P18004 bacterioph	199	9	81.8	62	1	CSKA_PSWA	P17420 pseudomonas
117	9	81.8	53	1	YHAM_ECOLI	P45807 escherichia	190	9	81.8	62	1	YHAM_ECOLI	P17420 escherichia
118	9	81.8	53	1	YFMI_PPPH	P12909 trypsinoma	191	9	81.8	62	1	YFMI_PPPH	P17420 simian virus
119	9	81.8	54	1	AT18_NDPCR	P08656 neosporea	192	9	81.8	62	1	YFMI_PPPH	P17420 cricetus
120	9	81.8	54	1	HBO_MACDU	P11041 macropus eu	193	9	81.8	62	1	YFMI_PPPH	P17420 dusicyan th
121	9	81.8	54	1	YVVO_SYRHI	P12245 syriacus	194	9	81.8	62	1	YFMI_PPPH	P17420 fowlpox vir
122	9	81.8	54	1	YVVO_SYRHI	P13940 enterobacte	195	9	81.8	62	1	YFMI_PPPH	P17420 fowlpox vir
123	9	81.8	55	1	PHNS_DESVH	P06173 desulfovib	196	9	81.8	62	1	YFMI_PPPH	P17420 fowlpox vir
124	9	81.8	55	1	PMR3_YEAST	P17284 saccharomyc	197	9	81.8	62	1	YFMI_PPPH	P17420 fowlpox vir
125	9	81.8	55	1	VXK1_BYOVP	P09518 barley yell	198	9	81.8	62	1	YFMI_PPPH	P17420 fowlpox vir
126	9	81.8	55	1	VXK1_CUSRE	P32035 cuscutea ref	199	9	81.8	62	1	YFMI_PPPH	P17420 fowlpox vir
127	9	81.8	55	1	YH62_PCOLI	P17770 escherichia	200	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
128	9	81.8	55	1	YH62_PCOLI	P12240 thermoprote	201	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
129	9	81.8	56	1	YVVO_SYRHI	P05685 thermoprote	202	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
130	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	203	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
131	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	204	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
132	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	205	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
133	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	206	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
134	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	207	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
135	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	208	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
136	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	209	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
137	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	210	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
138	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	211	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
139	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	212	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
140	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	213	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
141	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	214	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
142	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	215	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
143	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	216	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
144	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	217	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
145	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	218	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
146	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	219	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
147	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	220	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
148	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	221	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
149	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	222	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
150	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	223	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
151	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	224	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
152	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	225	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
153	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	226	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
154	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	227	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
155	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	228	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
156	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	229	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
157	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	230	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
158	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	231	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
159	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	232	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
160	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	233	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
161	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	234	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
162	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	235	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
163	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	236	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
164	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	237	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
165	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	238	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
166	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	239	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
167	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	240	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
168	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	241	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
169	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	242	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
170	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	243	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
171	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	244	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
172	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	245	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
173	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	246	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
174	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	247	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
175	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	248	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
176	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	249	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
177	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	250	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
178	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	251	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir
179	9	81.8	56	1	YVVO_SYRHI	P095232 homo sapien	252	9	81.8	63	1	YH62_PCOLI	P17420 fowlpox vir

[illegible]

545	88	1	Y6AD_SCHPO	013973	schizosacch	518	9	81.8	92	1	R819_F0RPH	P51316	porphyra po
546	88	1	YVAL_HUMAN	P29521	varicella vi	619	9	81.8	92	1	R319_E0PAA	P71967	bacteria ap
547	89	1	AP21_HUMAN	Q96210	homo sapien	620	9	81.8	92	1	R319_NEIMA	Q71967	neisseria m
548	89	1	BXA2_POMMO	P16471	bombx mori	621	9	81.8	92	1	R329_RICMA	Q2422	richestia
549	89	1	BXA8_POMMO	P16471	bombx mori	622	9	81.8	92	1	R329_RICMA	P43763	homo sapien
550	89	1	COX1_POMME	Q96524	drosofila	623	9	81.8	92	1	R329_RICMA	P18947	escheria coli
551	89	1	B42_PLPIA	P06516	bioparasma	624	9	81.8	92	1	R329_RICMA	Q97497	shistosoma m
552	89	1	EMPE_PPHH1	P17772	bacterioph	625	9	81.8	92	1	R319_BAINI	Q96461	halobacteri
553	89	1	P143_STAAM	Q95950	staphylococ	626	9	81.8	92	1	R319_XYLPA	Q96461	xyella las
554	89	1	P245_S-HPO	Q95950	schizosacch	627	9	81.8	92	1	R319_XYLPA	P12292	periss simp
555	89	1	PPOR_AAPPE	Q96439	aeropyrum p	628	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
556	89	1	R314_SIKPN	Q95950	streptococ	629	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
557	89	1	Z27A_ASRPE	P58322	aeropyrum p	630	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
558	89	1	Y055_SRYN3	P71811	spirochaeta	631	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
559	89	1	Y070_P0ISA	Q92759	staphylococ	632	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
560	89	1	YF19_MYCTU	Q95950	mycobacteri	633	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
561	89	1	YF03_BACST	Q95950	mycobacteri	634	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
562	89	1	YF03_S-YBN	P24274	lysine max	635	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
563	90	1	L1M1_LILLO	Q43533	lilium long	636	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
564	90	1	L1M2_LILLO	Q43534	lilium long	637	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
565	90	1	N015_THIME	Q92975	thimbium m	638	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
566	90	1	NUOC_SHOCE	P27758	secale cere	639	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
567	90	1	R319_SHPPO	Q96435	streptococ	640	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
568	90	1	R316_LACLA	Q96435	streptococ	641	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
569	90	1	YF17_P0Y11	Q96435	streptococ	642	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
570	90	1	R316_LISMO	Q96435	streptococ	643	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
571	90	1	R316_SHPNP	Q96435	streptococ	644	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
572	90	1	R316_SHPNP	P56124	streptococ	645	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
573	90	1	Y556_BOMPO	Q96424	mycobacteri	646	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
574	90	1	YF19_P0Y11	P43126	escheria coli	647	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
575	90	1	YF17_P0Y11	P73455	synchocyst	648	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
576	90	1	BXCL_BOMMO	P15410	bombx mori	649	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
577	90	1	GAIC_BORRU	Q51318	borrelia bu	650	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
578	90	1	GAIC_HALNI	Q96435	halobacteri	651	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
579	90	1	N012_BSAJA	P53418	trachytrichob	652	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
580	90	1	N011_PSPAE	P81651	fraxus arme	653	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
581	90	1	N011_PSPAE	P82534	prunus dora	654	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
582	90	1	N011_PSPAE	P81402	prunus pers	655	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
583	90	1	N011_PSPAE	Q96435	halobacteri	656	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
584	90	1	R316_SHPNP	P25798	spinacia ol	657	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
585	90	1	R316_SHPNP	Q96435	halobacteri	658	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
586	90	1	R316_SHPNP	Q96435	halobacteri	659	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
587	90	1	R316_SHPNP	Q96435	halobacteri	660	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
588	90	1	R316_SHPNP	Q96435	halobacteri	661	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
589	90	1	R316_SHPNP	Q96435	halobacteri	662	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
590	90	1	R316_SHPNP	Q96435	halobacteri	663	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
591	90	1	R316_SHPNP	Q96435	halobacteri	664	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
592	90	1	R316_SHPNP	Q96435	halobacteri	665	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
593	90	1	R316_SHPNP	Q96435	halobacteri	666	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
594	90	1	R316_SHPNP	Q96435	halobacteri	667	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
595	90	1	R316_SHPNP	Q96435	halobacteri	668	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
596	90	1	R316_SHPNP	Q96435	halobacteri	669	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
597	90	1	R316_SHPNP	Q96435	halobacteri	670	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
598	90	1	R316_SHPNP	Q96435	halobacteri	671	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
599	90	1	R316_SHPNP	Q96435	halobacteri	672	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
600	90	1	R316_SHPNP	Q96435	halobacteri	673	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
601	90	1	R316_SHPNP	Q96435	halobacteri	674	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
602	90	1	R316_SHPNP	Q96435	halobacteri	675	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
603	90	1	R316_SHPNP	Q96435	halobacteri	676	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
604	90	1	R316_SHPNP	Q96435	halobacteri	677	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
605	90	1	R316_SHPNP	Q96435	halobacteri	678	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
606	90	1	R316_SHPNP	Q96435	halobacteri	679	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
607	90	1	R316_SHPNP	Q96435	halobacteri	680	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
608	90	1	R316_SHPNP	Q96435	halobacteri	681	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
609	90	1	R316_SHPNP	Q96435	halobacteri	682	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
610	90	1	R316_SHPNP	Q96435	halobacteri	683	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
611	90	1	R316_SHPNP	Q96435	halobacteri	684	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
612	90	1	R316_SHPNP	Q96435	halobacteri	685	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
613	90	1	R316_SHPNP	Q96435	halobacteri	686	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
614	90	1	R316_SHPNP	Q96435	halobacteri	687	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
615	90	1	R316_SHPNP	Q96435	halobacteri	688	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
616	90	1	R316_SHPNP	Q96435	halobacteri	689	9	81.8	92	1	R319_XYLPA	P04874	homo sapien
617	90	1	R316_SHPNP	Q96435	halobacteri	690	9	81.8	92	1	R319_XYLPA	P04874	homo sapien

691	9	81.8	96	1	GATC_BACSD	Q94759	bacillus ba	764	9	81.8	99	1	GATC_RY110	Q94759	mycobacteri
692	9	81.8	96	1	GATC_BACSI	P58250	bacillus su	765	9	81.8	99	1	GATC_KALSO	Q94762	talstonia s
693	9	81.8	96	1	GATC_BACSI	Q06492	bacillus st	766	9	81.8	99	1	HPFA_KHRA	P40747	thiodactyl
694	9	81.8	96	1	GATC_DEIRA	Q94966	deinococcus	767	9	81.8	99	1	RECN_BBPB3	P07243	bacterioph
695	9	81.8	96	1	GATC_NEIMA	Q97266	neisseria m	768	9	81.8	99	1	RIN_RBP2	P04142	bacterioph
696	9	81.8	96	1	GATC_NEMH	Q97200	neisseria m	769	9	81.8	99	1	R114_ACAVA	P46761	aurantiimon
697	9	81.8	96	1	GATC_PSAF	Q96979	pseudomon	770	9	81.8	99	1	SPFG_FYFPA	P04107	pyrobacul
698	9	81.8	96	1	GATC_THEMA	Q96994	thermotoga	771	9	81.8	99	1	T400_AGRH	P04909	arabidacti
699	9	81.8	96	1	HXG6_PPAPE	R18652	fracthydian	772	9	81.8	99	1	TRP4_EHSH	P07247	thermofila
700	9	81.8	96	1	HXG6_SHEEP	Q28601	ovis aries	773	9	81.8	99	1	YTM2_MHVS	P09439	microthec
701	9	81.8	96	1	PUX3_MHSE	R15975	mus muscula	774	9	81.8	99	1	YXAV_FYALI	P17295	escherichia
702	9	81.8	96	1	PL4_XERP	R14117	xenopus tro	775	9	81.8	99	1	YORP_TTVI	P19286	thermoprote
703	9	81.8	96	1	RS20_THEMA	Q94777	thermotoga	776	9	81.8	99	1	YV07_MVTC	P07074	arabidacti
704	9	81.8	96	1	R124_SCHPO	Q43020	schizosacch	777	9	81.8	100	1	GATC_FYFPA	Q94774	thermotoga
705	9	81.8	96	1	V179_FYVIV	R15911	schizosac	778	9	81.8	100	1	YXAV_FYALI	P07247	thermotoga
706	9	81.8	96	1	Y64_TYLCU	P48612	tomato yell	779	9	81.8	100	1	GATC_STAAM	Q94708	staphylococ
707	9	81.8	96	1	YU62_EYALI	P46207	escherichia	780	9	81.8	100	1	H1S1_KHBN	P05149	klebsiella
708	9	81.8	96	1	YS98_MYCLE	Q33024	mycobacteri	781	9	81.8	100	1	H1FA_ZYRHO	Q94759	mycobacteri
709	9	81.8	96	1	COXD_POWIN	P07471	bos taurus	782	9	81.8	100	1	PAH0_MHSE	P10601	mus musculu
710	9	81.8	96	1	COXD_POWIN	Q52221	homo sapien	783	9	81.8	100	1	R272_FYKAE	P07247	thermotoga
711	9	81.8	96	1	COXD_POWIN	P43023	mus muscula	784	9	81.8	100	1	RK14_ASH10	P24354	chlamydom
712	9	81.8	96	1	CYTL_VIGON	Q06445	vigna ungui	785	9	81.8	100	1	RK14_CHLRE	Q94992	chlamydom
713	9	81.8	96	1	GATC_SULTO	Q97104	sulfolobus	786	9	81.8	100	1	RK14_CHLAV	P42776	chlorofila v
714	9	81.8	96	1	H1C2_TRYCR	P40258	trypanosoma	787	9	81.8	100	1	RK14_CYACA	Q94747	cyandium c
715	9	81.8	96	1	H411_BUEJA	P60737	blepharisma	788	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
716	9	81.8	96	1	H411_BUEJA	Q29430	blepharisma	789	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
717	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	790	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
718	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	791	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
719	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	792	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
720	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	793	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
721	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	794	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
722	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	795	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
723	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	796	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
724	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	797	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
725	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	798	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
726	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	799	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
727	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	800	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
728	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	801	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
729	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	802	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
730	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	803	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
731	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	804	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
732	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	805	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
733	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	806	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
734	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	807	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
735	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	808	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
736	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	809	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
737	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	810	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
738	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	811	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
739	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	812	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
740	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	813	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
741	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	814	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
742	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	815	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
743	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	816	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
744	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	817	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
745	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	818	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
746	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	819	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
747	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	820	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
748	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	821	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
749	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	822	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
750	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	823	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
751	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	824	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
752	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	825	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
753	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	826	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
754	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	827	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
755	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	828	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
756	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	829	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
757	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	830	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
758	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	831	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
759	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	832	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
760	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	833	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
761	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	834	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
762	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	835	9	81.8	100	1	RK14_CYACA	P11548	cyandium c
763	9	81.8	96	1	HPFA_MARSE	Q29430	blepharisma	836	9	81.8	100	1	RK14_CYACA	P11548	cyandium c

837	9	81.8	101	1	PS14_PAN_50	Q8325	ralstonia s	916	9	81.8	103	1	Y204_VAN3	P1104	synechocystis
838	9	81.8	101	1	ES14_VIRCH	Q8327	vibrio chol	911	9	81.8	103	1	V011_RHOF1	P5143	bacteriophag
839	9	81.8	101	1	PS14_VIRCH	Q8329	virginia po	912	9	81.8	103	1	V011_RHOF1	P5547	rhizobium s
840	9	81.8	101	1	PS16_UREFA	Q8331	ureaplasma	913	9	81.8	103	1	Y016_YEAS1	P5425	saccharomyc
841	9	81.8	101	1	PS18_ATRBB	P58920	atropa bell	914	9	81.8	104	1	Y016_YEAS1	P5427	saccharomyc
842	9	81.8	101	1	PS5_FUECH	P2439	thermus the	915	9	81.8	104	1	Y016_YEAS1	P5450	bradyrhizob
843	9	81.8	101	1	S104_HUMAN	P56447	homo sapien	916	9	81.8	104	1	GAL1_SYN3	P56450	synechocyst
844	9	81.8	101	1	S104_MOUSE	P07091	mus musculu	917	9	81.8	104	1	IAA_SIRIE	P01092	streptomyces
845	9	81.8	101	1	S104_RAT	P05942	rattus norv	918	9	81.8	104	1	HEB_NUHA	P01093	neisseria m
846	9	81.8	101	1	URE2_BALIN	P41392	haemophilus	919	9	81.8	104	1	LA1_FAI	P20717	ratifera t
847	9	81.8	101	1	URE3_UREFA	Q56557	ureaplasma	920	9	81.8	104	1	NEU2_YEAS1	P40097	lampyrida fi
848	9	81.8	101	1	URE3_UREFA	P17274	ureaplasma	921	9	81.8	104	1	P114_HUMAN	P40097	lampyrida fi
849	9	81.8	101	1	Y124_GMYV2	P15236	beet neocat	922	9	81.8	104	1	P421_MUHL	P24359	millardia
850	9	81.8	101	1	Y368_NYCE	P47628	haemophilus	923	9	81.8	104	1	P421_MUHL	P24359	millardia
851	9	81.8	101	1	Y060_HAFIN	P41138	haemophilus	924	9	81.8	104	1	P418_EGHA	P24359	millardia
852	9	81.8	101	1	Y060_HAFIN	P36660	escherichia	925	9	81.8	104	1	S019_ARCPO	P24359	millardia
853	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	926	9	81.8	104	1	Y060_HAFIN	P24359	millardia
854	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	927	9	81.8	104	1	Y060_HAFIN	P24359	millardia
855	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	928	9	81.8	104	1	Y060_HAFIN	P24359	millardia
856	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	929	9	81.8	104	1	Y060_HAFIN	P24359	millardia
857	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	930	9	81.8	104	1	Y060_HAFIN	P24359	millardia
858	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	931	9	81.8	104	1	Y060_HAFIN	P24359	millardia
859	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	932	9	81.8	104	1	Y060_HAFIN	P24359	millardia
860	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	933	9	81.8	104	1	Y060_HAFIN	P24359	millardia
861	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	934	9	81.8	104	1	Y060_HAFIN	P24359	millardia
862	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	935	9	81.8	104	1	Y060_HAFIN	P24359	millardia
863	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	936	9	81.8	104	1	Y060_HAFIN	P24359	millardia
864	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	937	9	81.8	104	1	Y060_HAFIN	P24359	millardia
865	9	81.8	101	1	Y060_HAFIN	P76162	escherichia	938	9	81.8	104	1	Y060_HAFIN	P24359	millardia
866	9	81.8	101	1	Y060_HAFIN	P76162	escherichia								

DE Insulin-like growth factor binding protein 4 (IGFBP-4) (Igf-4)
 DE (IGF-binding protein 4) (Fragment).
 GN IGFBP4.
 OS Sus scrofa (Pig).
 CC Eurythera; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE.
 RX MEDLINE=92109718; PubMed=1722398;
 RA Coleman M.E., Pan Y.-C.E., Ethernan T.D.;
 RT "Identification and NH2-terminal amino acid sequence of three
 RT insulin-like growth factor-binding proteins in porcine serum";
 RL Biochem. Biophys. Res. Commun. 181:1131-1136(1991).
 CC -1- FUNCTION: IGF-BINDING PROTEINS PROLONG THE HALF-LIFE OF THE IGFs
 CC AND HAVE BEEN SHOWN TO EITHER INHIBIT OR STIMULATE THE GROWTH
 CC PROMOTING EFFECTS OF THE IGFs ON CELL CULTURE. THEY ALTER THE
 CC INTERACTION OF IGFs WITH THEIR CELL SURFACE RECEPTORS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: CONTAINS 1 THYPOGLOBULIN TYPE-I DOMAIN.
 CC -1- SIMILARITY: BELONGS TO THE INSULIN-LIKE GROWTH FACTOR BINDING
 CC PROTEIN FAMILY.
 CC PIR; JH0517.
 DR InterPro: IPR000867; Ins_lgr_fac_pr
 DR InterPro: IPR000716; Thyroglobulin_1
 DR PROSITE: PS00322; IGF BINDING; PARTIAL.
 DR PROSITE: PS00484; THYROGLOBULIN_1; PARTIAL.
 KW Growth factor binding;
 FT NON-TER 16 16
 FT SEQUENCE 16 AA 164 MW 406604000.942 4964;
 Query Match 81.8%; Score 9; DB 1; Length 16;
 Best Local Similarity 66.7%; Pred. No. 4.7e+02;
 Matches 2; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 14 LAR 16
 RESULT 5
 YAA5_RH-PA
 ID YAA5_RH-PA STANDARD: PPT; 19 AA.
 AC Q02005;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 16-OCT-2001 (Rel. 43, Last annotation update)
 DE Hypothetical protein in AAP6 6-region (Fragment).
 OS Rhodospseudomonas palustris.
 CC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group.
 CC Bradyrhizobium group; Rhodospseudomonas
 OX NCBI_TaxID=1076;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CGA009;
 RX MEDLINE=92343492; PubMed 1522059;
 RA Dispensa M., Thomas C.T., Kim M.K., Furlong J.A., Bilsdorf J.,
 RA Harwood C.S.;
 RT "Anaerobic growth of Rhodospseudomonas palustris on 4-hydroxybenzoate
 RT is dependent on AadK, a member of the cyclic AMP receptor protein
 RT family of transcriptional regulators.";
 RL J. Bacteriol. 174:5803-5813(1992).
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non profit institutions as long as its content is in no way
 CC modified and this statement is not removed, added by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announcement/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: M92426; AAA26089.1;
 CC PIR: A43334; A43334.

KW Hypothetical protein.
 IT NON-TER 1
 SQ SEQUENCE 18 AA; 2173 HW; 61DAHDFE4E41740A CR064;
 Query Match 81.8%; Score 9; DB 1; Length 18;
 Best Local Similarity 66.7%; Pred. No. 5.4e+02;
 Matches 2; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 6 LAR 8
 RESULT 6
 LYC_FEL-CA
 ID LYC_FEL-CA STANDARD: PPT; 20 AA.
 AC P47155;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Lysocyme C (Lycocystin) (1.1 beta-D arabinofuranosylase C) (Fragment).
 GN LYZ.
 OS Felis silvestris catus (Cat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
 OX NCBI_TaxID=9685;
 RN [1]
 RP SEQUENCE.
 RC TISSUE=Milk;
 RX MEDLINE=96253493; PubMed 2447447;
 RA Halliday J.A., Bell K., McKenzie H.A., Shaw D.C.;
 RT "Feline whey proteases: identification, isolation and initial
 RT characterization of alpha-lactalbumin, beta-lactoglobulin and
 RT lysozyme";
 RL Comp. Biochem. Physiol. 95B:774-779(1990).
 CC -1- FUNCTION: Lysocymes have primarily a bacteriolytic function; those
 CC in tissues and body fluids are associated with the monocytes/
 CC macrophage system and enhance the activity of immunoproteas.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of the 1,4-beta-linkages between N-
 CC acetyl-D-glucosamine and N-acetylmuramic acid in peptidoglycan
 CC heteropolymers of the prokaryotes cell walls.
 CC -1- SUBUNIT: Monomer.
 CC -1- SIMILARITY: Lysocyme C is capable of both hydrolysis and
 CC transglutinylation; it shows also a slight esterase activity. It
 CC acts rapidly on both peptide substituted and unsubstituted
 CC peptidoglycan and slowly on gelatin carboxydehydrates.
 CC -1- SIMILARITY: BELONGS TO FAMILY 22 OF GLYCOSYL HYDROLASES.
 DR PIR; A09525; A09525.
 DR HSSP: P11376; 280L.
 DR InterPro: IPR001916; GH_22.
 DR Pfam: PF00962; 178; 1.
 DR PROSITE: PS00128; LACTALBUMIN_LYZOZYME; PARTIAL.
 KW Hydrolase; Glycosidase; Bacteriolytic enzyme; Milk.
 IT NON-TER 20 20
 SQ SEQUENCE 20 AA; 3214 HW; FERR24EA59425E13 CR064;
 Query Match 81.5%; Score 9; DB 1; Length 20;
 Best Local Similarity 66.7%; Pred. No. 6e+02;
 Matches 2; Conservative 9; Mismatches 7; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 8 LAR 10
 RESULT 7
 RECX_AZOVI
 ID RECX_AZOVI STANDARD: PPT; 20 AA.
 AC P37863;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-OCT-1994 (Rel. 30, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE Regulatory protein reoX (Fragment).
 GN

GN REXX.
 OS Acetobacter vinelandii.
 AC Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
 AC Acetobacter.
 CX NCBI_TaxID 354;
 PN (1)
 RP SEQUENCE FROM N.A.
 PX MEDLINE 94226477; PubMed 156342;
 RA Venkatesh T.V., Das H.K.;
 R1 "The Acetobacter vinelandii rxa gene: sequence analysis and
 R1 regulation of expression";
 RL Gene 114:47-54(1992).
 RL (2)
 PP IDENTIFICATION.
 PX MEDLINE 94218258; PubMed 8165147;
 RA de Mel R., Scholts G., Vanderheyden J.;
 R1 "A putative regulatory gene downstream of rxa is conserved in gram
 R1 negative and gram-positive bacteria";
 RL Nucleic Acids Res. 22:1313-1314(1994).
 CC -1- FUNCTION: MAY PLAY A REGULATORY ROLE POSSIBLY BY INTERACTING WITH
 CC REXX.
 CC -1- SIMILARITY: BELONGS TO THE REXX FAMILY.
 CC
 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC at the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license at <http://www.ebi.ac.uk/submit/submit.html>
 CC or send an email to license@ebi.ac.uk.
 CC
 CC EMBL: S96898; ; NOT_ANNOTATED_PDS.
 RL NCBI_TaxID 20 20
 SQ SEQUENCE 20 AA: 2111 MW: 680948636360655 CR654;
 Query Match 81.8%; Score 9; DB 1; Length 20;
 Best Local Similarity 66.7%; Pred. No. 66402;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 18 LAR 20
 RESULT 8
 ID SYA_RAI
 AC P50475;
 DT 01-OCT-1996 (rel. 34, Created)
 DT 01-OCT-1996 (rel. 34, Last sequence update)
 DE Alanine tRNA synthetase (EC 6.1.1.7) (Amino tRNA ligase) (AARS)
 DE (Fragment).
 DE
 GN AARS.
 OS Rattus norvegicus (Rat).
 AC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 AC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 CX NCBI_TaxID 10116;
 RN (1)
 RP SEQUENCE.
 PX MEDLINE 91447799; PubMed 2949289;
 RA Dittam J.D., Dittam S.S., Brunley L.L.;
 R1 "Alanine tRNA synthetase from Escherichia coli, Bombyx mori and Rattus
 R1 talpis. Existence of common structural features";
 RL Eur. J. Biochem. 198;201-210(1991).
 CC -1- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) -> AMP +
 CC diphosphate + L-alanyl-tRNA(Ala).
 CC -1- SUBUNIT: MONOMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic (cytosol).
 CC -1- SIMILARITY: BELONGS TO CLASS I AMINO-ACID tRNA SYNTHETASE FAMILY.
 DR InterPro: IPR002106; AARSRA1144seq11.
 DR PROSITE: PS50860; AA_TRNA_LIGASE_ILALA; PARTIAL.

KW Aminoacyl tRNA synthetase; Protein biosynthesis; Ligase; ATP binding.
 IT NRTIER 1
 FT NRTIER 21 21
 SQ SEQUENCE 21 AA: 2293 MW: 175935926143475 CR664;
 Query Match 81.8%; Score 9; DB 1; Length 21;
 Best Local Similarity 66.7%; Pred. No. 66402;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 18 LAR 20
 RESULT 9
 ID ANP_CHECK
 AC P21805;
 DT 01-MAY-1991 (rel. 18, Created)
 DT 01-MAY-1991 (rel. 18, Last sequence update)
 DT 16-OCT-2001 (rel. 40, Last annotation update)
 DE C-type natriuretic peptide (CNP).
 GN NPCC.
 OS Gallus gallus (Chicken).
 AC Fukuyama M., Choudhary Choudhary Choudhary Vert-Prata; Euteleostomi;
 AC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 CX NCBI_TaxID-9031;
 RN (1)
 RP SEQUENCE.
 RC TISSUE: Brain;
 RX MEDLINE-91113186; PubMed-1989595;
 RA Arimura J.J., Minamide N., Katsawa K., Matsuo H.;
 R1 "Isolation and identification of C-type natriuretic peptide in
 R1 chicken brain";
 RC Biochem. Biophys. Res. Commun. 174:142-148(1991).
 CC -1- FUNCTION: VASORELAXANT ACTIVITY. HAS A GMP-STIMULATING ACTIVITY.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NATRIURETIC PEPTIDES FAMILY.
 DR PIR: JT0581; J10581.
 DR InterPro: IPR000664; Natr_peptide.
 DR FLAM: P02212; ANP; 1
 DR PRINTS: PR00710; NATPEPTIDES.
 DR SMART: SM00183; NAT_PEP; 1.
 DR PROSITE: PS00264; NATRIURETIC_PEPTIDE; 1.
 KW Vasodilator.
 FT DISULFID 6 22
 SQ SEQUENCE 22 AA: 2244 MW: 172447861914025 CR664;
 Query Match 81.8%; Score 9; DB 1; Length 22;
 Best Local Similarity 66.7%; Pred. No. 66402;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 2 LSR 4
 RESULT 10
 ID GLNA_PRRP
 AC P20479;
 DT 01-FEB-1991 (rel. 17, Created)
 DT 01-FEB-1991 (rel. 17, Last sequence update)
 DT 15-JUL-1996 (rel. 37, Last annotation update)
 DE Glutamine synthetase (EC 6.3.1.2) (Glutamate
 DE (Fragment)).
 OS Phormidium laticum.
 AC Bacteriia; Cyanobacteria; Oscillatoriales; Phormidiales.
 CX NCBI_TaxID-32060;
 RN (1)
 RP SEQUENCE.
 RX MEDLINE-89214011; PubMed-2407514;

RA Sawa Y., Ichihara H., Yoshida K., Taniguchi Y., Taniguchi H., Soda K.,
 RI "Glutamine synthetase from a cyanobacterium, *Planktoniella lapidum*,
 RT purification, characterization, and comparison with other
 RI cyanobacterial enzymes.",
 RL J. Biochem. 104:917-927(1998).
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + NH(3) -> ADP + phosphate +
 CC L-glutamine.
 CC -1- SUBUNIT: OLIGOMER OF 12 SUBUNITS ARRANGED IN THE FORM OF TWO
 CC HEXAGONS.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE GLUTAMINE SYNTHETASE FAMILY.
 DR PR: PX0011; PX0011.
 DR InterPro: IPR001691; CLN_Synth.
 DR PROSITE: PS00180; GLNA_1; PARTIAL
 DR PROSITE: PS00181; GLNA_ATP; PARTIAL.
 KW Lysase.
 FT NONTER 23 23
 SQ SEQUENCE 25 AA: 2556 MW: 246925462A579 CR04.
 Query Match 81.8%; Score 9; DB 1; Length 23;
 Best Local Similarity 66.7%; Pred. No. 7692;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 3
 DB 1 1
 7 LSR 9

RESULT 11
 ID IPYR_PSEAN STANDARD; PRT: 25 AA.
 AC P80998;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15 JUN 2002 (Rel. 41, Last annotation update)
 DE Inorganic pyrophosphatase (EC 3.6.1.1) (pyrophosphate phospho-
 DE hydrolase) (ppase) (fragment).
 GN ppa.
 OS Pseudanabaena sp. (strain PCC 6901).
 CC Bacteria; Cyanobacteria; Oscillatoriales; Pseudanabaena.
 CX NCBI_TaxID=47918;
 RN [1]
 RP SEQUENCE.
 RA Gomez R., Serrano A.;
 RI Submitted (FEB-1997) to the SWISS-PROT data bank.
 CC -1- FUNCTION: Hydrolyses PPi generated in anabolic reactions.
 CC -1- CATALYTIC ACTIVITY: Diphosphate + H(2)O -> 2 phosphate.
 CC -1- COFACTOR: Requires the presence of divalent metal cation.
 CC Magnesium confers the highest activity. Binds 1 divalent cations
 CC per subunit (By similarity).
 CC -1- SUBUNIT: Homohexamer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE PPASE FAMILY.
 KW Hydrolase; Magnesium.
 FT NONTER 25 25
 SQ SEQUENCE 25 AA: 2530 MW: 191997APN4N14U CR04.
 Query Match 81.8%; Score 9; DB 1; Length 25;
 Best Local Similarity 66.7%; Pred. No. 7692;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 3
 DB 1 1
 3 LSR 5

RESULT 12
 ID NEUD_PANIE
 AC P20056;
 DT 01-FEB-1991 (Rel. 17, Created)
 DT 01-FEB-1991 (Rel. 17, Last sequence update)
 DT 15-JUN 2002 (Rel. 41, Last annotation update)

DE Serenaria 0.9% (Seq. 25).
 CC Same taxonomic (Bacteria, common trop).
 CC Eubacteria, Mollicutes, Chlamidia, Vertebrata, Euteleostomi;
 CC Amphibia, Batrachia, Anura, Neobatrachia; Ranidae; Rana.
 CX NCBI_TaxID 3407;
 RN [1]
 RP SEQUENCE.
 RA TISSUE: Intestine;
 EX MEDLINE 90078173; Pubmed 2592357;
 RA Smith J., Vignos Y., Sparks E.A., Aiken A., Parun E.B.,
 RA Chrysanthou K., Bloom S.R.;
 RI "The distribution, purification, and pharmacological action of an
 RI amphibian neuromedin U.",
 RL J. Biol. Chem. 264:20981-20987(1989).
 CC -1- FUNCTION: STIMULATES HYPERTENSIVE SMOOTH MUSCLE CONTRACTION AND CAUSES
 CC SELECTIVE VASOCONSTRICTION.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE RMU FAMILY.
 DR PR: A34179; A34179.
 DR PIR: A34179; A34179.
 DR PIR: P02075; RMU_1.
 DR PIR: P02075; RMU_1.
 DR PIR: P02075; RMU_1.
 DR PROSITE: PS00967; NMD; 1.
 KW Amidation; Hormone.
 FT MODRES 25 25
 SQ SEQUENCE 25 AA: 2842 MW: 5A0199549A06F04 CR04.
 Query Match 81.8%; Score 9; DB 1; Length 25;
 Best Local Similarity 66.7%; Pred. No. 7692;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 3
 DB 1 1
 14 LSR 15

RESULT 13
 ID SPUG_PSEUS STANDARD; PRT: 25 AA.
 AC P82457;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Spingerin.
 OS Pseudocanthohermes spingeri.
 CC Eubacteria, Mollicutes, Actinoptera, Mandibulata, Euteleostomi, Eupoda;
 CC Insecta, Platyptera, Neoptera, Coleoptera, Polyptera, Isoptera;
 CC Formicidae; Macrotermitidae; Pseudocanthohermes
 CX NCBI_TaxID=115113;
 RN [1]
 RP SEQUENCE, MASS SPECTROMETRY, AND FUNCTION.
 RA Lambert M., Zachary L., Lanot R., Bonjourn C., Robert A.,
 RA Hoffmann J.A., Huet P.;
 RI "Characterization of the spingerin, a cysteine-rich
 RI antifungal and a linear antibacterial peptide in a termite insect.",
 RL J. Biol. Chem. 276:4495-4499(2001).
 CC -1- FUNCTION: ACTIVE AGAINST GRAM POSITIVE BACTERIA IN MIDGUT OF RMU
 CC K. PNEUMONIAE, S. TYPHIMURUM AND P. AERUGINOSA, Y. ENTEROCOLITICA AND
 CC AND FLAVENTRICUS FURGI F. COLUMBUM, H. CRASSA, H. HERMANNI AND
 CC T. VIRIDAE. INACTIVE AGAINST GRAM NEGATIVE BACTERIA P. SUPPLIS,
 CC S. PNEUMONIAE, E. TYPHIMURUM AND Y. ENTEROCOLITICA, GRAM NEGATIVE BACTERIA
 CC S. GLAUCAE AND E. CACIOTURA AND EUKARYOTIC FUNGUS B. BASILLANA.
 CC -1- INDUCTION: by bacterial infection.
 CC -1- MASS SPECTROMETRY: MW 4001.6; METHIONINE.
 CC -1- MISCELLANEOUS: THERE ARE THREE ISOPREES OF SPINGERIN.
 KW Antibiotic; Peptide.
 FT VARIANT 22 25
 FT VARIANT 22 25
 FT VARIANT 22 25
 SQ SEQUENCE 25 AA: 4001 MW: AA7947024262F00 CR04.

```

Query Match      81.8%; Score 9; DB 1; Length 25;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 2; Conservative 0; Mismatches 1; Gaps 0.

QY 1 LXR 3
DB 22 LXR 24

RESULT 14
UBQL_BOVIN
ID UBQL_BOVIN STANDARD; PRI: 25 AA.
AC P23356;
DT 01-NOV-1991 (rel. 20, Created)
DT 01-NOV-1991 (rel. 20, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Ubiquitin carboxyl-terminal hydrolase isozyme L1 (EC 3.4.19.12) (UCH-
DE L1) (Ubiquitin thiolesterase L1) (Neuron cytoplasmic protein 9.5)
DE (P99 9.5) (P99 9.5) (Fragment).
GN UCHL1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Sumatran; Equidae; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN 111
RP SEQUENCE.
RC TISSUE: Brain;
RX MEDLINE 9209846; PubMed 1844249;
RA Giampapa L., Bianchi R., Cecaroli P., Pala G., Serci G.,
RA Antonelli S., Borchini V., Donato R.;
RA "Neuron-specific" protein gene product 9.5 (P99 9.5) is also
RA expressed in glioma cell lines and its expression depends on cellular
RA growth state.*
RL FEBS Lett. 290:131-134(1991).
CC 1- FUNCTION: UBIQUITIN PROTEIN HYDROLASE IS INVOLVED BOTH IN THE
CC PROCESSING OF UBIQUITIN PRECURSORS AND OF UBIQUITINATED PROTEINS.
CC THIS ENZYME IS A THIOLESTERASE THAT SPECIFICALLY HYDROLYSES
CC A PEPTIDE BOND AT THE C-TERMINAL GLYCINE OF UBIQUITIN.
CC 2- CATALYTIC ACTIVITY: Ubiquitin C-terminal thiolester + H(2)O =
CC ubiquitin + a thiol.
CC 3- SUBCELLULAR LOCATION: Cytoplasmic.
CC 4- TISSUE SPECIFICITY: NEURONS AND CELLS OF THE DIFFUSE
CC NEURONAL RETICULAR SYSTEM AND THEIR DENDRONS.
CC 5- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C12.
DR PIR: S17561; S17561.
DR MEROPS: C12.061.
DR InterPro: IPR001578; DCHL1.
DR Pfam: PF01088; Peptidase_C12; 1.
DR PROSITE: PS00140; DCHL1: PARTIAL.
KW Ubiquitin degradation pathway; Hydrolase; Thiol protease; Multidomain family.
FT NON_TER 25
SQ SEQUENCE 25 AA: 2812 MW: 26056.60A754255 CRC64.

Query Match      81.8%; Score 9; DB 1; Length 25;
Best Local Similarity 66.7%; Pred. No. 7.6e+02;
Matches 2; Conservative 0; Mismatches 1; Gaps 0.

QY 1 LXR 3
DB 17 LXR 19

RESULT 15
NTRC_RHLP
ID NTRC_RHLP STANDARD; PRI: 26 AA.
AC P41502;
DT 01-NOV-1995 (rel. 42, Created)
DT 01-NOV-1995 (rel. 42, Last sequence update)
DT 15-JUN-2002 (rel. 41, Last annotation update)
DE Nitrogen assimilation regulatory protein (fragment).
GN NTRC.
OS Rhizobium leguminosarum (bacterial phasid).

```

```

Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
CC Rhizobiaceae; Rhizobium.
CX NCBI_TaxID:385;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN:CF-4;
RX MEDLINE 94018651; PubMed 8412704;
RA Patriarca E.J., Riccio A., Tate R., Coloma-Romano S., Iacovino M.,
RA Defez R.;
RA "The ntrC genes of Rhizobium leguminosarum are part of a complex
RA operon subject to negative regulation.*"
RL Mol. Microbiol. 9:569-577(1993).
CC 1- FUNCTION: MEMBER OF THE TWO COMPONENT REGULATORY SYSTEM NTRC/NTRG.
CC INVOLVED IN THE ACTIVATION OF NITROGEN ASSIMILATORY GENES SUCH AS
CC GLN-AMC. NTRC IS PHOSPHORYLATED BY NTRG AND INTERACTS WITH SIGMA 54.
CC 2- SIMILARITY: CONTAINS 1 RESPONSE REGULATORY DOMAIN.
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC altered, republished, redistributed, or used for commercial
CC or sold at all to licensees (see http://www.ebi.ac.uk/edl/terms.html).
CC of send an email to license@ebi.ac.uk.
DR EMBL: A71435; 1 NOT_ANNOTATED_THIS.
DR PIR: S36203; S36203.
DR InterPro: IPR001789; Response_dom.
DR PROSITE: PS50110; RESPONSE_REGULATORY; 1.
KW Nitrogen fixation; Transcription regulation; Repressor; Activator;
KW DNA-binding; ATP-binding; Phosphorylation; Sensory transduction.
FT DOMAIN 1 26
FT NON_TER 26
SQ SEQUENCE 26 AA: 2767 MW: 41163.60A66304 CRC64.

Query Match      81.8%; Score 9; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 8e+02;
Matches 2; Conservative 0; Mismatches 1; Gaps 0.

QY 1 LXR 3
DB 22 LXR 24

RESULT 16
YFHA_KLEFN
ID YFHA_KLEFN STANDARD; PRI: 26 AA.
AC P21710;
DT 01-MAY-1991 (rel. 18, Created)
DT 01-MAY-1991 (rel. 18, Last sequence update)
DT 16-JUL-2001 (rel. 40, Last annotation update)
DE Hydrolytic protein in GNR 5' region (fragment).
GN YFHA.
OS Klebsiella pneumoniae.
CC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
CC Klebsiella.
CX NCBI_TaxID:574;
RN 111
RP SEQUENCE FROM N.A.
RC STRAIN:M5a1;
RX MEDLINE 89201233; PubMed-2907369;
RA Hotell A., Merrick M.;
RA "Identification of the Klebsiella pneumoniae alk gene nucleotide
RA sequence of wild-type and mutant alleles.*"
RL Mol. Gen. Genet. 215:134-138(1988).
CC 1- FUNCTION: PROBABLE MEMBER OF A TWO COMPONENT REGULATORY SYSTEM
CC YFHA/YFHK.
CC 2- PFM: THUS REVEALED BY YFHK (POTENTIAL).
CC 3- SIMILARITY: THE N-TERMINAL REGION IS SIMILAR TO THAT OF OTHER
CC RESPONSE REGULATORY DOMAINS OF SENSAORY TRANSDUCTION SYSTEMS.
CC 4- SIMILARITY: THE CENTRAL REGION CONTAINS A SIGMA 54 FACTOR
CC INTERACTION AND BINDING DOMAIN.
CC 5- SIMILARITY: TO EQUIVALENT PROTEIN IN E. COLI.

```


CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/edm/>)
 CC or send an email to license@ebi.ac.uk.

DR EMBL: X14012; CAA32176.1; -
 DR PIR: S04376; S04376.
 DR InterPro: IPR002078; Sig54 INTERACT.
 DR PROSITE: PS00675; SIGMA54_INTERACT_1; PARTIAL.
 DR PROSITE: PS00676; SIGMA54_INTERACT_2; PARTIAL.
 DR PROSITE: PS00698; SIGMA54_INTERACT_3; PARTIAL.
 DR PROSITE: PS00695; SIGMA54_INTERACT_4; PARTIAL.
 KW Hypothetical protein. *Genes* *transcription* *phosphorylation*
 KW Transcription regulation. DNA-binding. ATP-binding.
 FT NON_TER 1
 SQ SEQUENCE 26 AA; 3198 MW; 510C88BA443BF0C5 CRC64.

Query Match 81.8%; Score 9; DB 1; Length 26;
 Best local Similarity 56.7%; Pred. No. gaps 0;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 14 LSR 16

RESULT 17
 CXXR_CONRA STANDARD; PRT; 27 AA.
 AC PS8806;
 DI 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Conantokin-R (Con-R).
 OS Conus radiatus (Rayed cone).
 OC Eukaryota, Metazoa, Mollusca, Gastropoda, Conoquasidifida,
 OC Nectopoda, Conoidea, Conidae, Conus.
 OX NCBI_TaxID=61198;
 FN [1]
 RP SEQUENCE, SYNTHESIS, AND MASS SPECTROMETRY.
 RC TISSUE=Venom;
 RX MEDLINE=20072842; PubMed=10604979;
 RA White H S., McCabe P.T., Armstrong H., Donavan S.D., Cruz L.J.,
 RA Aboodie F.C., Torres J., Rivier J.E., Paarmann I., Hollmann M.,
 RA Olivera B.M.;
 RT "In vitro and in vivo characterization of conantokin R, a selective
 RT NMDA receptor antagonist isolated from the venom of the fish-hunting
 RT snail *Conus radiatus*."
 RL J. Pharmacol. Exp. Ther. 292:425-432(2000).
 CC -1- FUNCTION: Induces sleep-like symptoms in young mice. Inhibits
 CC N-methyl-D-aspartate (NMDA) receptor-mediated calcium influx in
 CC central nervous system neurons.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
 CC -1- MASS SPECTROMETRY: MW=3098.
 CC -1- SIMILARITY: BELONGS TO THE CONANTOKIN FAMILY.
 KW Toxin; Vitamin K; Gamma-carboxyglutamic acid; Calcium.
 FT DISULFID 21 25
 FT MOD_RES 3 4
 FT MOD_RES 4 4
 FT MOD_RES 11 11
 FT MOD_RES 15 15
 SQ SEQUENCE 27 AA; 292; MW; 25120A734E6134364.

Query Match 81.8%; Score 9; DB 1; Length 27;
 Best local Similarity 56.7%; Pred. No. gaps 0;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3

RESULT 19
 CXXR_CONRA STANDARD; PRT; 27 AA.
 AC PS2947;
 DI 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Secretin.
 GN SCL.
 OS *Cryptolagus cuniculus* (Rabbit).
 OC Eukaryota, Metazoa, Chordata, Grantaria, Vertebrata, Eutelestomii,
 OC Mammalia, Eutheria, Lagomorpha, Leporidae, Cryptolagus.
 OX NCBI_TaxID=9980;
 FN [1]
 RP SEQUENCE.
 RC TISSUE=Small Intestine;
 RX MEDLINE=6025994; PubMed=2412988;
 RA Gasser D., Buscail L., Gaudin A., Gaudin P., de Meel P., Rathe J.,
 RA Robberecht P., Vandermeeers P., M.C., Vandermeeers A., Christophe J.,
 RA "Amino acid sequence of VIP, PHI and secretin from the rabbit small
 RA intestine."
 RL Peptides 11:124-128(1990).
 FT DISULFID 11 12
 FT MOD_RES 11 12
 SQ SEQUENCE 27 AA; 3198 MW; 510C88BA443BF0C5 CRC64.

Query Match 81.8%; Score 9; DB 1; Length 27;
 Best local Similarity 56.7%; Pred. No. gaps 0;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3

DB 12 LAR 14
 RESULT 18
 CXXR_CONRA STANDARD; PRT; 27 AA.
 AC PS0910;
 DI 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE Secretin.
 GN SCL.
 OS *Canis familiaris* (Dog).
 OC Eukaryota, Metazoa, Vertebrata, Grantaria, Vertebrata, Eutelestomii,
 OC Mammalia, Eutheria, Carnivora, Fissipedia, Canidae, Canis.
 OX NCBI_TaxID=9615;
 FN [1]
 RP SEQUENCE.
 RC TISSUE=Intestine;
 RX MEDLINE=87314294; PubMed=626755;
 RA Shimamura Y., Ing J., Yalow R.S.;
 RA "Partial secretion, release, and release inhibition."
 RL Life Sci. 41:1243-1248(1987).
 CC -1- FUNCTION: STIMULATES FORMATION OF NADPH(+) RICH PANCREATIC JUICE
 CC AND SECRETION OF NADPH(+) RICH BILE AND INHIBITS BIL. PRODUCTION
 CC BY THE STOMACH.
 CC -1- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
 DR PIR: A27267; A27267.
 DR InterPro: IPR000532; Glucagon.
 DR Pfam: PF00123; hormone2; 1.
 DR PRINTS: PR00275; GHVAG5FN.
 DR SMART: SM00670; GLDFA; 1.
 DR PROSITE: PS00269; GLUCAGON; 1.
 KW Glucagon family, Hormone, Amidation.
 FT MOD_RES 27 27
 FT MOD_RES 27 27
 SQ SEQUENCE 27 AA; 3376 MW; 244015B147955B78 CRC64;

Query Match 81.8%; Score 9; DB 1; Length 27;
 Best local Similarity 56.7%; Pred. No. gaps 0;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 10 LSR 12

RESULT 19
 CXXR_CONRA STANDARD; PRT; 27 AA.
 AC PS2947;
 DI 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Secretin.
 GN SCL.
 OS *Cryptolagus cuniculus* (Rabbit).
 OC Eukaryota, Metazoa, Chordata, Grantaria, Vertebrata, Eutelestomii,
 OC Mammalia, Eutheria, Lagomorpha, Leporidae, Cryptolagus.
 OX NCBI_TaxID=9980;
 FN [1]
 RP SEQUENCE.
 RC TISSUE=Small Intestine;
 RX MEDLINE=6025994; PubMed=2412988;
 RA Gasser D., Buscail L., Gaudin A., Gaudin P., de Meel P., Rathe J.,
 RA Robberecht P., Vandermeeers P., M.C., Vandermeeers A., Christophe J.,
 RA "Amino acid sequence of VIP, PHI and secretin from the rabbit small
 RA intestine."
 RL Peptides 11:124-128(1990).
 FT DISULFID 11 12
 FT MOD_RES 11 12
 SQ SEQUENCE 27 AA; 3376 MW; 244015B147955B78 CRC64;

Query Match 81.8%; Score 9; DB 1; Length 27;
 Best local Similarity 56.7%; Pred. No. gaps 0;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 10 LSR 12

RESULT 19
 CXXR_CONRA STANDARD; PRT; 27 AA.
 AC PS2947;
 DI 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Secretin.
 GN SCL.
 OS *Cryptolagus cuniculus* (Rabbit).
 OC Eukaryota, Metazoa, Chordata, Grantaria, Vertebrata, Eutelestomii,
 OC Mammalia, Eutheria, Lagomorpha, Leporidae, Cryptolagus.
 OX NCBI_TaxID=9980;
 FN [1]
 RP SEQUENCE.
 RC TISSUE=Small Intestine;
 RX MEDLINE=6025994; PubMed=2412988;
 RA Gasser D., Buscail L., Gaudin A., Gaudin P., de Meel P., Rathe J.,
 RA Robberecht P., Vandermeeers P., M.C., Vandermeeers A., Christophe J.,
 RA "Amino acid sequence of VIP, PHI and secretin from the rabbit small
 RA intestine."
 RL Peptides 11:124-128(1990).
 FT DISULFID 11 12
 FT MOD_RES 11 12
 SQ SEQUENCE 27 AA; 3376 MW; 244015B147955B78 CRC64;

Query Match 81.8%; Score 9; DB 1; Length 27;
 Best local Similarity 56.7%; Pred. No. gaps 0;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 10 LSR 12

RESULT 19
 CXXR_CONRA STANDARD; PRT; 27 AA.
 AC PS2947;
 DI 01-OCT-1993 (Rel. 27, Created)
 DT 01-OCT-1993 (Rel. 27, Last sequence update)
 DT 01-OCT-1993 (Rel. 27, Last annotation update)
 DE Secretin.
 GN SCL.
 OS *Cryptolagus cuniculus* (Rabbit).
 OC Eukaryota, Metazoa, Chordata, Grantaria, Vertebrata, Eutelestomii,
 OC Mammalia, Eutheria, Lagomorpha, Leporidae, Cryptolagus.
 OX NCBI_TaxID=9980;
 FN [1]
 RP SEQUENCE.
 RC TISSUE=Small Intestine;
 RX MEDLINE=6025994; PubMed=2412988;
 RA Gasser D., Buscail L., Gaudin A., Gaudin P., de Meel P., Rathe J.,
 RA Robberecht P., Vandermeeers P., M.C., Vandermeeers A., Christophe J.,
 RA "Amino acid sequence of VIP, PHI and secretin from the rabbit small
 RA intestine."
 RL Peptides 11:124-128(1990).
 FT DISULFID 11 12
 FT MOD_RES 11 12
 SQ SEQUENCE 27 AA; 3376 MW; 244015B147955B78 CRC64;

```

DR PIR: C60415; C60415.
DR InterPro: IPR000532; Glucagon.
DR Pfam: PF00124; Hormone2; 1.
DR PRINTS: PR00275; GLUCAG-N.
DR SMART: SM00070; GLUCA; 1.
DR PROSITE: PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone; Amidation.
FT MOD_RES: 27.
SQ SEQUENCE 27 AA; 4105 MW; 48A158000D0G18 CR64;

Query Match 81.8% Score 9; DB 1; Length 27;
Best Local Similarity 66.7% Pred. No. 9; 4e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
DB 10 LSR 12

RESULT 20
SECR_SHEEP
ID SECR_SHEEP STANDARD; PRT: 27 AA.
AC P01299;
DT 01-JUL-1993 (rel. 26, Created)
DI 01-JUL-1993 (rel. 26, last sequence update)
DE Secretin.
GN SEC.
OS Bovine (Sheep).
OC Eukaryota; Metazoa; Chordata; Granulata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Caprinae; Ovis.
OX NCBI_TaxID 9940;
RN 1;
RP SEQUENCE.
RE TISSUE: Small intestine;
RX MEDLINE 91209434; PubMed 2034421;
RA Rongjona Y., Vandermeers A., Potherecht P., Vandermeers-Piret M.G.,
RA Christophe J.;
RT "Purification and amino acid sequence of vasoactive intestinal
RT peptide, peptide histidine isoleucamide and secretin from the ovine
RT small intestine.";
RC Regal, Pept. 32:169-179(1991).
CC -!- FUNCTION: STIMULATES FORMATION OF NAIRN(2) (3) KICH FARKINATE JUNE
CC AND SECRETION OF NAIRN(2) (3) KICH FARKINATE JUNE PRODUCTION
CC BY THE STOMACH.
CC -!- SIMILARITY: BELONGS TO THE GLUCAGON FAMILY.
DR PIR: C60072; SESU.
DR InterPro: IPR000532; Glucagon.
DR Pfam: PF00124; Hormone2; 1.
DR PRINTS: PR00275; GLUCAG-N.
DR SMART: SM00070; GLUCA; 1.
DR PROSITE: PS00260; GLUCAGON; 1.
KW Glucagon family; Hormone; Amidation.
FT MOD_RES: 27.
SQ SEQUENCE 27 AA; 4056 MW; 2D4015804ED95B78 CR64;

Query Match 81.8% Score 9; DB 1; Length 27;
Best Local Similarity 66.7% Pred. No. 9; 4e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
DB 10 LSR 12

RESULT 21
V103_VACU
ID V103_VACU STANDARD; PRT: 28 AA.
AC 900434;
DI 01 APR 1993 (rel. 25, Created)
DI 01 APR 1993 (rel. 25, last sequence update)
DI 01 APR 1993 (rel. 25, last annotation update)
DT 01 FEB 1994 (rel. 26, last annotation update)

```

```

DE Protein 14 (Fragment).
GN 13L.
OS Vaccinia virus (strain L-1VP).
CC Viruses; 4528A Viruses; no RNA stage; Poxviridae; Chordopoxvirinae;
CC Orthopoxvirus.
CX NCBI_TaxID 31531;
RN 1;
RP SEQUENCE FROM H.A.
RX MEDLINE 91066899; PubMed 2250685;
RA Ryazanova O.I., Shchegoleva S.N., Mordukhai A.I., Nefedova N.A.,
RA Yefremov N.H., Gerasimov V.V., Gerasimov A.P., Koltakov V.A.;
RA Malygin E.G.;
RT "Molecular-biological study of vaccinia virus genome, II.
RT Localization and nucleotide sequence of vaccinia virus genes coding
RT for proteins 46K and 12K.";
RC Mol. Biol. (Mosk) 24:968-976(1990).
CC -!- MISCELLANEOUS: THIS PROTEIN IS SYNTHESIZED IN THE EARLY AS WELL AS
CC THE LATE PHASE OF INFECTION.
CC -!- This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.ebi.ac.uk/edlib/).
CC or send an email to license@ebi.ac.uk.
DR EMBL: X61165; CAA43473.1; -.
DR F02; PS0395; PS0395.
KW Early protein; Late protein.
FT NON_TER: 1.
SQ SEQUENCE 28 AA; 3238 MW; CE10813AC944F010 CR64;

Query Match 81.8% Score 9; DB 1; Length 28;
Best Local Similarity 66.7% Pred. No. 6; 6e+02;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
DB 2 LAR 4

RESULT 22
HSP98_HSP98
ID HSP98_HSP98 STANDARD; PRT: 29 AA.
AC P01540;
DI 01-JUL-1993 (rel. 26, Created)
DI 01-JUL-1993 (rel. 26, last sequence update)
DI 01-JUL-1993 (rel. 26, last annotation update)
DE Heat shock protein HSP98 (Fragment).
OX Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariiales; Sordariaceae; Neurospora.
CX NCBI_TaxID 5141;
RN 1;
RP SEQUENCE.
RC STRAIN-74A;
RX MEDLINE 94112646; PubMed 1472534;
RA Vassiliev A.G., Plekostsky V.D., Frankl R.;
RT "Isolation, partial amino acid sequence, and cellular distribution of
RT heat-shock protein hsp98 from Neurospora crassa.";
RC Biochim. Biophys. Acta 1196:116(1992).
CC -!- SUBCELLULAR LOCATION: MORE CONCENTRATED IN POLYMEROMES THAN
CC IN MONOMEROMES, AND PREFERENTIALLY LOCALIZED IN THE LARGE
CC SUBUNIT.
CC -!- SIMILARITY: BELONGS TO THE CLP/AP/108 FAMILY.
DR PIR: S28174; S28174.
DR InterPro: IPR001270; Claprinin_c1pA/B.
DR PROSITE: PS00870; CLPAP_1; 1.
DR PROSITE: PS00871; CLPAP_2; PARTIAL.
KW Chaperone; Heat shock; ATP-binding.
FT NON_TER: 1.
FT NON_TER: 29

```



```

QY 1 LXR 3
  1
DB 8 LAR 10
  1

RESULT 26
ID ORCC_PSEP0 STANDARD; PRT: 33 AA.
AC P11727;
DT 01-01-1989 (Rel. 12, Created)
DI 01-01-1989 (Rel. 12, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE ornithine carbamoyltransferase, partial (EC 2.3.3.13) (catalase)
DE (fragment).
DB ACh.
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; gamma subphylum; Pseudomonadaceae;
OC Pseudomonas.
OX NCBI_TaxID: 404;
FN 11
RP SEQUENCE.
RX MEDLINE: 85104759; PubMed: 3968046;
RA Faiman P., Portetle D., Stalon V.;
RT "Immunological and structural relatedness of catabolic ornithine
RT carbamoyltransferases and the bacterial enzymes of enterobacteria."
RI J. Bacteriol. 161:714-719(1985)
RN 12
RP SEQUENCE OR 1 12 FROM N.A.
RC STRAIN ATCC 4359;
RA Wilson S.D., Wang M., Filpula D.;
RT Submitted (FPI-1664) to the European Bioinformatics Institute
OC 1- CATALYTIC ACTIVITY: Carbamoyl phosphate + L-ornithine ->
OC L-citrulline.
OC 1- PATHWAY: Arginine degradation via arginine deiminase; second step.
OC 1- SUBUNIT: PREPAREDLY 2-AMINO-3K-PHOSPHAMIDE.
OC 1- SUBCELLULAR LOCATION: Cytoplasmic.
OC 1- SIMILARITY: BELONGS TO THE ATCASES/GTPASES FAMILY.
OC
OC This SWISS-PROT entry is copyright. It is produced through a collaboration
OC between the Swiss Institute of Bioinformatics and the EMBL Outstation
OC at the European Bioinformatics Institute. There are no restrictions on its
OC use by non-profit institutions as long as its content is in no way
OC modified and this statement is not removed, usage by and for commercial
OC entities requires a license agreement (See http://www.ebi.ac.uk/infocentre/
OC or send an email to license@ebi.ac.uk).
EMBL: 007185; AAA16965.1; -
DB BSSP: P08408; LOR1.
DB InterPro: IPR002029; Asp/Arg/Gln-conf.
DB PROSITE: PS00097; CARBAMOYLTRANSFERASE; PARTIAL.
KW Transferase; Arginine metabolism.
FT NLSIER 44 43
SEQUENCE 44 AA: 4016 MW: 841806.34282097 CRG64;
Query Match 81.8%; Score 9; DB 1; Length 33;
Best local similarity 66.7%; Pred. No. 16-03;
Matches 2; Conservation 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LXR 3
  1
DB 26 LAR 26
  1

RESULT 27
ID PKL_DIC01 STANDARD; PRT: 33 AA.
AC P-4101;
DT 01-FEB-1994 (Rel. 28, Created)
DI 01-FEB-1994 (Rel. 28, Last sequence update)
DI 16-01-2001 (Rel. 40, Last annotation update)
DE Protein kinase 1 (EC 2.7.1.7) (Fragment).
DE

```

DR PIR: A33627; A33627;
 DR InterPro: IPR001427; PNAS-A
 DR Problem: P0000535; PNAS-A; 1.
 DR PROSITE: PS00127; PNAS-A; CREATING, PARTIAL.
 KW Hydrolase, Nuclease; Endonuclease; Glycoprotein.
 FT CARBOHYD 4 4 N LINKED (GLCNAC...) (PARTIAL)
 FT CARRHYD 4 4
 FT NON_TER 34 34
 SQ SEQUENCE 34 AA; 9331 MW; F2176DE8A6F517B3 CRC64;
 Query Match 81.8%; Score 9; DB 1; Length 34;
 Best Local Similarity 66.7%; Pred. No. 1.1e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 5 LTR 7
 RESULT 29
 ID CDK6_MOUSE STANDARD; PRT; 35 AA.
 AC Q64261;
 DT 01-NOV-1997 (Rel. 35, Created)
 DI 01-NOV-1997 (Rel. 35, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Cell division protein kinase 6 (P32711); (Serine/threonine protein
 DE kinase PLSTIPK) (CKP2) (Fragment).
 GN CDK6 OR CKP2.
 OS Mus musculus (Mouse).
 OC Euparyota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CBA; TISSUE=Bone marrow.
 RX MEDLINE:9185411; PubMed:944355;
 FA Ersler M.A., Nagorskaya T.V., Vasser J.W.M., Belyarsky A.V.;
 RT "Novel CDK2-related protein kinases produced in murine hematopoietic
 RT stem cells";
 RL Gene 124:305-306(1993).
 RN [2]
 PP SEQUENCE FROM N.A.
 RC STRAIN=CBA; TISSUE=Bone marrow.
 RX MEDLINE:93092802; PubMed:1459039;
 RA Ersler M.A., Nagorskaya T.V., Vasser J.W.M., Belyarsky A.V.;
 RT "Identification of new protein kinase genes, similar to kinases of
 RT the cdk2 family and expressed in murine hematopoietic stem cells";
 RL Lecl. Acad. Rank 5589:324-393-897(1997).
 CC -1- FUNCTION: PROBABLY INVOLVED IN THE CONTROL OF THE CELL CYCLE.
 CC INTERACTS WITH D-TYPE G1 CYCLINS (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC CDK2/CDKX SUBFAMILY.
 CC
 CC This SWISS-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.org/announcement>
 CC or send an email to license@sib-sib.ch).
 CC
 CC EMRL: X65058; CAA46201 1;
 DR MDL: M011272162; Cdk6.
 DR InterPro: IPR0000719; Euk_Pkinase.
 DR InterPro: IPR0022590; Ser_Thr_Pkinase.
 DR Pfam: PF00059; pkinase; 1.
 DR Problem: P0000601; Euk_Pkinase; 1
 DR PROSITE: PS00107; PROTEIN_KINASE_ATP; PARTIAL.
 DR PROSITE: PS00108; PROTEIN_KINASE_ST; PARTIAL.
 DR PROSITE: PS00111; PROTEIN_KINASE_DOM; 1;
 KW Tricardine; Serine/threonine protein kinase; ATF binding; Cell cycle;
 KW Cell division.

FT NON_TER 1 1
 FT DOMAIN 31 35
 FT NON_TER 35 35
 SQ SEQUENCE 35 AA; 1735 MW; 65271662751464 CRC64;
 Query Match 81.8%; Score 9; DB 1; Length 35;
 Best Local Similarity 66.7%; Pred. No. 1.1e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 18 LAR 20
 RESULT 30
 ID F4RE_METHOS STANDARD; PRT; 36 AA.
 AC F80951;
 DT 01-NOV-1997 (Rel. 35, Created)
 DI 01-NOV-1997 (Rel. 35, Last sequence update)
 DI 15-DEC-1998 (Rel. 37, Last annotation update)
 DE F420-dependent NADPH reductase (EC 1.1.1.17) (Fragment).
 OS Methanogenium ordanophilum.
 OC Archaea; Euryarchaeota; Methanococci; Methanomicrobiales;
 OC Methanomicrobiaceae; Methanococcus.
 OX NCBI_TaxID=2199;
 RN [1]
 RP SEQUENCE.
 RC STRAIN DSM 4596;
 RX MEDLINE:98004566; PubMed:9325428;
 RA Berk H., Thauer R.K.;
 RT "Function of coenzyme F420-dependent alcohol dehydrogenase";
 RL Arch. Microbiol. 168:396-402(1997).
 CC -1- FUNCTION: CATALYSES THE REDUCTION OF F420 WITH NADPH(+) (OPTIMAL PH
 CC 5.5), AND THE REDUCTION OF NADP(+) WITH F420H(2) (OPTIMAL PH 9.2).
 CC PROBABLY COMPLETES THE NADPH-DEPENDENT CATALATION OF THE ALCOHOL TO
 CC THE ALKYLE WITH OF F420 DEPENDENT REDUCTION OF 20(2) TO METHANE
 CC (ANABOLIC FUNCTION).
 CC -1- CATALYTIC ACTIVITY: NADPH + coenzyme F420 + NADP(+) + reduced
 CC coenzyme F420.
 CC -1- SIMILARITY: MONOMER.
 CC -1- SIMILARITY: TO A PUTATIVE M.JARNAKSHI1 (ETH-0-03 (M11501)).
 KW oxidoreductase, NADP.
 FT UNSURE 32 36
 FT NON_TER 36 36
 SQ SEQUENCE 36 AA; 3774 MW; 91A52A184A47D03 CRC64;
 Query Match 81.8%; Score 9; DB 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 1.1e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 14 LAR 18
 RESULT 31
 ID NEVY_F13 STANDARD; PRT; 36 AA.
 AC P01304;
 DT 21-JUL-1986 (Rel. 01, Created)
 DI 21-JUL-1986 (Rel. 01, Last sequence update)
 DI 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuropeptide Y (NPY).
 OS NPY.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
 OX NCBI_TaxID=923;
 RN [1]
 RP SEQUENCE.
 RC MEDLINE:83819395; PubMed:6959476;
 RX

KA Iatamoto K.;
 RI "Neuropeptide Y: complete amino acid sequence of the brain peptide.";
 RL Proc. Natl. Acad. Sci. U.S.A. 79:5465-5469(1982).
 RN 121
 RP STRUCTURE BY NMR.
 RX MEDLINE 96121904; PubMed 2372534.
 RA Soudak V., Polton J.L.;
 RI "Sequence-specific 1H NMR assignment and secondary structure of
 RI neuropeptide Y in aqueous solution.";
 RL Biochemistry 29:4599-4515(1993).
 RN 131
 RP STRUCTURE BY NMR.
 RX MEDLINE 94249114; PubMed 1575994;
 RA Cowley D.J., Bellack J.M., Polton J.L., Soudak V.;
 RI "Structure of neuropeptide Y dimer in solution.";
 RL Eur. J. Biochem. 255:1599-1124(1992).
 RN 141
 RP FUNCTION: NPY IS IMPLICATED IN THE CONTROL OF FEEDING AND IN
 CC SECRETION OF GABA/BOMBESIN RELEASE HORMONE.
 CC SUBCELLULAR LOCATION: Secreted.
 CC TISSUE SPECIFICITY: ONE OF THE MOST ABUNDANT PEPTIDES IN THE
 CC NERVOUS SYSTEM. ALSO FOUND IN SOME CHROMAFFIN CELLS OF THE ADRENAL
 CC MEDULLA.
 CC SIMILARITY: BELONGS TO THE NPY / PYY / PPY FAMILY
 DR PIR: A01573; NPYCY.
 DR HSSP: P01303; IRON.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormones; 1.
 DR PRINTS: PR00278; PANCHEORMONE.
 DR ProDom: P0001267; Pancreatic_horm; 1
 DR SMART: SM00309; PAH; 1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS0276; PANCREATIC_HORMONE_2; 1.
 DR NeorepId: Amidation
 KW MOD_RES 36
 FT MOD_RES 36
 SQ SEQUENCE 36 AA: 4255 MW: 916921.60600000 CR664.

Query Match 81.8% Score 9; DB 1; Length 36;
 Best Local Similarity 66.7% Pred. No. 1,1e-03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 3
 1 1
 17 LAR 19

RESULT 42
 NEDY SHEEP
 ID NEDY_SHEEP STANDARD: PPT 46 AA
 AC P14765;
 DT 01-APR-1999 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuropeptide Y (NPY).
 GN NPY.
 OS Ovis aries (Sheep).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Artiodactyla; Pimantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxID=9940;
 RN 111
 RP MEDLINE 9009495; PubMed 2590994;
 RA Sillard R., Auerbach B., Mutt V., Jernvall H.;
 RI "Sheep neuropeptide Y. A third structural type of a highly conserved
 RI peptide.";
 RL FEBS Lett. 258:263-265(1989).
 RN 121
 RP FUNCTION: NPY IS IMPLICATED IN THE CONTROL OF FEEDING AND IN
 CC SECRETION OF GABA/BOMBESIN RELEASE HORMONE.
 CC SUBCELLULAR LOCATION: Secreted.
 CC TISSUE SPECIFICITY: ONE OF THE MOST ABUNDANT PEPTIDES IN THE
 CC NERVOUS SYSTEM. ALSO FOUND IN SOME CHROMAFFIN CELLS OF THE ADRENAL
 CC MEDULLA.
 CC SIMILARITY: BELONGS TO THE NPY / PYY / PPY FAMILY.

DR PIR: S07052; S07052.
 DR HSSP: P01303; IRON.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormones; 1.
 DR PRINTS: PR00278; PANCHEORMONE.
 DR ProDom: P0001267; Pancreatic_horm; 1.
 DR SMART: SM00309; PAH; 1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS0276; PANCREATIC_HORMONE_2; 1.
 DR NeorepId: Amidation
 KW MOD_RES 36
 FT MOD_RES 36
 SQ SEQUENCE 36 AA: 4241 MW: 9086940368000000 CR664.
 Query Match 81.8% Score 9; DB 1; Length 36;
 Best Local Similarity 66.7% Pred. No. 1,1e-03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 3
 1 1
 17 LAR 19

RESULT 43
 PAHO_CERSI
 ID PAHO_CERSI STANDARD: PPT 46 AA
 AC P47999;
 DT 01-OCT-1994 (Rel. 30, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pancreatic hormone (Pancreatic polypeptide) (PP).
 GN PPY.
 CC Celothetium alium (White rhinoceros) (Square tipped rhinoceros).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Perissodactyla; Rhinocerotidae; Ceratotherium.
 CC NCBI_TaxID=9807;
 RN 111
 RP SEQUENCE.
 DR PIR: S07052;
 DR HSSP: P01303; IRON.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormones; 1.
 DR PRINTS: PR00278; PANCHEORMONE.
 DR SMART: SM00309; PAH; 1.
 DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS0276; PANCREATIC_HORMONE_2; 1.
 DR Hormone: Amidation; Pancreas.
 KW MOD_RES 36
 FT MOD_RES 36
 SQ SEQUENCE 36 AA: 4214 MW: 76167163629086 CR664.
 Query Match 81.8% Score 9; DB 1; Length 36;
 Best Local Similarity 66.7% Pred. No. 1,1e-03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 3
 1 1
 31 LAR 43

RESULT 44
 PAHO_CHIRR
 ID PAHO_CHIRR STANDARD: PPT 46 AA
 AC P41519;
 DT 01-APR-1999 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Neuropeptide Y (NPY).
 GN NPY.
 OS Ovis aries (Sheep).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Artiodactyla; Pimantia; Pecora; Bovidae;
 CC Bovidae; Caprinae; Ovis.
 CC NCBI_TaxID=9940;
 RN 111
 RP MEDLINE 9009495; PubMed 2590994;
 RA Sillard R., Auerbach B., Mutt V., Jernvall H.;
 RI "Sheep neuropeptide Y. A third structural type of a highly conserved
 RI peptide.";
 RL FEBS Lett. 258:263-265(1989).
 RN 121
 RP FUNCTION: NPY IS IMPLICATED IN THE CONTROL OF FEEDING AND IN
 CC SECRETION OF GABA/BOMBESIN RELEASE HORMONE.
 CC SUBCELLULAR LOCATION: Secreted.
 CC TISSUE SPECIFICITY: ONE OF THE MOST ABUNDANT PEPTIDES IN THE
 CC NERVOUS SYSTEM. ALSO FOUND IN SOME CHROMAFFIN CELLS OF THE ADRENAL
 CC MEDULLA.
 CC SIMILARITY: BELONGS TO THE NPY / PYY / PPY FAMILY.

DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DR Pancreatic hormone (pancreatic polypeptide) (PP).
 GN *Chinchilla brevicauda* (Chinchilla).
 OC Eukaryota; Metazoa; Chordata; Gravidata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Cystodonta; Chinchillidae;
 OC Chinchilla.
 CX NCBI_TaxID=10152;
 RN [1]
 PP SEQUENCE.
 RC TISSUE-Pancreas;
 RX MEDLINE=9104537; PubMed 2235678;
 RA Fug J., Kleinman W.A., Chu L.S.;
 RT "Purification of peptide hormones from chinchilla pancreas by
 chemical assay."
 RL Peptides 11:683-685(1990).
 CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 GASTROINTESTINAL FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NPY / PPV / PYY FAMILY
 PIR: P01302; B60413.
 DR HSSP: P01302; IBBR.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormone3; 1.
 DR PRINTS: PR00278; PANCERHORM.
 DR SMART: SM00309; PAH; 1.
 DR PROSITE: PS00255; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation; Pancreas.
 FT MOD_RES 36 AMIDATION.
 SQ SEQUENCE 36 AA; 4215 MW; 7618717670R3309F CRC64;

 Query Match 81.8%; Score 9; DP 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 1,1e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 LXR 3
 DB 31 LTR 33

 RESULT 25
 PAHQ_DIDMA STANDARD; PRT; 36 AA.
 ID P18107;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pancreatic hormone (Pancreatic polypeptide) (PP).
 GN PPV.
 OS *Didelphis marsupialis virgata* (North American opossum).
 OC Eukaryota; Metazoa; Chordata; Gravidata; Vertebrata; Euteleostomi;
 OC Mammalia; Metatheria; Didelphimorphia; Didelphidae; Didelphus.
 CX NCBI_TaxID=9267.
 RN [1]
 PP SEQUENCE.
 RC TISSUE-Pancreas;
 RX MEDLINE 9016042; PubMed 2695959;
 RA Yu J.-H., Eng J., Kattan S., Yalow R.S.;
 RT "Opossum insulin, glucagon and pancreatic polypeptide: amino acid
 sequences."
 RL Peptides 10:1195-1197(1989).
 CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 GASTROINTESTINAL FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NPY / PPV / PYY FAMILY.
 PIR: JQ0365; JQ0365.
 DR HSSP: P01302; IBBR.
 DR InterPro: IPR001955; Pancreatic_horm.

DR Pfam: PF00159; hormone3; 1.
 DR SMART: SM00309; PAH; 1.
 DR PROSITE: PS00255; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation; Pancreas.
 FT MOD_RES 36 AMIDATION.
 SQ SEQUENCE 36 AA; 4215 MW; 761869281A+221F CRC64;

 Query Match 81.8%; Score 9; DP 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 1,1e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 LXR 3
 DB 31 LTR 33

 RESULT 36
 PAHQ_EUZE STANDARD; PRT; 36 AA.
 ID P48000;
 DT 01-OCT-1994 (Rel. 40, Created)
 DT 01-OCT-1994 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pancreatic hormone (pancreatic polypeptide) (PP).
 GN PPV.
 OS *Equus zebra* (Mountain zebra), and
 OS *Equus caballus przewalskii* (Przewalski's horse).
 OC Eukaryota; Metazoa; Chordata; Gravidata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
 CX NCBI_TaxID 9791, 9798.
 RN [1]
 PP SEQUENCE.
 RC TISSUE-Pancreas;
 RX MEDLINE 9225511; PubMed 1838025;
 RA Brady J.D., Langer V.A., Szolton J.M.;
 RT "Isolation and characterization of pancreatic polypeptide from test studies of
 Perissodactyla (Przewalski's horse, zebra, rhino, tapir)."
 RL Can. Comp. Endocrinol. 84:440-446(1991)
 CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
 OF LANGERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
 GASTROINTESTINAL FUNCTIONS.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: BELONGS TO THE NPY / PPV / PYY FAMILY.
 PIR: A61132; A61142.
 DR PIR: D61132; D61142.
 DR HSSP: P01302; IBBR.
 DR InterPro: IPR001955; Pancreatic_horm.
 DR Pfam: PF00159; hormone3; 1.
 DR PRINTS: PR00278; PANCERHORM.
 DR SMART: SM00309; PAH; 1.
 DR PROSITE: PS00255; PANCREATIC_HORMONE_1; 1.
 DR PROSITE: PS00276; PANCREATIC_HORMONE_2; 1.
 KW Hormone; Amidation; Pancreas.
 FT MOD_RES 36 AMIDATION.
 SQ SEQUENCE 36 AA; 4215 MW; 7618A60C1A6309F CRC64;

 Query Match 81.8%; Score 9; DP 1; Length 36;
 Best Local Similarity 66.7%; Pred. No. 1,1e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

 QY 1 LXR 3
 DB 31 LTR 33

 RESULT 37
 PAHQ_EUZE STANDARD; PRT; 36 AA.
 ID P41335;
 DT 01-FEB-1995 (Rel. 41, Created)
 DT 01-FEB-1995 (Rel. 41, Last sequence update)


```

RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=94130533; PubMed=8299350;
RA Marks N.J., Shaw C., Halton D.W., Curry W.J., Thim L.;
RI "Rabbit pancreatic polypeptide.";
RL Comp. Biochem. Physiol. 106B:883-887(1993).
CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
CC OF LANCERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
CC GASTROINTESTINAL FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PPV / PYY / PYY FAMILY.
DR HSP; P01302; IPIA.
DR InterPro: IPR001955; Pancreatic_horm.
DR Pfam: PF00159; hormone3; 1.
DR PRINTS: PR00278; PANCHORMONE.
DR SMART: SM00309; PAH; 1.
DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE: PS0276; PANCREATIC_HORMONE_2; 1.
KW Hormone; Amidation; Pancreas.
FT MOD_RES 36
FT SEQUENCE 36 AA; 4197 MW; A14M18931A7759D CRC64;

Query Match 81.8%; Score 9; DB 1; Length 46;
Best local similarity 66.7%; Pred. No. 1; 16-03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 3
DB 1 LTR 33

RESULT 41
PAAO_TAPPI STANDARD; PRT; 36 AA.
AC P39559;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pancreatic hormone (Pancreatic polypeptide) (TP).
GN PPI.
OS Tapirus pinchus (Mountain tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=30582;
RN 1
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=92225314; PubMed=1808025;
RA Henry J.S., Lance V.A., Conlon J.M.;
RI "Primary structure of pancreatic polypeptide from four species of
RL Gen. Comp. Endocrinol. 84:440-446(1991).
CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
CC OF LANCERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
CC GASTROINTESTINAL FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PPV / PYY / PYY FAMILY.
DR HSP; P01302; IPIA.
DR InterPro: IPR001955; Pancreatic_horm.
DR Pfam: PF00159; hormone3; 1.
DR PRINTS: PR00278; PANCHORMONE.
DR SMART: SM00309; PAH; 1.
DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE: PS0276; PANCREATIC_HORMONE_2; 1.
KW Hormone; Amidation; Pancreas.
FT MOD_RES 36
FT SEQUENCE 36 AA; 4197 MW; 761B717671A6308F CRC64;

Query Match 81.8%; Score 9; DB 1; Length 46;
Best local similarity 66.7%; Pred. No. 1; 16-03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 4

```

```

DB 41 LTR 33

PAAO_TAPPI STANDARD; PRT; 36 AA.
AC P39559;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pancreatic hormone (Pancreatic polypeptide) (TP).
GN PPI.
OS Tapirus pinchus (Mountain tapir).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Perissodactyla; Tapiridae; Tapirus.
OX NCBI_TaxID=30582;
RN 1
RP SEQUENCE.
RC TISSUE=Pancreas;
RX MEDLINE=92225314; PubMed=1808025;
RA Henry J.S., Lance V.A., Conlon J.M.;
RI "Primary structure of pancreatic polypeptide from four species of
RL Gen. Comp. Endocrinol. 84:440-446(1991).
CC -1- FUNCTION: PANCREATIC HORMONE IS SYNTHESIZED IN PANCREATIC ISLETS
CC OF LANCERHANS AND ACTS AS A REGULATOR OF PANCREATIC AND
CC GASTROINTESTINAL FUNCTIONS.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: BELONGS TO THE PPV / PYY / PYY FAMILY.
DR HSP; P01302; IPIA.
DR InterPro: IPR001955; Pancreatic_horm.
DR Pfam: PF00159; hormone3; 1.
DR PRINTS: PR00278; PANCHORMONE.
DR SMART: SM00309; PAH; 1.
DR PROSITE: PS00265; PANCREATIC_HORMONE_1; 1.
DR PROSITE: PS0276; PANCREATIC_HORMONE_2; 1.
KW Hormone; Amidation.
FT MOD_RES 36
FT SEQUENCE 36 AA; 4197 MW; 56B4E14C8C8C8C8C1 CRC64;

Query Match 81.8%; Score 9; DB 1; Length 46;
Best local similarity 66.7%; Pred. No. 1; 16-03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 4
DB 1 LTR 19

RESULT 44
PAAO_TAPPI STANDARD; PRT; 36 AA.
AC P01305;
DT 21-JUL-1986 (Rel. 01, Created)
DT 21-JUL-1986 (Rel. 01, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Peptide YY (PYY) (Peptide tyrosine tyrosine).
GN PYY.
OS Sus scrofa (Pig), and
OS Sus scrofa (Pig), and
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Suidae; Sus.
OX NCBI_TaxID=9824; 9615;
RN 1
RP SEQUENCE.
RC SPECIES=Pig;
RX MEDLINE=82222168; PubMed=405409;
RA Tatamoco K.;
RT "Isolation and characterization of peptide YY (PYY), a candidate gut
RI peptide that inhibits pancreatic secretions."
RL Proc. Natl. Acad. Sci. U.S.A. 79:2311-2316(1982).
GN PYY.
KW Peptide.
FT MOD_RES 121
FT SEQUENCE.
RC SPECIES=Canis familiaris;

```

```

RX MEDLINE 9025984; PubMed 2442986;
RA Eysselein V.E., Eborlein G.A., Grand D., Schaeffer M., Zehres B.,
RB Rein U., Schaeffer B., Goebel H., Davis M., Lee T.D., Shively J.E.,
RC Meyer H.E., Kozyra J.K., Jr.;
RD "Structural characterization of canine PYY.";
RE Peptides 11:111-116(1990).
CC 1 FUNCTION: THIS GUT PEPTIDE INHIBITS LAXATIVE SECRETION,
CC HAS A VASOCONSTRICTORY ACTION AND INHIBITS GUT AND COLONIC
CC MOTILITY.
CC 1 SUBCELLULAR LOCATION: Secreted.
CC 1 SIMILARITY: Ref. 2; 1-18 DB 1; 11; 13; 14; 15; 16; 17; 18; 19; 20; 21; 22; 23; 24; 25; 26; 27; 28; 29; 30; 31; 32; 33; 34; 35; 36; 37; 38; 39; 40; 41; 42; 43; 44; 45; 46; 47; 48; 49; 50; 51; 52; 53; 54; 55; 56; 57; 58; 59; 60; 61; 62; 63; 64; 65; 66; 67; 68; 69; 70; 71; 72; 73; 74; 75; 76; 77; 78; 79; 80; 81; 82; 83; 84; 85; 86; 87; 88; 89; 90; 91; 92; 93; 94; 95; 96; 97; 98; 99; 100; 101; 102; 103; 104; 105; 106; 107; 108; 109; 110; 111; 112; 113; 114; 115; 116; 117; 118; 119; 120; 121; 122; 123; 124; 125; 126; 127; 128; 129; 130; 131; 132; 133; 134; 135; 136; 137; 138; 139; 140; 141; 142; 143; 144; 145; 146; 147; 148; 149; 150; 151; 152; 153; 154; 155; 156; 157; 158; 159; 160; 161; 162; 163; 164; 165; 166; 167; 168; 169; 170; 171; 172; 173; 174; 175; 176; 177; 178; 179; 180; 181; 182; 183; 184; 185; 186; 187; 188; 189; 190; 191; 192; 193; 194; 195; 196; 197; 198; 199; 200; 201; 202; 203; 204; 205; 206; 207; 208; 209; 210; 211; 212; 213; 214; 215; 216; 217; 218; 219; 220; 221; 222; 223; 224; 225; 226; 227; 228; 229; 230; 231; 232; 233; 234; 235; 236; 237; 238; 239; 240; 241; 242; 243; 244; 245; 246; 247; 248; 249; 250; 251; 252; 253; 254; 255; 256; 257; 258; 259; 260; 261; 262; 263; 264; 265; 266; 267; 268; 269; 270; 271; 272; 273; 274; 275; 276; 277; 278; 279; 280; 281; 282; 283; 284; 285; 286; 287; 288; 289; 290; 291; 292; 293; 294; 295; 296; 297; 298; 299; 300; 301; 302; 303; 304; 305; 306; 307; 308; 309; 310; 311; 312; 313; 314; 315; 316; 317; 318; 319; 320; 321; 322; 323; 324; 325; 326; 327; 328; 329; 330; 331; 332; 333; 334; 335; 336; 337; 338; 339; 340; 341; 342; 343; 344; 345; 346; 347; 348; 349; 350; 351; 352; 353; 354; 355; 356; 357; 358; 359; 360; 361; 362; 363; 364; 365; 366; 367; 368; 369; 370; 371; 372; 373; 374; 375; 376; 377; 378; 379; 380; 381; 382; 383; 384; 385; 386; 387; 388; 389; 390; 391; 392; 393; 394; 395; 396; 397; 398; 399; 400; 401; 402; 403; 404; 405; 406; 407; 408; 409; 410; 411; 412; 413; 414; 415; 416; 417; 418; 419; 420; 421; 422; 423; 424; 425; 426; 427; 428; 429; 430; 431; 432; 433; 434; 435; 436; 437; 438; 439; 440; 441; 442; 443; 444; 445; 446; 447; 448; 449; 450; 451; 452; 453; 454; 455; 456; 457; 458; 459; 460; 461; 462; 463; 464; 465; 466; 467; 468; 469; 470; 471; 472; 473; 474; 475; 476; 477; 478; 479; 480; 481; 482; 483; 484; 485; 486; 487; 488; 489; 490; 491; 492; 493; 494; 495; 496; 497; 498; 499; 500; 501; 502; 503; 504; 505; 506; 507; 508; 509; 510; 511; 512; 513; 514; 515; 516; 517; 518; 519; 520; 521; 522; 523; 524; 525; 526; 527; 528; 529; 530; 531; 532; 533; 534; 535; 536; 537; 538; 539; 540; 541; 542; 543; 544; 545; 546; 547; 548; 549; 550; 551; 552; 553; 554; 555; 556; 557; 558; 559; 560; 561; 562; 563; 564; 565; 566; 567; 568; 569; 570; 571; 572; 573; 574; 575; 576; 577; 578; 579; 580; 581; 582; 583; 584; 585; 586; 587; 588; 589; 590; 591; 592; 593; 594; 595; 596; 597; 598; 599; 600; 601; 602; 603; 604; 605; 606; 607; 608; 609; 610; 611; 612; 613; 614; 615; 616; 617; 618; 619; 620; 621; 622; 623; 624; 625; 626; 627; 628; 629; 630; 631; 632; 633; 634; 635; 636; 637; 638; 639; 640; 641; 642; 643; 644; 645; 646; 647; 648; 649; 650; 651; 652; 653; 654; 655; 656; 657; 658; 659; 660; 661; 662; 663; 664; 665; 666; 667; 668; 669; 670; 671; 672; 673; 674; 675; 676; 677; 678; 679; 680; 681; 682; 683; 684; 685; 686; 687; 688; 689; 690; 691; 692; 693; 694; 695; 696; 697; 698; 699; 700; 701; 702; 703; 704; 705; 706; 707; 708; 709; 710; 711; 712; 713; 714; 715; 716; 717; 718; 719; 720; 721; 722; 723; 724; 725; 726; 727; 728; 729; 730; 731; 732; 733; 734; 735; 736; 737; 738; 739; 740; 741; 742; 743; 744; 745; 746; 747; 748; 749; 750; 751; 752; 753; 754; 755; 756; 757; 758; 759; 760; 761; 762; 763; 764; 765; 766; 767; 768; 769; 770; 771; 772; 773; 774; 775; 776; 777; 778; 779; 780; 781; 782; 783; 784; 785; 786; 787; 788; 789; 790; 791; 792; 793; 794; 795; 796; 797; 798; 799; 800; 801; 802; 803; 804; 805; 806; 807; 808; 809; 810; 811; 812; 813; 814; 815; 816; 817; 818; 819; 820; 821; 822; 823; 824; 825; 826; 827; 828; 829; 830; 831; 832; 833; 834; 835; 836; 837; 838; 839; 840; 841; 842; 843; 844; 845; 846; 847; 848; 849; 850; 851; 852; 853; 854; 855; 856; 857; 858; 859; 860; 861; 862; 863; 864; 865; 866; 867; 868; 869; 870; 871; 872; 873; 874; 875; 876; 877; 878; 879; 880; 881; 882; 883; 884; 885; 886; 887; 888; 889; 890; 891; 892; 893; 894; 895; 896; 897; 898; 899; 900; 901; 902; 903; 904; 905; 906; 907; 908; 909; 910; 911; 912; 913; 914; 915; 916; 917; 918; 919; 920; 921; 922; 923; 924; 925; 926; 927; 928; 929; 930; 931; 932; 933; 934; 935; 936; 937; 938; 939; 940; 941; 942; 943; 944; 945; 946; 947; 948; 949; 950; 951; 952; 953; 954; 955; 956; 957; 958; 959; 960; 961; 962; 963; 964; 965; 966; 967; 968; 969; 970; 971; 972; 973; 974; 975; 976; 977; 978; 979; 980; 981; 982; 983; 984; 985; 986; 987; 988; 989; 990; 991; 992; 993; 994; 995; 996; 997; 998; 999; 1000; 1001; 1002; 1003; 1004; 1005; 1006; 1007; 1008; 1009; 1010; 1011; 1012; 1013; 1014; 1015; 1016; 1017; 1018; 1019; 1020; 1021; 1022; 1023; 1024; 1025; 1026; 1027; 1028; 1029; 1030; 1031; 1032; 1033; 1034; 1035; 1036; 1037; 1038; 1039; 1040; 1041; 1042; 1043; 1044; 1045; 1046; 1047; 1048; 1049; 1050; 1051; 1052; 1053; 1054; 1055; 1056; 1057; 1058; 1059; 1060; 1061; 1062; 1063; 1064; 1065; 1066; 1067; 1068; 1069; 1070; 1071; 1072; 1073; 1074; 1075; 1076; 1077; 1078; 1079; 1080; 1081; 1082; 1083; 1084; 1085; 1086; 1087; 1088; 1089; 1090; 1091; 1092; 1093; 1094; 1095; 1096; 1097; 1098; 1099; 1100; 1101; 1102; 1103; 1104; 1105; 1106; 1107; 1108; 1109; 1110; 1111; 1112; 1113; 1114; 1115; 1116; 1117; 1118; 1119; 1120; 1121; 1122; 1123; 1124; 1125; 1126; 1127; 1128; 1129; 1130; 1131; 1132; 1133; 1134; 1135; 1136; 1137; 1138; 1139; 1140; 1141; 1142; 1143; 1144; 1145; 1146; 1147; 1148; 1149; 1150; 1151; 1152; 1153; 1154; 1155; 1156; 1157; 1158; 1159; 1160; 1161; 1162; 1163; 1164; 1165; 1166; 1167; 1168; 1169; 1170; 1171; 1172; 1173; 1174; 1175; 1176; 1177; 1178; 1179; 1180; 1181; 1182; 1183; 1184; 1185; 1186; 1187; 1188; 1189; 1190; 1191; 1192; 1193; 1194; 1195; 1196; 1197; 1198; 1199; 1200; 1201; 1202; 1203; 1204; 1205; 1206; 1207; 1208; 1209; 1210; 1211; 1212; 1213; 1214; 1215; 1216; 1217; 1218; 1219; 1220; 1221; 1222; 1223; 1224; 1225; 1226; 1227; 1228; 1229; 1230; 1231; 1232; 1233; 1234; 1235; 1236; 1237; 1238; 1239; 1240; 1241; 1242; 1243; 1244; 1245; 1246; 1247; 1248; 1249; 1250; 1251; 1252; 1253; 1254; 1255; 1256; 1257; 1258; 1259; 1260; 1261; 1262; 1263; 1264; 1265; 1266; 1267; 1268; 1269; 1270; 1271; 1272; 1273; 1274; 1275; 1276; 1277; 1278; 1279; 1280; 1281; 1282; 1283; 1284; 1285; 1286; 1287; 1288; 1289; 1290; 1291; 1292; 1293; 1294; 1295; 1296; 1297; 1298; 1299; 1300; 1301; 1302; 1303; 1304; 1305; 1306; 1307; 1308; 1309; 1310; 1311; 1312; 1313; 1314; 1315; 1316; 1317; 1318; 1319; 1320; 1321; 1322; 1323; 1324; 1325; 1326; 1327; 1328; 1329; 1330; 1331; 1332; 1333; 1334; 1335; 1336; 1337; 1338; 1339; 1340; 1341; 1342; 1343; 1344; 1345; 1346; 1347; 1348; 1349; 1350; 1351; 1352; 1353; 1354; 1355; 1356; 1357; 1358; 1359; 1360; 1361; 1362; 1363; 1364; 1365; 1366; 1367; 1368; 1369; 1370; 1371; 1372; 1373; 1374; 1375; 1376; 1377; 1378; 1379; 1380; 1381; 1382; 1383; 1384; 1385; 1386; 1387; 1388; 1389; 1390; 1391; 1392; 1393; 1394; 1395; 1396; 1397; 1398; 1399; 1400; 1401; 1402; 1403; 1404; 1405; 1406; 1407; 1408; 1409; 1410; 1411; 1412; 1413; 1414; 1415; 1416; 1417; 1418; 1419; 1420; 1421; 1422; 1423; 1424; 1425; 1426; 1427; 1428; 1429; 1430; 1431; 1432; 1433; 1434; 1435; 1436; 1437; 1438; 1439; 1440; 1441; 1442; 1443; 1444; 1445; 1446; 1447; 1448; 1449; 1450; 1451; 1452; 1453; 1454; 1455; 1456; 1457; 1458; 1459; 1460; 1461; 1462; 1463; 1464; 1465; 1466; 1467; 1468; 1469; 1470; 1471; 1472; 1473; 1474; 1475; 1476; 1477; 1478; 1479; 1480; 1481; 1482; 1483; 1484; 1485; 1486; 1487; 1488; 1489; 1490; 1491; 1492; 1493; 1494; 1495; 1496; 1497; 1498; 1499; 1500; 1501; 1502; 1503; 1504; 1505; 1506; 1507; 1508; 1509; 1510; 1511; 1512; 1513; 1514; 1515; 1516; 1517; 1518; 1519; 1520; 1521; 1522; 1523; 1524; 1525; 1526; 1527; 1528; 1529; 1530; 1531; 1532; 1533; 1534; 1535; 1536; 1537; 1538; 1539; 1540; 1541; 1542; 1543; 1544; 1545; 1546; 1547; 1548; 1549; 1550; 1551; 1552; 1553; 1554; 1555; 1556; 1557; 1558; 1559; 1560; 1561; 1562; 1563; 1564; 1565; 1566; 1567; 1568; 1569; 1570; 1571; 1572; 1573; 1574; 1575; 1576; 1577; 1578; 1579; 1580; 1581; 1582; 1583; 1584; 1585; 1586; 1587; 1588; 1589; 1590; 1591; 1592; 1593; 1594; 1595; 1596; 1597; 1598; 1599; 1600; 1601; 1602; 1603; 1604; 1605; 1606; 1607; 1608; 1609; 1610; 1611; 1612; 1613; 1614; 1615; 1616; 1617; 1618; 1619; 1620; 1621; 1622; 1623; 1624; 1625; 1626; 1627; 1628; 1629; 1630; 1631; 1632; 1633; 1634; 1635; 1636; 1637; 1638; 1639; 1640; 1641; 1642; 1643; 1644; 1645; 1646; 1647; 1648; 1649; 1650; 1651; 1652; 1653; 1654; 1655; 1656; 1657; 1658; 1659; 1660; 1661; 1662; 1663; 1664; 1665; 1666; 1667; 1668; 1669; 1670; 1671; 1672; 1673; 1674; 1675; 1676; 1677; 1678; 1679; 1680; 1681; 1682; 1683; 1684; 1685; 1686; 1687; 1688; 1689; 1690; 1691; 1692; 1693; 1694; 1695; 1696; 1697; 1698; 1699; 1700; 1701; 1702; 1703; 1704; 1705; 1706; 1707; 1708; 1709; 1710; 1711; 1712; 1713; 1714; 1715; 1716; 1717; 1718; 1719; 1720; 1721; 1722; 1723; 1724; 1725; 1726; 1727; 1728; 1729; 1730; 1731; 1732; 1733; 1734; 1735; 1736; 1737; 1738; 1739; 1740; 1741; 1742; 1743; 1744; 1745; 1746; 1747; 1748; 1749; 1750; 1751; 1752; 1753; 1754; 1755; 1756; 1757; 1758; 1759; 1760; 1761; 1762; 1763; 1764; 1765; 1766; 1767; 1768; 1769; 1770; 1771; 1772; 1773; 1774; 1775; 1776; 1777; 1778; 1779; 1780; 1781; 1782; 1783; 1784; 1785; 1786; 1787; 1788; 1789; 1790; 1791; 1792; 1793; 1794; 1795; 1796; 1797; 1798; 1799; 1800; 1801; 1802; 1803; 1804; 1805; 1806; 1807; 1808; 1809; 1810; 1811; 1812; 1813; 1814; 1815; 1816; 1817; 1818; 1819; 1820; 1821; 1822; 1823; 1824; 1825; 1826; 1827; 1828; 1829; 1830; 1831; 1832; 1833; 1834; 1835; 1836; 1837; 1838; 1839; 1840; 1841; 1842; 1843; 1844; 1845; 1846; 1847; 1848; 1849; 1850; 1851; 1852; 1853; 1854; 1855; 1856; 1857; 1858; 1859; 1860; 1861; 1862; 1863; 1864; 1865; 1866; 1867; 1868; 1869; 1870; 1871; 1872; 1873; 1874; 1875; 1876; 1877; 1878; 1879; 1880; 1881; 1882; 1883; 1884; 1885; 1886; 1887; 1888; 1889; 1890; 1891; 1892; 1893; 1894; 1895; 1896; 1897; 1898; 1899; 1900; 1901; 1902; 1903; 1904; 1905; 1906; 1907; 1908; 1909; 1910; 1911; 1912; 1913; 1914; 1915; 1916; 1917; 1918; 1919; 1920; 1921; 1922; 1923; 1924; 1925; 1926; 1927; 1928; 1929; 1930; 1931; 1932; 1933; 1934; 1935; 1936; 1937; 1938; 1939; 1940; 1941; 1942; 1943; 1944; 1945; 1946; 1947; 1948; 1949; 1950; 1951; 1952; 1953; 1954; 1955; 1956; 1957; 1958; 1959; 1960; 1961; 1962; 1963; 1964; 1965; 1966; 1967; 1968; 1969; 1970; 1971; 1972; 1973; 1974; 1975; 1976; 1977; 1978; 1979; 1980; 1981; 1982; 1983; 1984; 1985; 1986; 1987; 1988; 1989; 1990; 1991; 1992; 1993; 1994; 1995; 1996; 1997; 1998; 1999; 2000; 2001; 2002; 2003; 2004; 2005; 2006; 2007; 2008; 2009; 2010; 2011; 2012; 2013; 2014; 2015; 2016; 2017; 2018; 2019; 2020; 2021; 2022; 2023; 2024; 2025; 2026; 2027; 2028; 2029; 2030; 2031; 2032; 2033; 2034; 2035; 2036; 2037; 2038; 2039; 2040; 2041; 2042; 2043; 2044; 2045; 2046; 2047; 2048; 2049; 2050; 2051; 2052; 2053; 2054; 2055; 2056; 2057; 2058; 2059; 2060; 2061; 2062; 2063; 2064; 2065; 2066; 2067; 2068; 2069; 2070; 2071; 2072; 2073; 2074; 2075; 2076; 2077; 2078; 2079; 2080; 2081; 2082; 2083; 2084; 2085; 2086; 2087; 2088; 2089; 2090; 2091; 2092; 2093; 2094; 2095; 2096; 2097; 2098; 2099; 2100; 2101; 2102; 2103; 2104; 2105; 2106; 2107; 2108; 2109; 2110; 2111; 2112; 2113; 2114; 2115; 2116; 2117; 2118; 2119; 2120; 2121; 2122; 2123; 2124; 2125; 2126; 2127; 2128; 2129; 2130; 2131; 2132; 2133; 2134; 2135; 2136; 2137; 2138; 2139; 2140; 2141; 2142; 2143; 2144; 2145; 2146; 2147; 2148; 2149; 2150; 2151; 2152; 2153; 2154; 2155; 2156; 2157; 2158; 2159; 2160; 2161; 2162; 2163; 2164; 2165; 2166; 2167; 2168; 2169; 2170; 2171; 2172; 2173; 2174; 2175; 2176; 2177; 2178; 2179; 2180; 2181; 2182; 2183; 2184; 2185; 2186; 2187; 2188; 2189; 2190; 2191; 2192; 2193
```


90	9	81.8	15	16	Q9X144	Q9X144 Galinella	163	9	81.8	22	13	Q91105	Q91105 morone saxa
91	9	81.8	16	2	Q9K414	Q9K414 pseudomoras	164	9	81.8	22	13	Q91106	Q91106 morone saxa
92	9	81.8	16	2	Q9H103	Q9H103 trypanosoma	165	9	81.8	22	13	Q91107	Q91107 mus mus
93	9	81.8	16	6	Q9H105	Q9H105 bos taurus	166	9	81.8	22	13	Q91108	Q91108 morone saxa
94	9	81.8	16	7	Q97922	Q97922 crocebrachis	167	9	81.8	23	2	Q92232	Q92232 carya rostrata
95	9	81.8	16	7	Q97922	Q97922 crocebrachis	168	9	81.8	23	2	Q96705	Q96705 llyanassa o
96	9	81.8	16	8	Q91294	Q91294 homo sapien	169	9	81.8	23	5	Q96707	Q96707 llyanassa o
97	9	81.8	16	12	Q94797	Q94797 autographa	170	9	81.8	23	5	Q94781	Q94781 llyanassa o
98	9	81.8	17	4	Q91073	Q91074 homo sapien	171	9	81.8	23	5	Q95162	Q95162 halictus r
99	9	81.8	17	10	Q9S854	Q9S854 lithocarpus	172	9	81.8	23	5	Q95163	Q95163 halictus r
100	9	81.8	17	10	Q94F00	Q94F00 arabidopsis	173	9	81.8	23	5	Q95166	Q95166 halictus r
101	9	81.8	18	4	Q9H588	Q9H588 homo sapien	174	9	81.8	23	5	Q95169	Q95169 halictus r
102	9	81.8	18	6	Q9S116	Q9S116 scirex arane	175	9	81.8	23	11	Q96137	Q96137 mus musculus
103	9	81.8	18	7	Q97923	Q97923 oreochromis	176	9	81.8	23	12	Q96495	Q96495 pseudorhabdo
104	9	81.8	18	13	Q9S836	Q9S836 torpedo mar	177	9	81.8	23	12	Q96491	Q96491 pseudorhabdo
105	9	81.8	18	15	Q97587	Q97587 chimpanzee	178	9	81.8	23	12	Q94331	Q94331 simian vifu
106	9	81.8	18	15	Q97589	Q97589 chimpanzee	179	9	81.8	23	12	Q97078	Q97078 pseudorhabdo
107	9	81.8	18	15	Q97591	Q97591 chimpanzee	180	9	81.8	23	12	Q97079	Q97079 pseudorhabdo
108	9	81.8	18	15	Q97593	Q97593 chimpanzee	181	9	81.8	23	12	Q97080	Q97080 pseudorhabdo
109	9	81.8	19	4	Q99711	Q99711 homo sapien	182	9	81.8	23	12	Q97081	Q97081 pseudorhabdo
110	9	81.8	19	5	Q9CPK3	Q9CPK3 scutigerell	183	9	81.8	23	12	Q97082	Q97082 pseudorhabdo
111	9	81.8	19	5	Q96706	Q96706 lithobius v	184	9	81.8	23	12	Q97083	Q97083 pseudorhabdo
112	9	81.8	19	5	Q9H104	Q9H104 heliothis v	185	9	81.8	23	12	Q97086	Q97086 pseudorhabdo
113	9	81.8	19	6	Q9H104	Q9H104 mammathuc p	186	9	81.8	23	2	Q96W81	Q96W81 pseudorhabdo
114	9	81.8	19	11	Q911A2	Q911A2 rattus norv	187	9	81.8	24	2	Q94396	Q94396 heliothis v
115	9	81.8	19	12	Q96496	Q96496 pseudorhabdo	188	9	81.8	24	2	Q96607	Q96607 versinia en
116	9	81.8	19	12	Q96445	Q96445 human herpe	189	9	81.8	24	2	Q96547	Q96547 heliothis v
117	9	81.8	20	2	Q95919	Q95919 rhinobium m	190	9	81.8	24	2	Q95923	Q95923 streptomyces
118	9	81.8	20	2	Q9H498	Q9H498 pseudomoras	191	9	81.8	24	5	Q9H542	Q9H542 aedes aegypt
119	9	81.8	20	3	Q9H885	Q9H885 anatis leus fi	192	9	81.8	24	5	Q9H572	Q9H572 tenebrio mol
120	9	81.8	20	3	Q9H871	Q9H871 homo sapien	193	9	81.8	24	5	Q94197	Q94197 eumecobabio
121	9	81.8	20	5	Q9H885	Q9H885 heliothis v	194	9	81.8	24	5	Q94190	Q94190 quillia aor
122	9	81.8	20	6	Q9M225	Q9M225 ceratophther	195	9	81.8	24	6	Q9H781	Q9H781 ponzo pyema
123	9	81.8	20	6	Q9H104	Q9H104 sus scrofa	196	9	81.8	24	11	Q96209	Q96209 mus musculus
124	9	81.8	20	16	Q92024	Q92024 versinia pe	197	9	81.8	24	12	Q97881	Q97881 heliothis v
125	9	81.8	21	2	Q9X064	Q9X064 prochloroen	198	9	81.8	24	16	Q9H335	Q9H335 metacaria m
126	9	81.8	21	4	Q9H822	Q9H822 homo sapien	199	9	81.8	25	2	Q94331	Q94331 brexibacter
127	9	81.8	21	4	Q9H816	Q9H816 homo sapien	200	9	81.8	25	4	Q9H888	Q9H888 homo sapien
128	9	81.8	21	5	Q9S084	Q9S084 herdmania m	201	9	81.8	25	5	Q96540	Q96540 heliothis v
129	9	81.8	21	5	Q9S087	Q9S087 herdmania m	202	9	81.8	25	5	Q96383	Q96383 polyocelis n
130	9	81.8	21	6	Q9M214	Q9M214 callinectes v	203	9	81.8	25	5	Q96385	Q96385 polyocelis n
131	9	81.8	21	6	Q9M213	Q9M213 cebus sp. a	204	9	81.8	25	5	Q96087	Q96087 polyocelis n
132	9	81.8	21	6	Q9M212	Q9M212 macaca mula	205	9	81.8	25	5	Q96089	Q96089 polyocelis n
133	9	81.8	21	6	Q9M212	Q9M212 pan troglody	206	9	81.8	25	5	Q96090	Q96090 polyocelis n
134	9	81.8	21	6	Q9M210	Q9M210 ceratophther	207	9	81.8	25	5	Q95872	Q95872 polyocelis n
135	9	81.8	21	6	Q9M209	Q9M209 hylabates s	208	9	81.8	25	5	Q95872	Q95872 polyocelis n
136	9	81.8	21	6	Q9M208	Q9M208 ponzo pyema	209	9	81.8	25	5	Q95874	Q95874 polyocelis n
137	9	81.8	21	6	Q9M207	Q9M207 acrida aer	210	9	81.8	25	5	Q95875	Q95875 dendrobaela
138	9	81.8	21	12	Q95182	Q95182 polyocelis n	211	9	81.8	25	5	Q95876	Q95876 dendrobaela
139	9	81.8	21	12	Q95870	Q95870 polyocelis n	212	9	81.8	25	5	Q95877	Q95877 dendrobaela
140	9	81.8	21	12	Q95859	Q95859 polyomaviru	213	9	81.8	25	5	Q95185	Q95185 artemia sal
141	9	81.8	21	12	Q95858	Q95858 polyomaviru	214	9	81.8	25	5	Q95878	Q95878 artemia sal
142	9	81.8	21	12	Q95857	Q95857 polyomaviru	215	9	81.8	25	5	Q95879	Q95879 artemia sal
143	9	81.8	21	12	Q95856	Q95856 polyomaviru	216	9	81.8	25	5	Q95880	Q95880 artemia sal
144	9	81.8	21	12	Q95855	Q95855 polyomaviru	217	9	81.8	25	5	Q95881	Q95881 artemia sal
145	9	81.8	21	12	Q95854	Q95854 polyomaviru	218	9	81.8	25	5	Q95882	Q95882 artemia sal
146	9	81.8	21	12	Q95853	Q95853 polyomaviru	219	9	81.8	25	5	Q95883	Q95883 artemia sal
147	9	81.8	21	12	Q95852	Q95852 lampetra fi	220	9	81.8	25	5	Q95884	Q95884 artemia sal
148	9	81.8	22	2	Q94612	Q94612 buchonia ap	221	9	81.8	25	5	Q95885	Q95885 artemia sal
149	9	81.8	22	2	Q94611	Q94611 versinia pe	222	9	81.8	25	5	Q95886	Q95886 artemia sal
150	9	81.8	22	4	Q9NNY7	Q9NNY7 homo sapien	223	9	81.8	25	5	Q95887	Q95887 artemia sal
151	9	81.8	22	4	Q9NNY5	Q9NNY5 homo sapien	224	9	81.8	25	5	Q95888	Q95888 artemia sal
152	9	81.8	22	4	Q9NNY2	Q9NNY2 homo sapien	225	9	81.8	25	5	Q95889	Q95889 artemia sal
153	9	81.8	22	6	Q9H855	Q9H855 sus sp. ins	226	9	81.8	25	5	Q95890	Q95890 artemia sal
154	9	81.8	22	8	Q9H854	Q9H854 centropomus	227	9	81.8	25	5	Q95891	Q95891 artemia sal
155	9	81.8	22	8	Q9H853	Q9H853 centropomus	228	9	81.8	25	5	Q95892	Q95892 artemia sal
156	9	81.8	22	8	Q9H852	Q9H852 centropomus	229	9	81.8	25	5	Q95893	Q95893 artemia sal
157	9	81.8	22	8	Q9H851	Q9H851 centropomus	230	9	81.8	25	5	Q95894	Q95894 artemia sal
158	9	81.8	22	12	Q97084	Q97084 pseudorhabdo	231	9	81.8	25	11	Q96098	Q96098 latius norv
159	9	81.8	22	12	Q97085	Q97085 pseudorhabdo	232	9	81.8	25	11	Q96099	Q96099 latius norv
160	9	81.8	22	12	Q96446	Q96446 human herpe	233	9	81.8	25	11	Q96091	Q96091 latius norv
161	9	81.8	22	13	Q91103	Q91103 morone saxa	234	9	81.8	25	11	Q96095	Q96095 latius norv
162	9	81.8	22	13	Q91104	Q91104 morone saxa	235	9	81.8	25	11	Q96096	Q96096 latius norv

236	9	81.8	26	11	063987	Q63987 ratitis sp.	329	9	81.8	27	5	065526	Q65526 saccollossu
237	9	81.8	25	11	063988	Q63988 ratitis sp.	310	9	81.8	27	5	065527	Q65527 saccollossu
238	9	81.8	25	11	063992	Q63992 ratitis sp.	311	9	81.8	27	5	065528	Q65528 saccollossu
239	9	81.8	25	11	063993	Q63993 mus muscula	312	9	81.8	27	5	065529	Q65529 echinostoma
240	9	81.8	25	11	063994	Q63994 mus muscula	313	9	81.8	27	5	065530	Q65530 echinostoma
241	9	81.8	25	11	063995	Q63995 mus muscula	314	9	81.8	27	5	065531	Q65531 echinostoma
242	9	81.8	25	12	061459	Q61459 hepatis c	315	9	81.8	27	5	065532	Q65532 hepatis c
243	9	81.8	25	12	061460	Q61460 hepatis c	316	9	81.8	27	5	065533	Q65533 hepatis c
244	9	81.8	25	12	061461	Q61461 hepatis c	317	9	81.8	27	5	065534	Q65534 hepatis c
245	9	81.8	26	5	044261	Q44261 acanthokara	318	9	81.8	27	5	065535	Q65535 hepatis c
246	9	81.8	26	5	044262	Q44262 acanthokara	319	9	81.8	27	5	065536	Q65536 hepatis c
247	9	81.8	26	5	044263	Q44263 acanthokara	320	9	81.8	27	5	065537	Q65537 hepatis c
248	9	81.8	26	5	044264	Q44264 acanthokara	321	9	81.8	27	5	065538	Q65538 hepatis c
249	9	81.8	26	5	044265	Q44265 acanthokara	322	9	81.8	27	5	065539	Q65539 hepatis c
250	9	81.8	26	5	044266	Q44266 acanthokara	323	9	81.8	27	5	065540	Q65540 hepatis c
251	9	81.8	26	5	044267	Q44267 acanthokara	324	9	81.8	27	5	065541	Q65541 hepatis c
252	9	81.8	26	5	044268	Q44268 acanthokara	325	9	81.8	27	5	065542	Q65542 hepatis c
253	9	81.8	26	5	044269	Q44269 acanthokara	326	9	81.8	27	5	065543	Q65543 hepatis c
254	9	81.8	26	5	044270	Q44270 acanthokara	327	9	81.8	27	5	065544	Q65544 hepatis c
255	9	81.8	26	5	044271	Q44271 acanthokara	328	9	81.8	27	5	065545	Q65545 hepatis c
256	9	81.8	26	5	044272	Q44272 acanthokara	329	9	81.8	27	5	065546	Q65546 hepatis c
257	9	81.8	26	5	044273	Q44273 acanthokara	330	9	81.8	27	5	065547	Q65547 hepatis c
258	9	81.8	26	5	044274	Q44274 acanthokara	331	9	81.8	27	5	065548	Q65548 hepatis c
259	9	81.8	26	5	044275	Q44275 acanthokara	332	9	81.8	27	5	065549	Q65549 hepatis c
260	9	81.8	26	5	044276	Q44276 acanthokara	333	9	81.8	27	5	065550	Q65550 hepatis c
261	9	81.8	26	11	063464	Q63464 ratitis sp.	334	9	81.8	27	5	065551	Q65551 hepatis c
262	9	81.8	26	12	061901	Q61901 hepatis c	335	9	81.8	27	5	065552	Q65552 hepatis c
263	9	81.8	27	5	063648	Q63648 acanthokara	336	9	81.8	27	5	065553	Q65553 hepatis c
264	9	81.8	27	5	063649	Q63649 acanthokara	337	9	81.8	27	5	065554	Q65554 hepatis c
265	9	81.8	27	5	063650	Q63650 acanthokara	338	9	81.8	27	5	065555	Q65555 hepatis c
266	9	81.8	27	5	063651	Q63651 acanthokara	339	9	81.8	27	5	065556	Q65556 hepatis c
267	9	81.8	27	5	063652	Q63652 acanthokara	340	9	81.8	27	5	065557	Q65557 hepatis c
268	9	81.8	27	5	063653	Q63653 acanthokara	341	9	81.8	27	5	065558	Q65558 hepatis c
269	9	81.8	27	5	063654	Q63654 acanthokara	342	9	81.8	27	5	065559	Q65559 hepatis c
270	9	81.8	27	5	063655	Q63655 acanthokara	343	9	81.8	27	5	065560	Q65560 hepatis c
271	9	81.8	27	5	063656	Q63656 acanthokara	344	9	81.8	27	5	065561	Q65561 hepatis c
272	9	81.8	27	5	063657	Q63657 acanthokara	345	9	81.8	27	5	065562	Q65562 hepatis c
273	9	81.8	27	5	063658	Q63658 acanthokara	346	9	81.8	27	5	065563	Q65563 hepatis c
274	9	81.8	27	5	063659	Q63659 acanthokara	347	9	81.8	27	5	065564	Q65564 hepatis c
275	9	81.8	27	5	063660	Q63660 acanthokara	348	9	81.8	27	5	065565	Q65565 hepatis c
276	9	81.8	27	5	063661	Q63661 acanthokara	349	9	81.8	27	5	065566	Q65566 hepatis c
277	9	81.8	27	5	063662	Q63662 acanthokara	350	9	81.8	27	5	065567	Q65567 hepatis c
278	9	81.8	27	5	063663	Q63663 acanthokara	351	9	81.8	27	5	065568	Q65568 hepatis c
279	9	81.8	27	5	063664	Q63664 acanthokara	352	9	81.8	27	5	065569	Q65569 hepatis c
280	9	81.8	27	5	063665	Q63665 acanthokara	353	9	81.8	27	5	065570	Q65570 hepatis c
281	9	81.8	27	5	063666	Q63666 acanthokara	354	9	81.8	27	5	065571	Q65571 hepatis c
282	9	81.8	27	5	063667	Q63667 acanthokara	355	9	81.8	27	5	065572	Q65572 hepatis c
283	9	81.8	27	5	063668	Q63668 acanthokara	356	9	81.8	27	5	065573	Q65573 hepatis c
284	9	81.8	27	5	063669	Q63669 acanthokara	357	9	81.8	27	5	065574	Q65574 hepatis c
285	9	81.8	27	5	063670	Q63670 acanthokara	358	9	81.8	27	5	065575	Q65575 hepatis c
286	9	81.8	27	5	063671	Q63671 acanthokara	359	9	81.8	27	5	065576	Q65576 hepatis c
287	9	81.8	27	5	063672	Q63672 acanthokara	360	9	81.8	27	5	065577	Q65577 hepatis c
288	9	81.8	27	5	063673	Q63673 acanthokara	361	9	81.8	27	5	065578	Q65578 hepatis c
289	9	81.8	27	5	063674	Q63674 acanthokara	362	9	81.8	27	5	065579	Q65579 hepatis c
290	9	81.8	27	5	063675	Q63675 acanthokara	363	9	81.8	27	5	065580	Q65580 hepatis c
291	9	81.8	27	5	063676	Q63676 acanthokara	364	9	81.8	27	5	065581	Q65581 hepatis c
292	9	81.8	27	5	063677	Q63677 acanthokara	365	9	81.8	27	5	065582	Q65582 hepatis c
293	9	81.8	27	5	063678	Q63678 acanthokara	366	9	81.8	27	5	065583	Q65583 hepatis c
294	9	81.8	27	5	063679	Q63679 acanthokara	367	9	81.8	27	5	065584	Q65584 hepatis c
295	9	81.8	27	5	063680	Q63680 acanthokara	368	9	81.8	27	5	065585	Q65585 hepatis c
296	9	81.8	27	5	063681	Q63681 acanthokara	369	9	81.8	27	5	065586	Q65586 hepatis c
297	9	81.8	27	5	063682	Q63682 acanthokara	370	9	81.8	27	5	065587	Q65587 hepatis c
298	9	81.8	27	5	063683	Q63683 acanthokara	371	9	81.8	27	5	065588	Q65588 hepatis c
299	9	81.8	27	5	063684	Q63684 acanthokara	372	9	81.8	27	5	065589	Q65589 hepatis c
300	9	81.8	27	5	063685	Q63685 acanthokara	373	9	81.8	27	5	065590	Q65590 hepatis c
301	9	81.8	27	5	063686	Q63686 acanthokara	374	9	81.8	27	5	065591	Q65591 hepatis c
302	9	81.8	27	5	063687	Q63687 acanthokara	375	9	81.8	27	5	065592	Q65592 hepatis c
303	9	81.8	27	5	063688	Q63688 acanthokara	376	9	81.8	27	5	065593	Q65593 hepatis c
304	9	81.8	27	5	063689	Q63689 acanthokara	377	9	81.8	27	5	065594	Q65594 hepatis c
305	9	81.8	27	5	063690	Q63690 acanthokara	378	9	81.8	27	5	065595	Q65595 hepatis c
306	9	81.8	27	5	063691	Q63691 acanthokara	379	9	81.8	27	5	065596	Q65596 hepatis c
307	9	81.8	27	5	063692	Q63692 acanthokara	380	9	81.8	27	5	065597	Q65597 hepatis c
308	9	81.8	27	5	063693	Q63693 acanthokara	381	9	81.8	27	5	065598	Q65598 hepatis c
309	9	81.8	27	5	063694	Q63694 acanthokara	382	9	81.8	27	5	065599	Q65599 hepatis c

382	9	81.8	27	12	089124	089124 citrus tris	355	9	81.8	27	12	089117	089117 petromyzon
383	9	81.8	27	12	089126	089126 citrus tris	356	9	81.8	27	12	089118	089118 chimpanzee
384	9	81.8	27	12	089128	089128 citrus tris	357	9	81.8	27	12	089119	089119 heliobacter
385	9	81.8	27	12	089130	089130 citrus tris	358	9	81.8	28	2	089120	089120 pseudomorus
386	9	81.8	27	12	089131	089131 citrus tris	359	9	81.8	28	2	089121	089121 homo sapien
387	9	81.8	27	12	0891467	0891467 citrus tris	360	9	81.8	28	4	089126	089126 homo sapien
388	9	81.8	27	12	089164	089164 porcine cir	361	9	81.8	28	4	089127	089127 scuticell
389	9	81.8	27	12	089166	089166 porcine cir	362	9	81.8	28	4	089128	089128 scuticell
390	9	81.8	27	12	089175	089175 hepatitis c	363	9	81.8	28	4	089129	089129 scuticell
391	9	81.8	27	12	089177	089177 hepatitis c	364	9	81.8	28	4	089130	089130 scuticell
392	9	81.8	27	12	089179	089179 hepatitis c	365	9	81.8	28	4	089131	089131 scuticell
393	9	81.8	27	12	089199	089199 hepatitis c	366	9	81.8	28	4	089132	089132 scuticell
394	9	81.8	27	12	0891201	0891201 hepatitis c	367	9	81.8	28	4	089133	089133 scuticell
395	9	81.8	27	12	0891562	0891562 bovine herp	368	9	81.8	28	4	089134	089134 scuticell
396	9	81.8	27	12	089159	089159 hepatitis c	369	9	81.8	28	4	089135	089135 scuticell
397	9	81.8	27	12	089134	089134 hepatitis c	370	9	81.8	28	4	089136	089136 scuticell
398	9	81.8	27	12	0891502	0891502 hepatitis c	371	9	81.8	28	4	089137	089137 scuticell
399	9	81.8	27	12	0891004	0891004 hepatitis c	372	9	81.8	28	4	089138	089138 scuticell
400	9	81.8	27	12	0891003	0891003 hepatitis c	373	9	81.8	28	4	089139	089139 scuticell
401	9	81.8	27	12	0891001	0891001 hepatitis c	374	9	81.8	28	4	089140	089140 scuticell
402	9	81.8	27	12	0891050	0891050 hepatitis c	375	9	81.8	28	4	089141	089141 scuticell
403	9	81.8	27	12	0891228	0891228 hepatitis c	376	9	81.8	28	4	089142	089142 scuticell
404	9	81.8	27	12	0891227	0891227 hepatitis c	377	9	81.8	28	4	089143	089143 scuticell
405	9	81.8	27	12	0891226	0891226 hepatitis c	378	9	81.8	28	4	089144	089144 scuticell
406	9	81.8	27	12	0891225	0891225 hepatitis c	379	9	81.8	28	4	089145	089145 scuticell
407	9	81.8	27	12	0891224	0891224 hepatitis c	380	9	81.8	28	4	089146	089146 scuticell
408	9	81.8	27	12	0891004	0891004 hepatitis c	381	9	81.8	28	4	089147	089147 scuticell
409	9	81.8	27	12	0891002	0891002 hepatitis c	382	9	81.8	28	4	089148	089148 scuticell
410	9	81.8	27	12	0891001	0891001 hepatitis c	383	9	81.8	28	4	089149	089149 scuticell
411	9	81.8	27	12	0891000	0891000 hepatitis c	384	9	81.8	28	4	089150	089150 scuticell
412	9	81.8	27	12	0891000	0891000 hepatitis c	385	9	81.8	28	4	089151	089151 scuticell
413	9	81.8	27	12	0891000	0891000 hepatitis c	386	9	81.8	28	4	089152	089152 scuticell
414	9	81.8	27	12	0891000	0891000 hepatitis c	387	9	81.8	28	4	089153	089153 scuticell
415	9	81.8	27	12	0891000	0891000 hepatitis c	388	9	81.8	28	4	089154	089154 scuticell
416	9	81.8	27	12	0891000	0891000 hepatitis c	389	9	81.8	28	4	089155	089155 scuticell
417	9	81.8	27	12	0891000	0891000 hepatitis c	390	9	81.8	28	4	089156	089156 scuticell
418	9	81.8	27	12	0891000	0891000 hepatitis c	391	9	81.8	28	4	089157	089157 scuticell
419	9	81.8	27	12	0891000	0891000 hepatitis c	392	9	81.8	28	4	089158	089158 scuticell
420	9	81.8	27	12	0891000	0891000 hepatitis c	393	9	81.8	28	4	089159	089159 scuticell
421	9	81.8	27	12	0891000	0891000 hepatitis c	394	9	81.8	28	4	089160	089160 scuticell
422	9	81.8	27	12	0891000	0891000 hepatitis c	395	9	81.8	28	4	089161	089161 scuticell
423	9	81.8	27	12	0891000	0891000 hepatitis c	396	9	81.8	28	4	089162	089162 scuticell
424	9	81.8	27	12	0891000	0891000 hepatitis c	397	9	81.8	28	4	089163	089163 scuticell
425	9	81.8	27	12	0891000	0891000 hepatitis c	398	9	81.8	28	4	089164	089164 scuticell
426	9	81.8	27	12	0891000	0891000 hepatitis c	399	9	81.8	28	4	089165	089165 scuticell
427	9	81.8	27	12	0891000	0891000 hepatitis c	400	9	81.8	28	4	089166	089166 scuticell
428	9	81.8	27	12	0891000	0891000 hepatitis c	401	9	81.8	28	4	089167	089167 scuticell
429	9	81.8	27	12	0891000	0891000 hepatitis c	402	9	81.8	28	4	089168	089168 scuticell
430	9	81.8	27	12	0891000	0891000 hepatitis c	403	9	81.8	28	4	089169	089169 scuticell
431	9	81.8	27	12	0891000	0891000 hepatitis c	404	9	81.8	28	4	089170	089170 scuticell
432	9	81.8	27	12	0891000	0891000 hepatitis c	405	9	81.8	28	4	089171	089171 scuticell
433	9	81.8	27	12	0891000	0891000 hepatitis c	406	9	81.8	28	4	089172	089172 scuticell
434	9	81.8	27	12	0891000	0891000 hepatitis c	407	9	81.8	28	4	089173	089173 scuticell
435	9	81.8	27	12	0891000	0891000 hepatitis c	408	9	81.8	28	4	089174	089174 scuticell
436	9	81.8	27	12	0891000	0891000 hepatitis c	409	9	81.8	28	4	089175	089175 scuticell
437	9	81.8	27	12	0891000	0891000 hepatitis c	410	9	81.8	28	4	089176	089176 scuticell
438	9	81.8	27	12	0891000	0891000 hepatitis c	411	9	81.8	28	4	089177	089177 scuticell
439	9	81.8	27	12	0891000	0891000 hepatitis c	412	9	81.8	28	4	089178	089178 scuticell
440	9	81.8	27	12	0891000	0891000 hepatitis c	413	9	81.8	28	4	089179	089179 scuticell
441	9	81.8	27	12	0891000	0891000 hepatitis c	414	9	81.8	28	4	089180	089180 scuticell
442	9	81.8	27	12	0891000	0891000 hepatitis c	415	9	81.8	28	4	089181	089181 scuticell
443	9	81.8	27	12	0891000	0891000 hepatitis c	416	9	81.8	28	4	089182	089182 scuticell
444	9	81.8	27	12	0891000	0891000 hepatitis c	417	9	81.8	28	4	089183	089183 scuticell
445	9	81.8	27	12	0891000	0891000 hepatitis c	418	9	81.8	28	4	089184	089184 scuticell
446	9	81.8	27	12	0891000	0891000 hepatitis c	419	9	81.8	28	4	089185	089185 scuticell
447	9	81.8	27	12	0891000	0891000 hepatitis c	420	9	81.8	28	4	089186	089186 scuticell
448	9	81.8	27	12	0891000	0891000 hepatitis c	421	9	81.8	28	4	089187	089187 scuticell
449	9	81.8	27	12	0891000	0891000 hepatitis c	422	9	81.8	28	4	089188	089188 scuticell
450	9	81.8	27	12	0891000	0891000 hepatitis c	423	9	81.8	28	4	089189	089189 scuticell
451	9	81.8	27	12	0891000	0891000 hepatitis c	424	9	81.8	28	4	089190	089190 scuticell
452	9	81.8	27	12	0891000	0891000 hepatitis c	425	9	81.8	28	4	089191	089191 scuticell
453	9	81.8	27	12	0891000	0891000 hepatitis c	426	9	81.8	28	4	089192	089192 scuticell
454	9	81.8	27	12	0891000	0891000 hepatitis c	427	9	81.8	28	4	089193	089193 scuticell

528	9	91.8	31	16	Q9X124	Q9X124 thermotoga	601	9	81.8	31	16	Q9X124	Q9X124 arabidopsis
529	9	81.8	31	16	Q9X125	Q9X125 vibrio chol	602	9	81.8	31	16	Q9X125	Q9X125 rattus norv
530	9	81.8	31	16	Q9X126	Q9X126 yersinia fe	603	9	81.8	31	16	Q9X126	Q9X126 asia porc
531	9	81.8	31	16	Q9X127	Q9X127 anrobacteri	604	9	81.8	31	16	Q9X127	Q9X127 hepatitis b
532	9	81.8	32	2	Q9X128	Q9X128 actinophiliu	605	9	81.8	34	14	Q9X128	Q9X128 notophala
533	9	81.8	32	2	Q9X129	Q9X129 mycobacteri	606	9	81.8	34	14	Q9X129	Q9X129 aspergillu
534	9	81.8	32	2	Q9X130	Q9X130 yersinia fe	607	9	81.8	31	16	Q9X130	Q9X130 vibrio chol
535	9	81.8	32	2	Q9X131	Q9X131 bacillus su	608	9	81.8	34	14	Q9X131	Q9X131 aspergillu
536	9	81.8	32	2	Q9X132	Q9X132 bacillus su	609	9	81.8	35	2	Q9X132	Q9X132 synchrospo
537	9	81.8	32	2	Q9X133	Q9X133 streptococ	610	9	81.8	35	2	Q9X133	Q9X133 baculovira
538	9	81.8	32	2	Q9X134	Q9X134 schizosacch	611	9	81.8	35	2	Q9X134	Q9X134 pseudomonas
539	9	81.8	32	2	Q9X135	Q9X135 bacillus su	612	9	81.8	35	2	Q9X135	Q9X135 pseudomonas
540	9	81.8	32	2	Q9X136	Q9X136 bacillus su	613	9	81.8	35	2	Q9X136	Q9X136 pseudomonas
541	9	81.8	32	2	Q9X137	Q9X137 bacillus su	614	9	81.8	35	2	Q9X137	Q9X137 pseudomonas
542	9	81.8	32	2	Q9X138	Q9X138 bacillus su	615	9	81.8	35	2	Q9X138	Q9X138 pseudomonas
543	9	81.8	32	2	Q9X139	Q9X139 bacillus su	616	9	81.8	35	2	Q9X139	Q9X139 pseudomonas
544	9	81.8	32	2	Q9X140	Q9X140 bacillus su	617	9	81.8	35	2	Q9X140	Q9X140 pseudomonas
545	9	81.8	32	2	Q9X141	Q9X141 bacillus su	618	9	81.8	35	2	Q9X141	Q9X141 pseudomonas
546	9	81.8	32	2	Q9X142	Q9X142 bacillus su	619	9	81.8	35	2	Q9X142	Q9X142 pseudomonas
547	9	81.8	32	2	Q9X143	Q9X143 bacillus su	620	9	81.8	35	2	Q9X143	Q9X143 pseudomonas
548	9	81.8	32	2	Q9X144	Q9X144 bacillus su	621	9	81.8	35	2	Q9X144	Q9X144 pseudomonas
549	9	81.8	32	2	Q9X145	Q9X145 bacillus su	622	9	81.8	35	2	Q9X145	Q9X145 pseudomonas
550	9	81.8	32	2	Q9X146	Q9X146 bacillus su	623	9	81.8	35	2	Q9X146	Q9X146 pseudomonas
551	9	81.8	32	2	Q9X147	Q9X147 bacillus su	624	9	81.8	35	2	Q9X147	Q9X147 pseudomonas
552	9	81.8	32	2	Q9X148	Q9X148 bacillus su	625	9	81.8	35	2	Q9X148	Q9X148 pseudomonas
553	9	81.8	32	2	Q9X149	Q9X149 bacillus su	626	9	81.8	35	2	Q9X149	Q9X149 pseudomonas
554	9	81.8	32	2	Q9X150	Q9X150 bacillus su	627	9	81.8	35	2	Q9X150	Q9X150 pseudomonas
555	9	81.8	32	2	Q9X151	Q9X151 bacillus su	628	9	81.8	35	2	Q9X151	Q9X151 pseudomonas
556	9	81.8	32	2	Q9X152	Q9X152 bacillus su	629	9	81.8	35	2	Q9X152	Q9X152 pseudomonas
557	9	81.8	32	2	Q9X153	Q9X153 bacillus su	630	9	81.8	35	2	Q9X153	Q9X153 pseudomonas
558	9	81.8	32	2	Q9X154	Q9X154 bacillus su	631	9	81.8	35	2	Q9X154	Q9X154 pseudomonas
559	9	81.8	32	2	Q9X155	Q9X155 bacillus su	632	9	81.8	35	2	Q9X155	Q9X155 pseudomonas
560	9	81.8	32	2	Q9X156	Q9X156 bacillus su	633	9	81.8	35	2	Q9X156	Q9X156 pseudomonas
561	9	81.8	32	2	Q9X157	Q9X157 bacillus su	634	9	81.8	35	2	Q9X157	Q9X157 pseudomonas
562	9	81.8	32	2	Q9X158	Q9X158 bacillus su	635	9	81.8	35	2	Q9X158	Q9X158 pseudomonas
563	9	81.8	32	2	Q9X159	Q9X159 bacillus su	636	9	81.8	35	2	Q9X159	Q9X159 pseudomonas
564	9	81.8	32	2	Q9X160	Q9X160 bacillus su	637	9	81.8	35	2	Q9X160	Q9X160 pseudomonas
565	9	81.8	32	2	Q9X161	Q9X161 bacillus su	638	9	81.8	35	2	Q9X161	Q9X161 pseudomonas
566	9	81.8	32	2	Q9X162	Q9X162 bacillus su	639	9	81.8	35	2	Q9X162	Q9X162 pseudomonas
567	9	81.8	32	2	Q9X163	Q9X163 bacillus su	640	9	81.8	35	2	Q9X163	Q9X163 pseudomonas
568	9	81.8	32	2	Q9X164	Q9X164 bacillus su	641	9	81.8	35	2	Q9X164	Q9X164 pseudomonas
569	9	81.8	32	2	Q9X165	Q9X165 bacillus su	642	9	81.8	35	2	Q9X165	Q9X165 pseudomonas
570	9	81.8	32	2	Q9X166	Q9X166 bacillus su	643	9	81.8	35	2	Q9X166	Q9X166 pseudomonas
571	9	81.8	32	2	Q9X167	Q9X167 bacillus su	644	9	81.8	35	2	Q9X167	Q9X167 pseudomonas
572	9	81.8	32	2	Q9X168	Q9X168 bacillus su	645	9	81.8	35	2	Q9X168	Q9X168 pseudomonas
573	9	81.8	32	2	Q9X169	Q9X169 bacillus su	646	9	81.8	35	2	Q9X169	Q9X169 pseudomonas
574	9	81.8	32	2	Q9X170	Q9X170 bacillus su	647	9	81.8	35	2	Q9X170	Q9X170 pseudomonas
575	9	81.8	32	2	Q9X171	Q9X171 bacillus su	648	9	81.8	35	2	Q9X171	Q9X171 pseudomonas
576	9	81.8	32	2	Q9X172	Q9X172 bacillus su	649	9	81.8	35	2	Q9X172	Q9X172 pseudomonas
577	9	81.8	32	2	Q9X173	Q9X173 bacillus su	650	9	81.8	35	2	Q9X173	Q9X173 pseudomonas
578	9	81.8	32	2	Q9X174	Q9X174 bacillus su	651	9	81.8	35	2	Q9X174	Q9X174 pseudomonas
579	9	81.8	32	2	Q9X175	Q9X175 bacillus su	652	9	81.8	35	2	Q9X175	Q9X175 pseudomonas
580	9	81.8	32	2	Q9X176	Q9X176 bacillus su	653	9	81.8	35	2	Q9X176	Q9X176 pseudomonas
581	9	81.8	32	2	Q9X177	Q9X177 bacillus su	654	9	81.8	35	2	Q9X177	Q9X177 pseudomonas
582	9	81.8	32	2	Q9X178	Q9X178 bacillus su	655	9	81.8	35	2	Q9X178	Q9X178 pseudomonas
583	9	81.8	32	2	Q9X179	Q9X179 bacillus su	656	9	81.8	35	2	Q9X179	Q9X179 pseudomonas
584	9	81.8	32	2	Q9X180	Q9X180 bacillus su	657	9	81.8	35	2	Q9X180	Q9X180 pseudomonas
585	9	81.8	32	2	Q9X181	Q9X181 bacillus su	658	9	81.8	35	2	Q9X181	Q9X181 pseudomonas
586	9	81.8	32	2	Q9X182	Q9X182 bacillus su	659	9	81.8	35	2	Q9X182	Q9X182 pseudomonas
587	9	81.8	32	2	Q9X183	Q9X183 bacillus su	660	9	81.8	35	2	Q9X183	Q9X183 pseudomonas
588	9	81.8	32	2	Q9X184	Q9X184 bacillus su	661	9	81.8	35	2	Q9X184	Q9X184 pseudomonas
589	9	81.8	32	2	Q9X185	Q9X185 bacillus su	662	9	81.8	35	2	Q9X185	Q9X185 pseudomonas
590	9	81.8	32	2	Q9X186	Q9X186 bacillus su	663	9	81.8	35	2	Q9X186	Q9X186 pseudomonas
591	9	81.8	32	2	Q9X187	Q9X187 bacillus su	664	9	81.8	35	2	Q9X187	Q9X187 pseudomonas
592	9	81.8	32	2	Q9X188	Q9X188 bacillus su	665	9	81.8	35	2	Q9X188	Q9X188 pseudomonas
593	9	81.8	32	2	Q9X189	Q9X189 bacillus su	666	9	81.8	35	2	Q9X189	Q9X189 pseudomonas
594	9	81.8	32	2	Q9X190	Q9X190 bacillus su	667	9	81.8	35	2	Q9X190	Q9X190 pseudomonas
595	9	81.8	32	2	Q9X191	Q9X191 bacillus su	668	9	81.8	35	2	Q9X191	Q9X191 pseudomonas
596	9	81.8	32	2	Q9X192	Q9X192 bacillus su	669	9	81.8	35	2	Q9X192	Q9X192 pseudomonas
597	9	81.8	32	2	Q9X193	Q9X193 bacillus su	670	9	81.8	35	2	Q9X193	Q9X193 pseudomonas
598	9	81.8	32	2	Q9X194	Q9X194 bacillus su	671	9	81.8	35	2	Q9X194	Q9X194 pseudomonas
599	9	81.8	32	2	Q9X195	Q9X195 bacillus su	672	9	81.8	35	2	Q9X195	Q9X195 pseudomonas
600	9	81.8	32	2	Q9X196	Q9X196 bacillus su	673	9	81.8	35	2	Q9X196	Q9X196 pseudomonas

820	9	91.8	41	5	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H5	Q950P5	classical
821	9	91.8	41	5	Q950H1	Q950P1	trypanosoma	894	9	91.8	42	12	Q950H2	Q950P2	classical
822	9	91.8	41	5	Q950H2	Q950P2	maraca radi	894	9	91.8	42	12	Q950H3	Q950P3	classical
823	9	91.8	41	6	Q950H6	Q950P6	canis famli	894	9	91.8	42	12	Q950H7	Q950P7	classical
824	9	91.8	41	6	Q950H8	Q950P8	sus scrofa	894	9	91.8	42	12	Q950H9	Q950P9	classical
825	9	91.8	41	8	Q950H4	Q950P4	acipenser f	894	9	91.8	42	12	Q950H4	Q950P4	classical
826	9	91.8	41	8	Q950H4	Q950P4	acipenser b	894	9	91.8	42	12	Q950H5	Q950P5	classical
827	9	91.8	41	8	Q950H4	Q950P4	acipenser b	894	9	91.8	42	12	Q950H6	Q950P6	classical
828	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H7	Q950P7	classical
829	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H8	Q950P8	classical
830	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H9	Q950P9	classical
831	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
832	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H5	Q950P5	classical
833	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H6	Q950P6	classical
834	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H7	Q950P7	classical
835	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H8	Q950P8	classical
836	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H9	Q950P9	classical
837	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
838	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H5	Q950P5	classical
839	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H6	Q950P6	classical
840	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H7	Q950P7	classical
841	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H8	Q950P8	classical
842	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H9	Q950P9	classical
843	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
844	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H5	Q950P5	classical
845	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H6	Q950P6	classical
846	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H7	Q950P7	classical
847	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H8	Q950P8	classical
848	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H9	Q950P9	classical
849	9	91.8	41	8	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
850	9	91.8	41	11	Q950H5	Q950P5	parachymetium	894	9	91.8	42	12	Q950H5	Q950P5	classical
851	9	91.8	41	11	Q950H5	Q950P5	parachymetium	894	9	91.8	42	12	Q950H5	Q950P5	classical
852	9	91.8	41	11	Q950H5	Q950P5	parachymetium	894	9	91.8	42	12	Q950H5	Q950P5	classical
853	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
854	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
855	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
856	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
857	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
858	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
859	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
860	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
861	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
862	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
863	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
864	9	91.8	41	12	Q950H6	Q950P6	parachymetium	894	9	91.8	42	12	Q950H6	Q950P6	classical
865	9	91.8	41	15	Q950H4	Q950P4	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
866	9	91.8	41	15	Q950H4	Q950P4	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
867	9	91.8	41	15	Q950H4	Q950P4	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
868	9	91.8	41	16	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
869	9	91.8	41	16	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
870	9	91.8	41	16	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
871	9	91.8	41	16	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
872	9	91.8	41	16	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
873	9	91.8	41	16	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
874	9	91.8	42	2	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
875	9	91.8	42	2	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
876	9	91.8	42	2	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
877	9	91.8	42	2	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
878	9	91.8	42	2	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
879	9	91.8	42	4	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
880	9	91.8	42	5	Q950H4	Q950P4	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
881	9	91.8	42	5	Q950H4	Q950P4	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
882	9	91.8	42	5	Q950H4	Q950P4	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
883	9	91.8	42	5	Q950H4	Q950P4	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
884	9	91.8	42	6	Q950H4	Q950P4	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
885	9	91.8	42	6	Q950H4	Q950P4	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
886	9	91.8	42	8	Q950H4	Q950P4	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
887	9	91.8	42	8	Q950H4	Q950P4	homo sapien	894	9	91.8	42	12	Q950H4	Q950P4	classical
888	9	91.8	42	9	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
889	9	91.8	42	9	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
890	9	91.8	42	11	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
891	9	91.8	42	11	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical
892	9	91.8	42	11	Q950H3	Q950P3	homo sapien	894	9	91.8	42	12	Q950H3	Q950P3	classical


```

DE Cytochrome c oxidase subunit I (Fragment).
GN COL.
OS Gecko gecko (Tokay gecko).
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Gekkota; Gekkonidae; Gekko.
OX NCBI_TaxID=36310.
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99343648; PubMed=10413626;
FA Macey J.P., Wang Y., Ananjeva N.B., Larson A., Papenfuss T.J.,
RI "Variant patterns of fragmentation among gekkonid lizards of the
RI genus Tarantula produced by the Indian collision: A molecular
RI phylogenetic perspective and an area cladogram for central Asia".
EL Mol. Phylogenet. Evol. 12:30-32(1999).
DR EMBL: AF14244; AAL1000.1; -
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 AA; 1188 MW; 428789C9B36411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 2 LTR 4

RESULT 5
Q94V18 ID Q94V18 PRELIMINARY; PRT; 9 AA.
AC Q94V18:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COL.
OS Varanus arenarius.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
OX NCBI_TaxID=169848;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanidae (Squamata).";
KL Cladistics 17:0-0(2001).
DR EMBL: AF407495; AAL1004.1; -
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 AA; 1124 MW; 9E80C733640D5731 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LTR 5

RESULT 6
Q94VH4 ID Q94VH4 PRELIMINARY; PRT; 9 AA.
AC Q94VH4:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COL.
OS Varanus glauerti.
OG Mitochondrion.

```

```

DE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
OX NCBI_TaxID=169841;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanidae (Squamata).";
KL Cladistics 17:0-0(2001).
DR EMBL: AF407560; AAL10054.1; -
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 AA; 1124 MW; 9E80C7336411A731 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LTR 5

RESULT 7
Q94VE1 ID Q94VE1 PRELIMINARY; PRT; 9 AA.
AC Q94VE1:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COL.
OS Varanus mertensi.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
OX NCBI_TaxID=62044;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanidae (Squamata).";
KL Cladistics 17:0-0(2001).
DR EMBL: AF407512; AAL10090.1; -
KW Mitochondrion.
FT NON_TER
SQ SEQUENCE 9 AA; 1154 MW; 9E80C7336411A731 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 6.7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LTR 5

RESULT 8
Q94VD8 ID Q94VD8 PRELIMINARY; PRT; 9 AA.
AC Q94VD8:
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit I (Fragment).
GN COL.
OS Varanus niloticus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Scleroglossa; Anguilliformia; Varanidae; Varanus.
OX NCBI_TaxID=62046;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
RT "Mitochondrial DNA evidence and evolution in Varanidae (Squamata).";

```

```

BL Cladistics 17:00(2001).
DB EMBL: AF407514; AAL10096.1; -.
KW Mitochondrion.
FT NON_TER 9
SQ SEQUENCE 9 AA: 1154 MW: 98007336411A731 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 6,7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LXR 5

RESULT 9
ID Q94V66 PRELIMINARY: PRT; 9 AA.
AC Q94V66;
DI 01-DEC-2001 (TrEMBLrel, 19, Created)
DI 01-DEC-2001 (TrEMBLrel, 19, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Cyt.
OS Varanus pilbarensis.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Sclerozoa; Anguimorpha; Varanidae; Varanus.
OX NCBI_TaxID 62048;
RN [1]
RP SEQUENCE FROM N.A.
RA Ast J.C.;
PI "Cladistics 17:00(2001).";
DB EMBL: AF407518; AAL10108.1; -.
KW Mitochondrion.
FT NON_TER 9
SQ SEQUENCE 9 AA: 1064 MW: 8740A5A36411A735 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 6,7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LXR 5

RESULT 10
ID Q9PYK1 PRELIMINARY: PRT; 9 AA.
AC Q9PYK1;
DI 01-MAY-2000 (TrEMBLrel, 13, Created)
DI 01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
DE Papovavirus HK (Carder) early transcription control region (Fragment).
GN
OS Simian virus 12.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomaviruses.
OX NCBI_TaxID 46771;
RN [1]
RP SEQUENCE FROM N.A.
RA Choke W.F.; Walker D.L.; Poltman L.B.; Frisque R.L.;
PI "Construction and characterization of hybrid polyomavirus genomes.";
DB EMBL: M14451; AAA06236.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA: 1130 MW: 07E015B746C40742 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 9;
Best Local Similarity 66.7%; Pred. No. 6,7e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LXR 5

```

```

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 6 LXR 8

RESULT 11
ID Q91H88 PRELIMINARY: PRT; 9 AA.
AC Q91H88;
DI 01-OCT-2000 (TrEMBLrel, 15, Created)
DI 01-OCT-2000 (TrEMBLrel, 15, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel, 19, Last annotation update)
DE Papovavirus HK (Carder derived clone HKV) early transcription control region (Fragment).
GN
OS Simian virus 12.
OC Viruses; dsDNA viruses, no RNA stage; Polyomaviridae; Polyomaviruses.
OX NCBI_TaxID 46771;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN-GARNER;
RX MEDLINE: 87061221; PubMed 4923684;
RA Choke W.F.; Walker D.L.; Poltman L.B.; Frisque R.L.;
PI "Construction and characterization of hybrid polyomavirus genomes.";
DB EMBL: M14451; AAA06236.1; -.
FT NON_TER 9
SQ SEQUENCE 9 AA: 1130 MW: 07E015B746C40742 CRC64;

Query Match 81.8%; Score 9; DB 12; Length 9;
Best Local Similarity 66.7%; Pred. No. 6,7e+05;
Matches 2; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 6 LXR 8

RESULT 12
ID Q9T3H6 PRELIMINARY: PRT; 10 AA.
AC Q9T3H6;
DI 01-MAY-2000 (TrEMBLrel, 13, Created)
DI 01-MAY-2000 (TrEMBLrel, 13, Last sequence update)
DI 01-MAY-2000 (TrEMBLrel, 13, Last annotation update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Cyt.
OS Diplolossus bilobatus.
OC Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; Sclerozoa; Anguimorpha; Anolis.
OC Diplolossus.
OX NCBI_TaxID 192189;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 99443613; PubMed 10413621;
RA Macey J.R.; Schulte J.A.; Latsch A.; Pauly G.P.; Hall W.R.;
KA Papadatos J.J.;
PI "Molecular phylogenetics, tRNA evolution, and historical biogeography in anole lizards and related taxonomic families.";
DB EMBL: AF085698; AAD51514.1; -.
FT NON_TER 10
SQ SEQUENCE 10 AA: 1255 MW: 51E6067346411A73 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 1

```

Db 3 LTR 5

RESULT 13

Q9TG47 PRELIMINARY: PRI: 10 AA.

AC Q9TG47
 DT 01-MAY-2000 (TRENBLER: 13, Created)
 DI 01-MAY-2000 (TRENBLER: 13, Last sequence update)
 DI 01-MAY-2000 (TRENBLER: 13, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Col.
 OS Ophisaurus koellikeri.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Clariata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Annirothera; Annirothera;
 OC Ophisaurus.
 OC NCBI_TaxID=102194;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:99343613; PubMed-10413621;
 RA Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
 RA Papenfuss T.J.,
 RA "Molecular phylogenetics, rRNA evolution, and historical biogeography
 in anolis lizards and related taxonomic families."
 PL Mol. Phylogenet. Evol. 12:259-272(1999).
 DR EMBL: AF085621; AAB51563.1;
 KW Mitochondrion.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 10 AA: 1255 MW: 55E80C7336411A7 CRC64.

Query Match 81.8%; Score 9; DB 8; Length 10;

Best local Similarity 66.7%; Pred. No. 36+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

I I

Db 3 LTR 5

RESULT 14

Q9TG38 PRELIMINARY: PRI: 10 AA.

AC Q9TG38
 DT 01-MAY-2000 (TRENBLER: 13, Created)
 DI 01-MAY-2000 (TRENBLER: 13, Last sequence update)
 DI 01-MAY-2000 (TRENBLER: 13, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Col.
 OS Ophisaurus harti.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Clariata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Annirothera; Annirothera;
 OC Ophisaurus.
 OC NCBI_TaxID=102193;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:99343613; PubMed 10413621;
 RA Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
 RA Papenfuss T.J.,
 RA "Molecular phylogenetics, rRNA evolution, and historical biogeography
 in anolis lizards and related taxonomic families."
 PL Mol. Phylogenet. Evol. 12:259-272(1999).
 DR EMBL: AF085624; AAB51563.1;
 KW Mitochondrion.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 10 AA: 1255 MW: 55E80C7336411A7 CRC64.

Query Match 81.8%; Score 9; DB 8; Length 10;

Best local Similarity 66.7%; Pred. No. 36+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

Db 3 LTR 5

RESULT 15

Q9TG35 PRELIMINARY: PRI: 10 AA.

AC Q9TG35
 DT 01-MAY-2000 (TRENBLER: 13, Created)
 DI 01-MAY-2000 (TRENBLER: 13, Last sequence update)
 DI 01-MAY-2000 (TRENBLER: 13, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Col.
 OS Ophisaurus attenuatus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Clariata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Annirothera; Annirothera;
 OC Ophisaurus.
 OC NCBI_TaxID=102192;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:99343613; PubMed 10413621;
 RA Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
 RA Papenfuss T.J.,
 RA "Molecular phylogenetics, rRNA evolution, and historical biogeography
 in anolis lizards and related taxonomic families."
 PL Mol. Phylogenet. Evol. 12:259-272(1999).
 DR EMBL: AF085625; AAB51565.1;
 KW Mitochondrion.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 10 AA: 1255 MW: 55E80C7336411A7 CRC64.

Query Match 81.8%; Score 9; DB 8; Length 10;

Best local Similarity 66.7%; Pred. No. 36+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

I I

Db 3 LTR 5

RESULT 16

Q9TG42 PRELIMINARY: PRI: 10 AA.

AC Q9TG42
 DT 01-MAY-2000 (TRENBLER: 13, Created)
 DI 01-MAY-2000 (TRENBLER: 13, Last sequence update)
 DI 01-MAY-2000 (TRENBLER: 13, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Col.
 OS Ophisaurus ventralis.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Clariata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Annirothera; Annirothera;
 OC Ophisaurus.
 OC NCBI_TaxID=102195;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:99343613; PubMed 10413621;
 RA Macey J.R., Schulte J.A. II, Larson A., Tuniyev B.S., Orlov N.,
 RA Papenfuss T.J.,
 RA "Molecular phylogenetics, rRNA evolution, and historical biogeography
 in anolis lizards and related taxonomic families."
 PL Mol. Phylogenet. Evol. 12:259-272(1999).
 DR EMBL: AF085626; AAB51568.1;
 KW Mitochondrion.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 10 AA: 1255 MW: 55E80C7336411A7 CRC64.

Query Match 81.8%; Score 9; DB 8; Length 10;

Best local Similarity 66.7%; Pred. No. 36+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

```

QY 1 LXR 3
DB 3 LXR 5

RESULT 17
Q91FV5 PRELIMINARY: PRT: 10 AA.
AC Q91FV5:
DI 01-MAY-2000 (TREMBLrel. 14, Last sequence update)
DI 01-MAY-2000 (TREMBLrel. 14, Last sequence update)
DI 01-MAY-2000 (TREMBLrel. 14, Last annotation update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Eublepharus turkmenicus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; ScleroGLOSSa; Gekkota; Eublepharidae;
OX NCBI_TaxID:52219;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:99444613; PubMed:10414621;
RA Macey J.R., Schulte J.A. II, Larson A., Ananjeva N.B., Orlov N.,
RT "Molecular phylogenetics, rRNA evolution, and historical biogeography
in anolis lizards and related taxonomic families."
RL Mol. Phylogenet. Evol. 12:250-272(1999).
DR EMBL: U71345; AA02821.1;
KW Mitochondrion.
FT NON_CODING 10 10
SQ SEQUENCE 10 AA: 1290 MW: 506800936411A7 CR604;
Query Match 81.8%; Score 9; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LXR 5

RESULT 18
Q92771 PRELIMINARY: PRT: 10 AA.
AC Q92771:
DI 01-MAY-1997 (TREMBLrel. 03, Created)
DI 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DI 01-DEC-2000 (TREMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Xenosaurus grandis.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; ScleroGLOSSa; Anouromorpha; Xenosauridae;
OX NCBI_TaxID:52183;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:97154826; PubMed:9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Faur 2., Papenfuss T.J.,
RT "Two novel gene orders and the role of light-strand replication in
rearrangement of the vertebrate mitochondrial genome."
RL Mol. Biol. Evol. 14:91-104(1997).
DR EMBL: U71345; AA02821.1;
KW Mitochondrion.
FT NON_CODING 10 10
SQ SEQUENCE 10 AA: 1241 MW: 5068007336415B7 CR604;
Query Match 81.8%; Score 9; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LXR 5

RESULT 19
Q92576 PRELIMINARY: PRT: 10 AA.
AC Q92576:
DI 01-MAY-1997 (TREMBLrel. 03, Created)
DI 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DI 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Rana biporus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; ScleroGLOSSa; Amphibiana; Ranae;
OX NCBI_TaxID:52188;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:97154826; PubMed:9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Faur 2., Papenfuss T.J.,
RT "Two novel gene orders and the role of light-strand replication in
rearrangement of the vertebrate mitochondrial genome."
RL Mol. Biol. Evol. 14:91-104(1997).
DR EMBL: U71345; AA02821.1;
KW Mitochondrion.
FT NON_CODING 10 10
SQ SEQUENCE 10 AA: 1176 MW: 506800405A411A7 CR604;
Query Match 81.8%; Score 9; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LXR 5

RESULT 20
Q958K9 PRELIMINARY: PRT: 10 AA.
AC Q958K9:
DI 01-DEC-2001 (TREMBLrel. 19, Created)
DI 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DI 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Rana boylei.
OG Mitochondrion.

```

```

QY 1 LXR 3
DB 3 LXR 5

RESULT 19
Q92576 PRELIMINARY: PRT: 10 AA.
AC Q92576:
DI 01-MAY-1997 (TREMBLrel. 03, Created)
DI 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
DI 01-NOV-1998 (TREMBLrel. 08, Last annotation update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Rana biporus.
OG Mitochondrion.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosauria; Squamata; ScleroGLOSSa; Amphibiana; Ranae;
OX NCBI_TaxID:52188;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE:97154826; PubMed:9000757;
RA Macey J.R., Larson A., Ananjeva N.B., Faur 2., Papenfuss T.J.,
RT "Two novel gene orders and the role of light-strand replication in
rearrangement of the vertebrate mitochondrial genome."
RL Mol. Biol. Evol. 14:91-104(1997).
DR EMBL: U71345; AA02821.1;
KW Mitochondrion.
FT NON_CODING 10 10
SQ SEQUENCE 10 AA: 1176 MW: 506800405A411A7 CR604;
Query Match 81.8%; Score 9; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
DB 3 LXR 5

RESULT 20
Q958K9 PRELIMINARY: PRT: 10 AA.
AC Q958K9:
DI 01-DEC-2001 (TREMBLrel. 19, Created)
DI 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DI 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Rana boylei.
OG Mitochondrion.

```

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana;
 OC NCBITaxID=160499;
 RN [1];
 RP SEQUENCE FROM N.A.
 PX MESLINE=21184290; PubMed 11286199;
 RA Macey J.R., Strasburg J.H., Brisson J.A., Vredenburg V.I.,
 RA Jennings M., Larson A.;
 RT "Molecular Phylogenetics of Western North American Frogs of the Rana
 RT boylii Species Group", 19:131-142(2001).
 RL Mol. Phylogenet. Evol., 19:131-142(2001).
 DR EMBL: AF314019; AAF56477 1; -
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1320 MW; 42D380C9D36411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LXR 5

RESULT 21

Q94VF0
 ID Q94VF0 PRELIMINARY; PRI; 10 AA.
 AC Q94VF0;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit 1 (Fragment).
 GN Col.
 OS Varanus kingorum.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OC NCBITaxID=169845;
 RN [1];
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidae (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407509; AAL10041 1; -
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1255 MW; 5B8E90C7A36411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LXR 5

RESULT 22

Q94VF5
 ID Q94VF5 PRELIMINARY; PRI; 10 AA.
 AC Q94VF5;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit 1 (Fragment).
 GN Col.
 OS Varanus olivaceus.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OC NCBITaxID=62047;
 RN [1];

RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidae (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407516; AAL10099 1; -
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1234 MW; 5B4C4CA5A36411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;
 Best Local Similarity 66.7%; Pred. No. 3e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LXR 5

RESULT 23

Q94VD2
 ID Q94VD2 PRELIMINARY; PRI; 10 AA.
 AC Q94VD2;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit 1 (Fragment).
 GN Col.
 OS Varanus panoptes panoptes.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OC NCBITaxID=169849;
 RN [1];
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidae (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407519; AAL10102 1; -
 KW Mitochondrion.
 FT NON_TER 10 10
 SQ SEQUENCE 10 AA; 1219 MW; 5B2B00A146411A7 CRC64;

Query Match 41.8%; Score 9; DB 8; Length 10;
 Best Local Similarity 56.7%; Pred. No. 3e-04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 Db 3 LXR 5

RESULT 24

Q94VC9
 ID Q94VC9 PRELIMINARY; PRI; 10 AA.
 AC Q94VC9;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Cytochrome c oxidase subunit 1 (Fragment).
 GN Col.
 OS Varanus panoptes horn.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Anguimorpha; Varanidae; Varanus.
 OC NCBITaxID=169848;
 RN [1];
 RP SEQUENCE FROM N.A.
 RA Ast J.C.;
 RT "Mitochondrial DNA evidence and evolution in Varanoidae (Squamata).";
 RL Cladistics 17:0-0(2001).
 DR EMBL: AF407517; AAL10105 1; -
 KW Mitochondrion.
 FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1255 MW; 5DDE80C7336411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 3e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 3 LXR 5

RESULT 25

Q94V97

ID Q94V97 PRELIMINARY; PRI; 10 AA;

AC Q94V97;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

EE Cytochrome c oxidase subunit 1 (Fragment).

GN Col.

OS Varanus spenceri.

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; ScleroGLOSSa; Anguimorpha; Varanidae; Varanus.

OX NCBI_TaxID=169854;

PN 111

RP SEQUENCE FROM N.A.

RA Ast J.C.;

RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";

KL Cladistics 17:0-0(2001).

DR EMBL; AF407530; AAL10142.1;

KW Mitochondrion.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1255 MW; 5DDE80C7336411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;

Best Local Similarity 66.7%; Pred. No. 3e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 3 LXR 5

RESULT 26

Q94V85

ID Q94V85 PRELIMINARY; PRI; 10 AA;

AC Q94V85;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

EE Cytochrome c oxidase subunit 1 (Fragment).

GN Col.

OS Varanus varius (Lace monitor).

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; ScleroGLOSSa; Anguimorpha; Varanidae; Varanus.

OX NCBI_TaxID=8550;

PN 111

RP SEQUENCE FROM N.A.

RA Ast J.C.;

RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";

KL Cladistics 17:0-0(2001)

DR EMBL; AF407534; AAL10154.1;

KW Mitochondrion.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1255 MW; 5DEE90C7336411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;

Best Local Similarity 66.7%; Pred. No. 3e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 3 LXR 5

RESULT 27

Q94F08

ID Q94F08 PRELIMINARY; PRI; 10 AA;

AC Q94F08;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)

DI 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)

DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

EE Cytochrome c oxidase subunit 1 (Fragment).

GN Col.

OS Varanus scalaris.

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; ScleroGLOSSa; Anguimorpha; Varanidae; Varanus.

OX NCBI_TaxID=169852;

PN 111

RP SEQUENCE FROM N.A.

RA Ast J.C.;

RT "Mitochondrial DNA evidence and evolution in Varanoidea (Squamata).";

KL Cladistics 17:0-0(2001).

DR EMBL; AF407527; AAL10133.1;

DR EMBL; AF407528; AAL10136.1;

KW Mitochondrion.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1255 MW; 5DDE80C7336411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;

Best Local Similarity 66.7%; Pred. No. 3e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

DB 3 LXR 5

RESULT 28

Q95H01

ID Q95H01 PRELIMINARY; PRI; 10 AA;

AC Q95H01;

DT 01-JUN-2002 (TrEMBLrel. 21, Created)

DI 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)

DE 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

EE Cytochrome c oxidase subunit 1 (Fragment).

GN Col.

OS Bradyopodion tavetanum

OC Mitochondrion.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Lepidosauria; Squamata; Iguanata; Actosomatia; Chamaeleonidae;

OC Bradyopodion.

OX NCBI_TaxID=179888;

PN 111

RP SEQUENCE FROM N.A.

RA Townsend L.M.; Larson A.L.;

RT "Mitochondrial Phylogenetics and Mitochondrial Genome Evolution in the Chamaeleonidae (Reptilia, Squamata).";

KL Systematic Zoology 51:1-19; 1998; 51:13-19; 1998 databases.

DR EMBL; AF448730; AAL90472.1;

KW Mitochondrion.

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1427 MW; 5E2D6C2230411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 10;

Best Local Similarity 66.7%; Pred. No. 3e+03;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 3 LXR 5

RESULT 29

QC1K7
ID Q6C1R7 PRELIMINARY: PRT: 11 AA.
AC Q6C1R7
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DI 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TrEMBLrel. 21, Last annotation update)
GN Sslp (Fragment).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycetia; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetaceae.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-T73;
RA Perez-Orellana J.E.;
FL Submitted (FEB-2005); 1 kb; EMBL/GenBank/DBJ databases.
DR EMBL: AF239758; AAK15080.1; -;
FT NON_TER 11
SQ SEQUENCE 11 AA: 1274 MW: 1256761407.420374 CRC64;

Query Match 81.8%; Score 9; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. No. 3, 3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 9 LXR 11

RESULT 30

077899
ID 077899 PRELIMINARY: PRT: 11 AA.
AC 077899
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oryzomys niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Mochleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
OC Cichlidae; Oryzomys.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
FA Malaga-Trillo E., Zaleska-Raczynska Z., McAndrew B., Vincek V.,
FA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among eichlid mhc
RT class II B loci";
RL Genetics 149:1527-1537(1998).
DR EMBL: AF050009; AAC41348.1; -;
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA: 1349 MW: 81C12D8E7341B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 3, 3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 7 LXR 9

RESULT 31

077900
ID 077900 PRELIMINARY: PRT: 11 AA.
AC 077900
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oryzomys niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Mochleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
OC Cichlidae; Oryzomys.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
FA Malaga-Trillo E., Zaleska-Raczynska Z., McAndrew B., Vincek V.,
FA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among eichlid mhc
RT class II B loci";
RL Genetics 149:1527-1537(1998).
DR EMBL: AF050010; AAC41349.1; -;
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA: 1349 MW: 81C12D8E7341B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 3, 3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 7 LXR 9

RESULT 32

077901
ID 077901 PRELIMINARY: PRT: 11 AA.
AC 077901
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE MHC class II B locus 14 (Fragment).
OS Oryzomys niloticus (Nile tilapia) (Tilapia nilotica).
OC Eukaryota; Metazoa; Chordata; Gracilata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Mochleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Labroidel;
OC Cichlidae; Oryzomys.
OX NCBI_TaxID=8128;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=98315113; PubMed=9649539;
FA Malaga-Trillo E., Zaleska-Raczynska Z., McAndrew B., Vincek V.,
FA Figueroa F., Sultmann H., Klein J.;
RT "Linkage relationships and haplotype polymorphism among eichlid mhc
RT class II B loci";
RL Genetics 149:1527-1537(1998).
DR EMBL: AF050011; AAC41350.1; -;
FT NON_TER 11
FT NON_TER 11
SQ SEQUENCE 11 AA: 1349 MW: 81C12D8E7341B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 3, 3e+03;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 7 LXR 9

RESULT 33

077902
ID 077902 PRELIMINARY: PRT: 11 AA.
AC 077902
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DE MHC class II B locus 14 (Fragment).
 OS orochromis niloticus (Nile tilapia) (tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
 OC Cichlidae; orochromis.
 CX NCBI_taxid 8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 98415113; PubMed 9649549;
 RA Malara-Trillo E., Zaleska Patryszka Z., McAndrew B., Vinick V.,
 FA Funerua F., Sultmann H., Klein J.;
 RI "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci";
 RL Genetics 149:1527-1547(1998).
 DR EMBL: AF050014; AAC41352.1;
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1349 MW: 810120867441841 CRC64;
 Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3,3e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 7 LSR 9

RESULT 44
 077904
 ID 077904 PRELIMINARY: PRI: 11 AA.
 AC 077904;
 DT 01-NOV-1998 (TRIMBLrel. 08, Created)
 DT 01-NOV-1998 (TRIMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TRIMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS orochromis niloticus (Nile tilapia) (tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
 OC Cichlidae; orochromis.
 CX NCBI_taxid 8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 98415113; PubMed 9649549;
 RA Malara-Trillo E., Zaleska Patryszka Z., McAndrew B., Vinick V.,
 FA Funerua F., Sultmann H., Klein J.;
 RI "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci";
 RL Genetics 149:1527-1547(1998).
 DR EMBL: AF050014; AAC41352.1;
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1349 MW: 810120867441841 CRC64;
 Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3,3e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 7 LSR 9

RESULT 45
 077904
 ID 077904 PRELIMINARY: PRI: 11 AA.
 AC 077904;
 DT 01-NOV-1998 (TRIMBLrel. 08, Created)
 DT 01-NOV-1998 (TRIMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TRIMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS orochromis niloticus (Nile tilapia) (tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
 OC Cichlidae; orochromis.
 CX NCBI_taxid 8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 98415113; PubMed 9649549;
 RA Malara-Trillo E., Zaleska Patryszka Z., McAndrew B., Vinick V.,
 FA Funerua F., Sultmann H., Klein J.;
 RI "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci";
 RL Genetics 149:1527-1547(1998).
 DR EMBL: AF050014; AAC41352.1;
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1349 MW: 810120867441841 CRC64;
 Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3,3e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 7 LSR 9

OS orochromis niloticus (Nile tilapia) (tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
 OC Cichlidae; orochromis.
 CX NCBI_taxid 8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 98415113; PubMed 9649549;
 RA Malara-Trillo E., Zaleska Patryszka Z., McAndrew B., Vinick V.,
 FA Funerua F., Sultmann H., Klein J.;
 RI "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci";
 RL Genetics 149:1527-1547(1998).
 DR EMBL: AF050014; AAC41352.1;
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1349 MW: 810120867441841 CRC64;
 Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3,3e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 7 LSR 9

RESULT 46
 077905
 ID 077905 PRELIMINARY: PRI: 11 AA.
 AC 077905;
 DT 01-NOV-1998 (TRIMBLrel. 08, Created)
 DT 01-NOV-1998 (TRIMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TRIMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS orochromis niloticus (Nile tilapia) (tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
 OC Cichlidae; orochromis.
 CX NCBI_taxid 8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 98415113; PubMed 9649549;
 RA Malara-Trillo E., Zaleska Patryszka Z., McAndrew B., Vinick V.,
 FA Funerua F., Sultmann H., Klein J.;
 RI "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci";
 RL Genetics 149:1527-1547(1998).
 DR EMBL: AF050015; AAC41354.1;
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1349 MW: 810120867441841 CRC64;
 Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3,3e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 7 LSR 9

RESULT 47
 078121
 ID 078121 PRELIMINARY: PRI: 11 AA.
 AC 078121;
 DT 01-NOV-1998 (TRIMBLrel. 08, Created)
 DT 01-NOV-1998 (TRIMBLrel. 08, Last sequence update)
 DT 01-DEC-2001 (TRIMBLrel. 19, Last annotation update)
 DE MHC class II B locus 12 (Fragment).
 OS orochromis niloticus (Nile tilapia) (tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorpha; Perciformes; Labroidel;
 OC Cichlidae; orochromis.
 CX NCBI_taxid 8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE 98415113; PubMed 9649549;
 RA Malara-Trillo E., Zaleska Patryszka Z., McAndrew B., Vinick V.,
 FA Funerua F., Sultmann H., Klein J.;
 RI "Linkage relationships and haplotype polymorphism among cichlid mhc
 class II B loci";
 RL Genetics 149:1527-1547(1998).
 DR EMBL: AF050015; AAC41354.1;
 FT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA: 1349 MW: 810120867441841 CRC64;
 Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3,3e+04;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 7 LSR 9

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorphia; Perciformes; Labroidel;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98315113; PubMed:9649539;
 RA Malaga-Trillo F., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 PA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 R1 class II B loci";
 RL Genetics 149:1527-1537(1998);
 DR EMBL: AF050029; AAC41366.1;
 FT NON_LTER 1 1
 FT NON_LTER 11 11
 SQ SEQUENCE 11 AA: 1362 MW: 83C12D8EE741B54 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 4,4e-03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 I I
 DB 7 LSR 9

RESULT 38

077916
 ID 077916 PRELIMINARY; PRT; 11 AA.
 AC 077916;
 DT 01-NOV-1998 (EMBLrel. 08, Created)
 DI 01-NOV-1998 (EMBLrel. 08, Last sequence update)
 DE 01-DEC-2001 (EMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorphia; Perciformes; Labroidel;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98315113; PubMed:9649539;
 RA Malaga-Trillo F., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 PA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 R1 class II B loci";
 RL Genetics 149:1527-1537(1998);
 DR EMBL: AF050029; AAC41366.1;
 FT NON_LTER 1 1
 FT NON_LTER 11 11
 SQ SEQUENCE 11 AA: 1349 MW: 81C12D8EE741B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 4,4e-03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 I I
 DB 7 LSR 9

RESULT 39

077917
 ID 077917 PRELIMINARY; PRT; 11 AA.
 AC 077917;
 DT 01-NOV-1998 (EMBLrel. 08, Created)
 DI 01-NOV-1998 (EMBLrel. 08, Last sequence update)
 DE 01-DEC-2001 (EMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Oreochromis niloticus (Nile tilapia) (Tilapia nilotica).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

AC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorphia; Perciformes; Labroidel;
 OC Cichlidae; Oreochromis.
 OX NCBI_TaxID=8128;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98315113; PubMed:9649539;
 RA Malaga-Trillo F., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 PA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 R1 class II B loci";
 RL Genetics 149:1527-1537(1998);
 DR EMBL: AF050029; AAC41366.1;
 FT NON_LTER 1 1
 FT NON_LTER 11 11
 SQ SEQUENCE 11 AA: 1449 MW: 81C12D8EE741B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 4,4e-03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 I I
 DB 7 LSR 9

RESULT 40

077921
 ID 077921 PRELIMINARY; PRT; 11 AA.
 AC 077921;
 DT 01-NOV-1998 (EMBLrel. 08, Created)
 DI 01-NOV-1998 (EMBLrel. 08, Last sequence update)
 DE 01-DEC-2001 (EMBLrel. 19, Last annotation update)
 DE MHC class II B locus 14 (Fragment).
 OS Pseudotropheus sp. "Pseudotropheus tropheops complex".
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 OC Acanthomorpha; Acanthopterygii; Percomorphia; Perciformes; Labroidel;
 OC Cichlidae; Pseudotropheus.
 OX NCBI_TaxID=51796;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE:98315113; PubMed:9649539;
 RA Malaga-Trillo F., Zaleska-Rutczynska Z., McAndrew B., Vincek V.,
 PA Figueroa F., Sultmann H., Klein J.;
 RT "Linkage relationships and haplotype polymorphism among cichlid mhc
 R1 class II B loci";
 RL Genetics 149:1527-1537(1998);
 DR EMBL: AF050034; AAC41373.1;
 FT NON_LTER 1 1
 FT NON_LTER 11 11
 SQ SEQUENCE 11 AA: 1449 MW: 81C12D8EE741B41 CRC64;

Query Match 81.8%; Score 9; DB 7; Length 11;
 Best Local Similarity 66.7%; Pred. No. 4,4e-03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 I I
 DB 7 LSR 9

RESULT 41

090368
 ID 090368 PRELIMINARY; PRT; 11 AA.
 AC 090368;
 DT 01-MAR-2001 (EMBLrel. 16, Created)
 DI 01-MAR-2001 (EMBLrel. 16, Last sequence update)
 DE 01-DEC-2001 (EMBLrel. 19, Last annotation update)
 DE cytochrome c oxidase subunit I (Fragment).
 GN COI.
 OS Draco blanfordi.
 OG Mitochondrion.

```

oc Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
oc Lepidosauria; Squamata; Iguania; Arodonta; Anomidae; Draconinae;
oc Crocodylia;
ox NCBI_TaxID 89021;
rn [1]
rp SEQUENCE FROM N.A.
rx MEDLINE 97154820; PubMed 9006751;
ra Macey J.R., Larson A., Ananjeva N.B., Papenfuss T.J.;
rt "Replication slippage may cause parallel evolution in the secondary
ri structures of mitochondrial transfer RNAs."
rl Syst. Biol. 49:257-277(1997).
rn [2]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schultze J.A., Larson A.
rt "Evolution and information content of the mitochondrial genomic
ri structural features illustrated with acrodont lizards."
rl Syst. Biol. 49:257-277(2000).
rn [3]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schultze J.A., Larson A., Ananjeva N.B., Wang Y.,
ra Pothiyandara R., Rastegar-Pooyani N., Papenfuss T.J.;
rt "Evaluation of trans-species migration: An example using Acrodont lizard
ri phylogenetics."
rl Syst. Biol. 49:233-256(2000).
rn [4]
rp EMBL; AF128477; AA006686.1; -.
kw Mitochondrion.
ft NON_TER 11 11
sq SEQUENCE 11 AA; 1441 MW; 482637163641587 CR264;

Query Match 81.88; Score 9; DR 8; Length 11;
Best local Similarity 66.78; Pred. No. 3,6e-04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
IB 4 LXR 6

RESULT 42
Q96340 PRELIMINARY; PRI; 11 AA.
AC Q96340;
DT 01-MAR-2001 (TREMBLE; 16, Created)
DI 01-MAR-2001 (TREMBLE; 16, Last sequence update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Calotes cyclanoides.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
oc Lepidosauria; Squamata; Iguania; Arodonta; Anomidae; Draconinae;
oc Crocodylia;
ox NCBI_TaxID 118094;
rn [1]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schultze J.A., Larson A.
rt "Evolution and information content of the mitochondrial genomic
ri structural features illustrated with acrodont lizards."
rl Syst. Biol. 49:257-277(2000).
rn [2]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schultze J.A., Larson A., Ananjeva N.B., Wang Y.,
ra Pothiyandara R., Rastegar-Pooyani N., Papenfuss T.J.;
rt "Evaluation of trans-species migration: An example using Acrodont lizard
ri phylogenetics."
rl Syst. Biol. 49:233-256(2000).
rn [3]
rp EMBL; AF128484; AA006686.1; -.
kw Mitochondrion.
ft NON_TER 11 11
sq SEQUENCE 11 AA; 1455 MW; 482637163641147 CR264;

Query Match 81.88; Score 9; DR 8; Length 11;
Best local Similarity 66.79; Pred. No. 3,6e-04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
IB 4 LXR 6

RESULT 43
Q96347 PRELIMINARY; PRI; 11 AA.
AC Q96347;
DT 01-MAR-2001 (TREMBLE; 16, Created)
DI 01-MAR-2001 (TREMBLE; 16, Last sequence update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Calotes liocephalus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
oc Lepidosauria; Squamata; Iguania; Arodonta; Anomidae; Draconinae;
oc Crocodylia;
ox NCBI_TaxID 118095;
rn [1]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schultze J.A., Larson A.
rt "Evolution and information content of the mitochondrial genomic
ri structural features illustrated with acrodont lizards."
rl Syst. Biol. 49:257-277(2000).
rn [2]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schultze J.A., Larson A., Ananjeva N.B., Wang Y.,
ra Pothiyandara R., Rastegar-Pooyani N., Papenfuss T.J.;
rt "Evaluation of trans-species migration: An example using Acrodont lizard
ri phylogenetics."
rl Syst. Biol. 49:233-256(2000).
rn [3]
rp EMBL; AF128484; AA006686.1; -.
kw Mitochondrion.
ft NON_TER 11 11
sq SEQUENCE 11 AA; 1425 MW; 4706371013641007 CR264;

Query Match 81.88; Score 9; DR 8; Length 11;
Best local Similarity 66.78; Pred. No. 3,6e-04;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
IB 4 LXR 6

RESULT 44
Q96344 PRELIMINARY; PRI; 11 AA.
AC Q96344;
DT 01-MAR-2001 (TREMBLE; 16, Created)
DI 01-MAR-2001 (TREMBLE; 16, Last sequence update)
DE Cytochrome c oxidase subunit 1 (Fragment).
GN Col.
OS Calotes liocephalus.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
oc Lepidosauria; Squamata; Iguania; Arodonta; Anomidae; Draconinae;
oc Crocodylia;
ox NCBI_TaxID 118096;
rn [1]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schultze J.A., Larson A.
rt "Evolution and information content of the mitochondrial genomic
ri structural features illustrated with acrodont lizards."
rl Syst. Biol. 49:257-277(2000).
rn [2]
rp SEQUENCE FROM N.A.
rx Macey J.R., Schultze J.A., Larson A., Ananjeva N.B., Wang Y.,

```

RA Pethiyagoda R., Rastegar-Pouyani N., Papenfuss T.J.:
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL: AF128485; AAG00692.1; -.
 KW Mitochondrion.
 FT NON_TFR 11 11
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 3
 | |
 Db 4 LIR 6

RESULT 45

Q9G631 PRELIMINARY; PRT: 11 AA.
 AC Q9G631;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
 DE Cytochrome c oxidase subunit I (Fragment).
 GN Col.
 OS Calotes nigrilabris.
 OG Mitochondrion.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Acrodonta; Acanthodactylidae; Brachycephalus;
 OC Calotes.
 OX NCBI_TaxID=118098;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Macey J.R., Schulte J.A. II, Larson A.:
 RT "Evolution and information content of the mitochondrial genomic
 structural features illustrated with acrodont lizards.";
 RL Syst. Biol. 49:257-277(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Macey J.P., Schulte J.A. II, Larson A., Anderson M.B., King Y.:
 RT "Evaluating Trans-Tethys migration: An example using Acrodont lizard
 phylogenetics.";
 RL Syst. Biol. 49:233-256(2000).
 DR EMBL: AF128486; AAG00695.1; -.
 KW Mitochondrion.
 FT NON_TFR 11 11
 SQ SEQUENCE 11 AA; 1355 MW; 4B2D371E336411A7 CRC64;

Query Match 81.8%; Score 9; DB 8; Length 11;
 Best Local Similarity 66.7%; Pred. No. 3.3e+03;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 3
 | |
 Db 4 LIR 6

Search completed: April 30, 2003, 13:36:56
 Job time : 56.8182 secs



GenCore version: 5.1.4.ps-4578
Copyright (c) 1993 - 2003 GenCore Ltd.

OM protein - protein search, using sw model

Run on: April 30, 2003, 13:30:48 ; Search time 8.72727 seconds

Title: US-09-498-556c-357
Perfect score: 11
Sequence: 1 LXRK 4

Scoring table: BLOSUM62
Gapop 10.0 ; Gapext 0.5

Searched: 762574 seqs, 2942292 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database : Issued Patents_AA:*

- 1: /seq2/seqdata/1/aa/seqs/seqs.fdb
- 2: /seq2/seqdata/1/aa/seqs/seqs.fdb
- 3: /seq2/seqdata/1/aa/seqs/seqs.fdb
- 4: /seq2/seqdata/1/aa/seqs/seqs.fdb
- 5: /seq2/seqdata/1/aa/seqs/seqs.fdb
- 6: /seq2/seqdata/1/aa/seqs/seqs.fdb

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	81.8	3	1	US-08-470-937-7
2	9	81.8	3	4	US-08-868-452-7
3	9	81.8	4	1	US-08-288-405A-4
4	9	81.8	4	1	US-08-336-343A-36
5	9	81.8	4	4	US-09-142-079-19
6	9	81.8	4	4	US-09-357-141-19
7	9	81.8	4	4	US-09-533-889-19
8	9	81.8	5	1	US-07-620-023A-12
9	9	81.8	5	1	US-08-357-264-5
10	9	81.8	5	1	US-08-456-840-38
11	9	81.8	5	1	US-08-672-514-5
12	9	81.8	5	1	US-07-782-184-173
13	9	81.8	5	1	US-08-406-192-12
14	9	81.8	5	1	US-08-460-343B-37
15	9	81.8	5	1	US-08-460-343B-37
16	9	81.8	5	1	US-08-475-263-173
17	9	81.8	5	1	US-08-398-028B-37
18	9	81.8	5	1	US-08-398-028B-38
19	9	81.8	5	1	US-08-365-407A-38
20	9	81.8	5	1	US-08-485-886-173
21	9	81.8	5	2	US-08-504-265B-37
22	9	81.8	5	2	US-08-504-265B-38
23	9	81.8	5	2	US-08-545-171-12
24	9	81.8	5	2	US-08-392-973A-7
25	9	81.8	5	2	US-08-392-973A-8
26	9	81.8	5	2	US-08-392-973A-9
27	9	81.8	5	2	US-09-477-362-173

28	9	81.8	5	2	US-08-477-144-173
29	9	81.8	5	2	US-08-392-973A-48
30	9	81.8	5	2	US-08-173-189A-173
31	9	81.8	5	3	US-08-485-695-173
32	9	81.8	5	4	US-08-018-760-173
33	9	81.8	5	4	US-09-246-500B-17
34	9	81.8	5	6	5169943-16
35	9	81.8	5	6	5169943-16
36	9	81.8	5	6	5169943-16
37	9	81.8	5	6	5169943-16
38	9	81.8	5	6	5169943-16
39	9	81.8	5	6	5169943-16
40	9	81.8	5	6	5169943-16
41	9	81.8	5	6	5169943-16
42	9	81.8	5	6	5169943-16
43	9	81.8	5	6	5169943-16
44	9	81.8	5	6	5169943-16
45	9	81.8	5	6	5169943-16
46	9	81.8	5	6	5169943-16
47	9	81.8	5	6	5169943-16
48	9	81.8	5	6	5169943-16
49	9	81.8	5	6	5169943-16
50	9	81.8	5	6	5169943-16
51	9	81.8	5	6	5169943-16
52	9	81.8	5	6	5169943-16
53	9	81.8	5	6	5169943-16
54	9	81.8	5	6	5169943-16
55	9	81.8	5	6	5169943-16
56	9	81.8	5	6	5169943-16
57	9	81.8	5	6	5169943-16
58	9	81.8	5	6	5169943-16
59	9	81.8	5	6	5169943-16
60	9	81.8	5	6	5169943-16
61	9	81.8	5	6	5169943-16
62	9	81.8	5	6	5169943-16
63	9	81.8	5	6	5169943-16
64	9	81.8	5	6	5169943-16
65	9	81.8	5	6	5169943-16
66	9	81.8	5	6	5169943-16
67	9	81.8	5	6	5169943-16
68	9	81.8	5	6	5169943-16
69	9	81.8	5	6	5169943-16
70	9	81.8	5	6	5169943-16
71	9	81.8	5	6	5169943-16
72	9	81.8	5	6	5169943-16
73	9	81.8	5	6	5169943-16
74	9	81.8	5	6	5169943-16
75	9	81.8	5	6	5169943-16
76	9	81.8	5	6	5169943-16
77	9	81.8	5	6	5169943-16
78	9	81.8	5	6	5169943-16
79	9	81.8	5	6	5169943-16
80	9	81.8	5	6	5169943-16
81	9	81.8	5	6	5169943-16
82	9	81.8	5	6	5169943-16
83	9	81.8	5	6	5169943-16
84	9	81.8	5	6	5169943-16
85	9	81.8	5	6	5169943-16
86	9	81.8	5	6	5169943-16
87	9	81.8	5	6	5169943-16
88	9	81.8	5	6	5169943-16
89	9	81.8	5	6	5169943-16
90	9	81.8	5	6	5169943-16
91	9	81.8	5	6	5169943-16
92	9	81.8	5	6	5169943-16
93	9	81.8	5	6	5169943-16
94	9	81.8	5	6	5169943-16
95	9	81.8	5	6	5169943-16
96	9	81.8	5	6	5169943-16
97	9	81.8	5	6	5169943-16
98	9	81.8	5	6	5169943-16
99	9	81.8	5	6	5169943-16
100	9	81.8	5	6	5169943-16

101	9	81.8	8	4	US-08-444-818-685	Sequence 685, App	174	9	81.8	10	1	US-08-166-195A-43	Sequence 43, App
102	9	81.8	8	4	US-08-444-818-686	Sequence 686, App	175	9	81.8	10	1	US-08-166-195A-44	Sequence 44, App
103	9	81.8	8	4	US-08-444-818-687	Sequence 687, App	176	9	81.8	10	1	US-08-212-43A-33	Sequence 33, App
104	9	81.8	8	4	US-09-258-754-41	Sequence 41, App	177	9	81.8	10	1	US-08-217-186-8	Sequence 8, App
105	9	81.8	8	4	US-08-948-483B-6	Sequence 6, App	178	9	81.8	10	1	US-08-261-160A-8	Sequence 8, App
106	9	81.8	8	4	US-09-942-107-41	Sequence 41, App	179	9	81.8	10	1	US-08-316-333-61	Sequence 61, App
107	9	81.8	8	4	US-08-676-418A-14	Sequence 14, App	180	9	81.8	10	1	US-08-299-285-7	Sequence 7, App
108	9	81.8	8	4	US-09-133-521-14	Sequence 14, App	181	9	81.8	10	1	US-08-299-285-8	Sequence 8, App
109	9	81.8	8	4	US-09-193-263-2	Sequence 2, App	182	9	81.8	10	1	US-08-299-285-10	Sequence 10, App
110	9	81.8	8	4	US-04-556-111-45	Sequence 45, App	183	9	81.8	10	1	US-08-299-285-19	Sequence 19, App
111	9	81.8	8	1	US-07-969-941-3	Sequence 3, App	184	9	81.8	10	1	US-08-299-285-24	Sequence 24, App
112	9	81.8	9	1	US-07-955-417A-3	Sequence 3, App	185	9	81.8	10	1	US-09-299-385-26	Sequence 26, App
113	9	81.8	9	1	US-08-217-187-2	Sequence 2, App	186	9	81.8	10	1	US-08-299-285-27	Sequence 27, App
114	9	81.8	9	1	US-08-288-435A-6	Sequence 6, App	187	9	81.8	10	1	US-08-299-285-28	Sequence 28, App
115	9	81.8	9	1	US-08-288-435A-8	Sequence 8, App	188	9	81.8	10	1	US-08-299-285-29	Sequence 29, App
116	9	81.8	9	1	US-08-217-186-2	Sequence 2, App	189	9	81.8	10	1	US-08-299-285-30	Sequence 30, App
117	9	81.8	9	1	US-08-251-160A-2	Sequence 2, App	190	9	81.8	10	1	US-08-299-285-41	Sequence 41, App
118	9	81.8	9	1	US-08-403-634-5	Sequence 5, App	191	9	81.8	10	1	US-09-299-285-42	Sequence 42, App
119	9	81.8	9	1	US-08-403-634-6	Sequence 6, App	192	9	81.8	10	1	US-08-299-285-43	Sequence 43, App
120	9	81.8	9	1	US-08-487-890A-140	Sequence 140, App	193	9	81.8	10	1	US-08-299-285-44	Sequence 44, App
121	9	81.8	9	1	US-08-214-650-12	Sequence 12, App	194	9	81.8	10	1	US-08-299-285-45	Sequence 45, App
122	9	81.8	9	1	US-08-116-650-3	Sequence 3, App	195	9	81.8	10	1	US-08-299-285-46	Sequence 46, App
123	9	81.8	9	1	US-08-787-547-56	Sequence 56, App	196	9	81.8	10	1	US-08-299-285-47	Sequence 47, App
124	9	81.8	9	1	US-08-464-245-1	Sequence 1, App	197	9	81.8	10	1	US-08-214-650-41	Sequence 41, App
125	9	81.8	9	2	US-08-299-281A-2	Sequence 2, App	198	9	81.8	10	1	US-09-503-362-18	Sequence 18, App
126	9	81.8	9	2	US-08-704-655-15	Sequence 15, App	199	9	81.8	10	1	US-08-094-851-4	Sequence 4, App
127	9	81.8	9	2	US-08-478-435-140	Sequence 140, App	200	9	81.8	10	1	US-08-406-192-11	Sequence 11, App
128	9	81.8	9	2	US-08-227-483-140	Sequence 140, App	201	9	81.8	10	1	US-08-627-497-8	Sequence 8, App
129	9	81.8	9	2	US-08-478-372-140	Sequence 140, App	202	9	81.8	10	1	US-08-787-547-28	Sequence 28, App
130	9	81.8	9	2	US-08-469-840-2	Sequence 2, App	203	9	81.8	10	1	US-08-290-401-41	Sequence 41, App
131	9	81.8	9	2	US-08-755-728-14	Sequence 14, App	204	9	81.8	10	1	US-08-117-1170-127	Sequence 127, App
132	9	81.8	9	2	US-08-974-655-14	Sequence 14, App	205	9	81.8	10	2	US-08-436-772-8	Sequence 8, App
133	9	81.8	9	3	US-08-474-671-140	Sequence 140, App	206	9	81.8	10	2	US-08-436-772-9	Sequence 9, App
134	9	81.8	9	3	US-08-483-577A-140	Sequence 140, App	207	9	81.8	10	2	US-08-436-772-10	Sequence 10, App
135	9	81.8	9	3	US-08-568-560-2	Sequence 2, App	208	9	81.8	10	2	US-08-436-772-42	Sequence 42, App
136	9	81.8	9	3	US-08-159-339A-275	Sequence 275, App	209	9	81.8	10	2	US-08-436-772-43	Sequence 43, App
137	9	81.8	9	3	US-08-159-339A-643	Sequence 643, App	210	9	81.8	10	2	US-08-436-772-44	Sequence 44, App
138	9	81.8	9	3	US-08-159-339A-1094	Sequence 1094, App	211	9	81.8	10	2	US-08-436-772-45	Sequence 45, App
139	9	81.8	9	3	US-08-159-339A-1094	Sequence 1094, App	212	9	81.8	10	2	US-08-436-884B-8	Sequence 8, App
140	9	81.8	9	3	US-08-946-429A-45	Sequence 45, App	213	9	81.8	10	2	US-08-436-884B-10	Sequence 10, App
141	9	81.8	9	3	US-09-101-146-8	Sequence 8, App	214	9	81.8	10	2	US-08-436-884B-10	Sequence 10, App
142	9	81.8	9	4	US-08-513-441B-5	Sequence 5, App	215	9	81.8	10	2	US-08-436-884B-43	Sequence 43, App
143	9	81.8	9	4	US-08-913-441B-6	Sequence 6, App	216	9	81.8	10	2	US-08-436-884B-44	Sequence 44, App
144	9	81.8	9	4	US-09-258-754-253	Sequence 253, App	217	9	81.8	10	2	US-08-572-951-13	Sequence 13, App
145	9	81.8	9	4	US-04-283-011-14	Sequence 14, App	218	9	81.8	10	2	US-08-545-151-11	Sequence 11, App
146	9	81.8	9	4	US-04-042-107-253	Sequence 253, App	219	9	81.8	10	2	US-08-290-401A-9	Sequence 9, App
147	9	81.8	9	4	US-08-463-486-1	Sequence 1, App	220	9	81.8	10	2	US-08-383-624-11	Sequence 11, App
148	9	81.8	9	4	US-08-773-106-30	Sequence 30, App	221	9	81.8	10	2	US-08-556-597-133	Sequence 133, App
149	9	81.8	9	4	US-08-897-438-140	Sequence 140, App	222	9	81.8	10	2	US-08-556-597-143	Sequence 143, App
150	9	81.8	9	4	US-08-657-339A-4	Sequence 4, App	223	9	81.8	10	2	US-08-556-597-160	Sequence 160, App
151	9	81.8	9	4	US-08-657-339A-10	Sequence 10, App	224	9	81.8	10	2	US-08-556-597-160	Sequence 160, App
152	9	81.8	9	4	US-09-510-748A-35	Sequence 35, App	225	9	81.8	10	2	US-08-985-126-7	Sequence 7, App
153	9	81.8	9	4	US-09-510-748A-101	Sequence 101, App	226	9	81.8	10	2	US-08-985-126-8	Sequence 8, App
154	9	81.8	9	4	US-09-510-748A-147	Sequence 147, App	227	9	81.8	10	2	US-08-985-126-10	Sequence 10, App
155	9	81.8	9	4	US-09-510-748A-158	Sequence 158, App	228	9	81.8	10	2	US-08-985-126-19	Sequence 19, App
156	9	81.8	9	4	US-09-510-748A-159	Sequence 159, App	229	9	81.8	10	2	US-08-985-126-24	Sequence 24, App
157	9	81.8	9	4	US-09-133-521-16	Sequence 16, App	230	9	81.8	10	2	US-08-985-126-26	Sequence 26, App
158	9	81.8	9	4	US-09-142-481-11	Sequence 11, App	231	9	81.8	10	2	US-08-985-126-26	Sequence 26, App
159	9	81.8	9	4	US-08-457-694A-10	Sequence 4, App	232	9	81.8	10	2	US-08-985-126-28	Sequence 28, App
160	9	81.8	9	4	US-08-457-694A-10	Sequence 10, App	233	9	81.8	10	2	US-08-985-126-28	Sequence 28, App
161	9	81.8	9	4	US-09-349-797-2	Sequence 2, App	234	9	81.8	10	2	US-08-985-126-29	Sequence 29, App
162	9	81.8	9	4	US-08-627-654-110	Sequence 110, App	235	9	81.8	10	2	US-08-985-126-30	Sequence 30, App
163	9	81.8	9	4	US-08-649-518-140	Sequence 140, App	236	9	81.8	10	2	US-08-985-126-41	Sequence 41, App
164	9	81.8	9	4	US-09-044-718-59	Sequence 59, App	237	9	81.8	10	2	US-08-985-126-42	Sequence 42, App
165	9	81.8	9	4	US-09-160-513-218	Sequence 218, App	238	9	81.8	10	2	US-08-985-126-43	Sequence 43, App
166	9	81.8	9	4	US-08-459-260A-166	Sequence 166, App	239	9	81.8	10	2	US-08-985-126-44	Sequence 44, App
167	9	81.8	9	5	PCT-US94-02195-1	Sequence 1, App	240	9	81.8	10	2	US-08-985-126-45	Sequence 45, App
168	9	81.8	9	6	5217969-116	Patent No. 5217969	241	9	81.8	10	2	US-08-985-126-46	Sequence 46, App
169	9	81.8	10	1	US-07-841-997A-31	Sequence 31, App	242	9	81.8	10	2	US-08-985-126-47	Sequence 47, App
170	9	81.8	10	1	US-08-166-195A-8	Sequence 8, App	243	9	81.8	10	2	US-09-174-060-19	Sequence 19, App
171	9	81.8	10	1	US-08-166-195A-9	Sequence 9, App	244	9	81.8	10	3	US-09-139-742A-22	Sequence 22, App
172	9	81.8	10	1	US-08-166-195A-10	Sequence 10, App	245	9	81.8	10	3	US-09-139-742A-26	Sequence 26, App
173	9	81.8	10	1	US-08-166-195A-42	Sequence 42, App	246	9	81.8	10	3	US-09-139-742A-46	Sequence 46, App

393 9 81.8 12 3 US-08-482-508-204 Sequence 204, App
394 9 81.8 12 3 US-08-473-489A-170 Sequence 170, App
395 9 81.8 12 3 US-08-655-352-14 Sequence 14, App
396 9 81.8 12 3 US-08-573-225-21 Sequence 21, App
397 9 81.8 12 3 US-08-573-225-211 Sequence 211, App
398 9 81.8 12 3 US-09-244-298A-83 Sequence 83, App
399 9 81.8 12 3 US-08-485-695-170 Sequence 170, App
400 9 81.8 12 3 US-08-101-146-46 Sequence 46, App
401 9 81.8 12 4 US-08-981-601-6 Sequence 6, App
402 9 81.8 12 4 US-09-207-223-1 Sequence 1, App
403 9 81.8 12 4 US-09-082-420-2 Sequence 2, App
404 9 81.8 12 4 US-09-082-420-2 Sequence 3, App
405 9 81.8 12 4 US-09-082-420-2 Sequence 4, App
406 9 81.8 12 4 US-09-082-420-2 Sequence 19, App
407 9 81.8 12 4 US-08-018-760-170 Sequence 170, App
408 9 81.8 12 4 US-08-460-003-216 Sequence 216, App
409 9 81.8 12 4 US-09-516-704-83 Sequence 83, App
410 9 81.8 12 4 US-09-133-521-22 Sequence 22, App
411 9 81.8 12 4 US-09-203-945-249 Sequence 213, App
412 9 81.8 12 4 US-09-203-945-249 Sequence 218, App
413 9 81.8 12 4 US-09-258-016-14 Sequence 14, App
414 9 81.8 12 4 US-09-257-845B-14 Sequence 14, App
415 9 81.8 12 4 US-09-150-513-216 Sequence 216, App
416 9 81.8 12 4 US-08-835-281-14 Sequence 14, App
417 9 81.8 12 4 US-08-845-281-15 Sequence 15, App
418 9 81.8 12 4 US-08-845-281-16 Sequence 16, App
419 9 81.8 12 4 US-09-190-428-13 Sequence 13, App
420 9 81.8 12 4 US-08-459-260A-480 Sequence 480, App
421 9 81.8 12 4 US-09-549-090-82 Sequence 82, App
422 9 81.8 12 4 US-09-549-090-211 Sequence 211, App
423 9 81.8 12 5 PCT-US95-02478-3 Sequence 3, App
424 9 81.8 12 5 PCT-US95-05471-7 Sequence 7, App
425 9 81.8 12 5 PCT-US95-05471-40 Sequence 40, App
426 9 81.8 12 5 PCT-US95-11495-5 Sequence 5, App
427 9 81.8 12 5 PCT-US95-11495-11 Sequence 11, App
428 9 81.8 12 5 PCT-US96-09809-141 Sequence 141, App
429 9 81.8 13 1 US-08-630-731A-17 Sequence 17, App
430 9 81.8 13 1 US-08-456-840-16 Sequence 16, App
431 9 81.8 13 1 US-08-330-727-2 Sequence 2, App
432 9 81.8 13 1 US-08-330-727-3 Sequence 3, App
433 9 81.8 13 1 US-08-330-727-4 Sequence 4, App
434 9 81.8 13 1 US-08-330-727-5 Sequence 5, App
435 9 81.8 13 1 US-08-548-540-146 Sequence 146, App
436 9 81.8 13 1 US-08-210-715-13 Sequence 13, App
437 9 81.8 13 1 US-08-366-665-13 Sequence 13, App
438 9 81.8 13 1 US-08-266-607A-16 Sequence 16, App
439 9 81.8 13 2 US-08-572-951-19 Sequence 19, App
440 9 81.8 13 2 US-08-572-951-20 Sequence 20, App
441 9 81.8 13 2 US-08-572-951-20 Sequence 30, App
442 9 81.8 13 2 US-08-572-951-20 Sequence 10, App
443 9 81.8 13 2 US-08-592-514-15 Sequence 15, App
444 9 81.8 13 2 US-08-323-685-7 Sequence 7, App
445 9 81.8 13 3 US-08-726-096A-97 Sequence 97, App
446 9 81.8 13 3 US-08-530-589A-20 Sequence 20, App
447 9 81.8 13 4 US-08-865-5410-47 Sequence 47, App
448 9 81.8 13 4 US-08-628-747-8 Sequence 8, App
449 9 81.8 13 4 US-09-266-059-28 Sequence 28, App
450 9 81.8 13 4 US-09-177-219-20 Sequence 20, App
451 9 81.8 13 4 US-08-855-525B-47 Sequence 47, App
452 9 81.8 13 4 US-08-854-039B-26 Sequence 26, App
453 9 81.8 13 4 US-08-854-039B-27 Sequence 27, App
454 9 81.8 13 4 US-09-339-838-10 Sequence 10, App
455 9 81.8 13 4 US-09-339-838-11 Sequence 11, App
456 9 81.8 13 4 US-09-599-781-20 Sequence 20, App
457 9 81.8 13 5 US-09-160-513-221 Sequence 221, App
458 9 81.8 13 5 PCT-US96-09809-146 Sequence 146, App
459 9 81.8 13 6 5171684-36 Patent No. 5171684
460 9 81.8 14 1 US-08-103-490A-156 Sequence 156, App
461 9 81.8 14 1 US-08-103-490A-157 Sequence 157, App
462 9 81.8 14 1 US-08-103-490A-158 Sequence 158, App
463 9 81.8 14 1 US-08-103-490A-159 Sequence 159, App
464 9 81.8 14 1 US-08-103-490A-160 Sequence 160, App
465 9 81.8 14 1 US-08-103-490A-161 Sequence 161, App
466 9 81.8 14 1 US-08-103-490A-168 Sequence 168, App
467 9 81.8 14 1 US-08-103-490A-169 Sequence 169, App
468 9 81.8 14 1 US-08-103-490A-170 Sequence 170, App
469 9 81.8 14 1 US-08-103-490A-171 Sequence 171, App
470 9 81.8 14 1 US-08-103-490A-172 Sequence 172, App
471 9 81.8 14 1 US-08-103-490A-173 Sequence 173, App
472 9 81.8 14 1 US-07-969-941-4 Sequence 4, App
473 9 81.8 14 1 US-07-969-941-24 Sequence 24, App
474 9 81.8 14 1 US-08-103-489A-29 Sequence 29, App
475 9 81.8 14 1 US-08-103-489A-46 Sequence 46, App
476 9 81.8 14 1 US-08-103-489A-66 Sequence 66, App
477 9 81.8 14 1 US-08-103-489A-77 Sequence 77, App
478 9 81.8 14 1 US-08-103-489A-115 Sequence 115, App
479 9 81.8 14 1 US-08-103-489A-116 Sequence 116, App
480 9 81.8 14 1 US-08-103-489A-117 Sequence 117, App
481 9 81.8 14 1 US-08-103-489A-118 Sequence 118, App
482 9 81.8 14 1 US-08-103-489A-119 Sequence 119, App
483 9 81.8 14 1 US-08-103-489A-120 Sequence 120, App
484 9 81.8 14 1 US-08-103-489A-121 Sequence 121, App
485 9 81.8 14 1 US-08-103-489A-122 Sequence 122, App
486 9 81.8 14 1 US-07-971-163-11 Sequence 11, App
487 9 81.8 14 1 US-07-855-417A-4 Sequence 4, App
488 9 81.8 14 1 US-07-855-417A-29 Sequence 29, App
489 9 81.8 14 1 US-08-232-433A-8 Sequence 8, App
490 9 81.8 14 1 US-08-232-433A-23 Sequence 23, App
491 9 81.8 14 1 US-08-242-433A-28 Sequence 28, App
492 9 81.8 14 1 US-08-242-433A-41 Sequence 41, App
493 9 81.8 14 1 US-08-179-632-16 Sequence 16, App
494 9 81.8 14 1 US-08-179-632-19 Sequence 19, App
495 9 81.8 14 1 US-08-179-632-20 Sequence 20, App
496 9 81.8 14 1 US-08-440-174A-16 Sequence 16, App
497 9 81.8 14 1 US-08-440-174A-19 Sequence 19, App
498 9 81.8 14 1 US-08-440-174A-20 Sequence 20, App
499 9 81.8 14 1 US-08-467-083-66 Sequence 66, App
500 9 81.8 14 1 US-08-447-411-7 Sequence 7, App
501 9 81.8 14 1 US-08-447-411-8 Sequence 8, App
502 9 81.8 14 1 US-08-447-411-9 Sequence 9, App
503 9 81.8 14 1 US-08-447-411-55 Sequence 55, App
504 9 81.8 14 1 US-08-447-411-56 Sequence 56, App
505 9 81.8 14 1 US-08-447-411-57 Sequence 57, App
506 9 81.8 14 1 US-08-536-241-11 Sequence 11, App
507 9 81.8 14 1 US-08-431-417B-66 Sequence 66, App
508 9 81.8 14 2 US-08-442-181-1 Sequence 1, App
509 9 81.8 14 2 US-08-458-508A-10 Sequence 10, App
510 9 81.8 14 2 US-08-486-488A-66 Sequence 66, App
511 9 81.8 14 2 US-08-465-273-11 Sequence 11, App
512 9 81.8 14 2 US-08-764-640-41 Sequence 41, App
513 9 81.8 14 2 US-08-468-545B-66 Sequence 66, App
514 9 81.8 14 2 US-08-632-227-12 Sequence 12, App
515 9 81.8 14 2 US-08-632-227-13 Sequence 13, App
516 9 81.8 14 2 US-08-632-227-14 Sequence 14, App
517 9 81.8 14 2 US-09-119-024-11 Sequence 11, App
518 9 81.8 14 2 US-08-417-226-11 Sequence 11, App
519 9 81.8 14 3 US-09-109-414B-25 Sequence 25, App
520 9 81.8 14 3 US-08-785-247-29 Sequence 29, App
521 9 81.8 14 3 US-08-466-688B-66 Sequence 66, App
522 9 81.8 14 3 US-09-413-452-7 Sequence 7, App
523 9 81.8 14 3 US-08-974-225-41 Sequence 41, App
524 9 81.8 14 3 US-09-244-298A-41 Sequence 41, App
525 9 81.8 14 1 US-09-403-927-27 Sequence 27, App
526 9 81.8 14 4 US-09-041-886-49 Sequence 49, App
527 9 81.8 14 4 US-09-041-886-55 Sequence 55, App
528 9 81.8 14 4 US-09-196-141-11 Sequence 11, App
529 9 81.8 14 4 US-09-516-754-41 Sequence 41, App
530 9 81.8 14 4 US-08-989-661-13 Sequence 13, App
531 9 81.8 14 4 US-09-413-068-7 Sequence 7, App
532 9 81.8 14 4 US-09-027-998A-11 Sequence 11, App
533 9 81.8 14 4 US-09-027-998A-17 Sequence 17, App
534 9 81.8 14 4 US-09-017-947-12 Sequence 12, App
535 9 81.8 14 4 US-09-017-947-13 Sequence 13, App
536 9 81.8 14 4 US-09-017-947-14 Sequence 14, App
537 9 81.8 14 4 US-09-017-947-14 Sequence 14, App
538 9 81.8 14 4 US-08-643-732-11 Sequence 11, App

539	9	81.8	14	4	US-08-669-656A-23	Sequence 22, Appl	612	9	81.8	15	5	PCT-US93-06751-119	Sequence 119, Appl
540	9	81.8	14	4	US-09-549-090-41	Sequence 41, Appl	613	9	81.8	15	5	PCT-US95-11405-7	Sequence 7, Appl
541	9	81.8	14	5	PCT-US94-01368-1	Sequence 1, Appl	614	9	81.8	15	5	PCT-US95-11405-13	Sequence 13, Appl
542	9	81.8	14	5	PCT-US95-00062-16	Sequence 16, Appl	615	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
543	9	81.8	14	5	PCT-US95-00072-13	Sequence 13, Appl	616	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
544	9	81.8	14	5	PCT-US95-00002-20	Sequence 20, Appl	617	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
545	9	81.8	14	6	5405452-5	Patent No. 5405452	618	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
546	9	81.8	14	6	5445054-2	Patent No. 5445054	619	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
547	9	81.8	15	1	US-08-330-047-28	Sequence 28, Appl	620	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
548	9	81.8	15	1	US-08-208-181A-15	Sequence 15, Appl	621	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
549	9	81.8	15	1	US-08-423-399B-21	Sequence 21, Appl	622	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
550	9	81.8	15	1	US-09-470-314-1	Sequence 1, Appl	623	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
551	9	81.8	15	1	US-08-467-084-47	Sequence 47, Appl	624	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
552	9	81.8	15	1	US-08-466-468-13	Sequence 13, Appl	625	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
553	9	81.8	15	1	US-08-416-692-3	Sequence 3, Appl	626	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
554	9	81.8	15	1	US-08-787-547-25	Sequence 25, Appl	627	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
555	9	81.8	15	1	US-08-414-417A-47	Sequence 47, Appl	628	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
556	9	81.8	15	2	US-08-488-451A-2	Sequence 2, Appl	629	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
557	9	81.8	15	2	US-08-460-502-9	Sequence 9, Appl	630	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
558	9	81.8	15	2	US-08-485-349A-17	Sequence 17, Appl	631	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
559	9	81.8	15	2	US-08-492-616A-22	Sequence 22, Appl	632	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
560	9	81.8	15	2	US-08-686-594-14	Sequence 14, Appl	633	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
561	9	81.8	15	2	US-08-369-834-5	Sequence 5, Appl	634	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
562	9	81.8	15	2	US-08-468-746-4	Sequence 4, Appl	635	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
563	9	81.8	15	2	US-08-458-545B-47	Sequence 47, Appl	636	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
564	9	81.8	15	2	US-08-867-149-2	Sequence 2, Appl	637	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
565	9	81.8	15	2	US-08-740-444-1	Sequence 1, Appl	638	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
566	9	81.8	15	2	US-08-876-874-3	Sequence 3, Appl	639	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
567	9	81.8	15	2	US-08-769-715-35	Sequence 35, Appl	640	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
568	9	81.8	15	2	US-08-447-154-5	Sequence 5, Appl	641	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
569	9	81.8	15	2	US-08-808-374-2	Sequence 2, Appl	642	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
570	9	81.8	15	2	US-07-894-063A-13	Sequence 13, Appl	643	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
571	9	81.8	15	2	US-08-553-257A-51	Sequence 51, Appl	644	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
572	9	81.8	15	2	US-08-553-257A-51	Sequence 51, Appl	645	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
573	9	81.8	15	2	US-08-100-114B-23	Sequence 23, Appl	646	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
574	9	81.8	15	3	US-08-466-680A-47	Sequence 47, Appl	647	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
575	9	81.8	15	3	US-08-413-452-11	Sequence 11, Appl	648	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
576	9	81.8	15	3	US-08-406-405A-8	Sequence 8, Appl	649	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
577	9	81.8	15	3	US-08-391-122-85	Sequence 85, Appl	650	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
578	9	81.8	15	4	US-08-676-242-4	Sequence 4, Appl	651	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
579	9	81.8	15	4	US-08-468-208-13	Sequence 13, Appl	652	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
580	9	81.8	15	4	US-08-789-239P-20	Sequence 20, Appl	653	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
581	9	81.8	15	4	US-08-160-015-24	Sequence 24, Appl	654	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
582	9	81.8	15	4	US-08-256-104-5	Sequence 5, Appl	655	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
583	9	81.8	15	4	US-08-937-228-13	Sequence 13, Appl	656	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
584	9	81.8	15	4	US-08-112-681-6	Sequence 6, Appl	657	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
585	9	81.8	15	4	US-08-303-323-22	Sequence 22, Appl	658	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
586	9	81.8	15	4	US-08-982-274P-1202	Sequence 1202, Appl	659	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
587	9	81.8	15	4	US-09-264-693-1	Sequence 1, Appl	660	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
588	9	81.8	15	4	US-09-413-068-11	Sequence 11, Appl	661	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
589	9	81.8	15	4	US-08-132-644-24	Sequence 24, Appl	662	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
590	9	81.8	15	4	US-08-406-781-60	Sequence 60, Appl	663	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
591	9	81.8	15	4	US-08-089-090-7	Sequence 7, Appl	664	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
592	9	81.8	15	4	US-09-770-176-9	Sequence 9, Appl	665	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
593	9	81.8	15	4	US-08-421-593-13	Sequence 13, Appl	666	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
594	9	81.8	15	4	US-08-115-304B-1202	Sequence 1202, Appl	667	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
595	9	81.8	15	4	US-08-115-304B-1202	Sequence 1202, Appl	668	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
596	9	81.8	15	4	US-09-208-827-20	Sequence 20, Appl	669	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
597	9	81.8	15	4	US-08-347-504-46	Sequence 46, Appl	670	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
598	9	81.8	15	4	US-09-053-611-34	Sequence 34, Appl	671	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
599	9	81.8	15	4	US-08-006-053-137	Sequence 137, Appl	672	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
600	9	81.8	15	4	US-09-009-958-145	Sequence 145, Appl	673	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
601	9	81.8	15	4	US-08-006-054-155	Sequence 155, Appl	674	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
602	9	81.8	15	4	US-09-513-784A-104	Sequence 104, Appl	675	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
603	9	81.8	15	4	US-09-914-479A-13	Sequence 13, Appl	676	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
604	9	81.8	15	4	US-09-148-711A-9	Sequence 9, Appl	677	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
605	9	81.8	15	4	US-09-225-202-1	Sequence 1, Appl	678	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
606	9	81.8	15	4	US-08-190-132B-17	Sequence 17, Appl	679	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
607	9	81.8	15	4	US-08-469-260A-304	Sequence 304, Appl	680	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
608	9	81.8	15	4	US-08-787-748A-25	Sequence 25, Appl	681	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
609	9	81.8	15	4	US-08-629-242A-13	Sequence 13, Appl	682	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
610	9	81.8	15	4	US-09-157-748-31	Sequence 31, Appl	683	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl
611	9	81.8	15	5	PCT-US93-06751-115	Sequence 115, Appl	684	9	81.8	15	5	PCT-US95-13841-5	Sequence 5, Appl

Sequence 28, Appl
Sequence 18, Appl
Sequence 98, Appl
Sequence 5, Appl
Sequence 10, Appl
Sequence 3, Appl
Sequence 10, Appl
Sequence 17, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 10, Appl
Sequence 15, Appl
Sequence 17, Appl
Sequence 22, Appl
Sequence 77, Appl
Sequence 141, Appl
Sequence 138, Appl
Sequence 145, Appl
Sequence 1, Appl
Sequence 13, Appl
Sequence 4, Appl
Sequence 123, Appl
Sequence 28, Appl

977 9 81.8 24 1 95 09 227 357 282
978 9 81.8 24 4 05 08 981 527A 18
979 9 81.8 24 4 05 09 257 179 98
980 9 81.8 24 4 05 08 835 281 5
981 9 81.8 24 4 05 09 492 418 10
982 9 81.8 24 4 05 08 476 501 3
983 9 81.8 24 5 021 0594 06176 10
984 9 81.8 24 5 021 0595 00862 17
985 9 81.8 24 5 021 0595 04435 10
986 9 81.8 24 5 021 0595 04718 10
987 9 81.8 24 5 021 0595 09348 10
988 9 81.8 24 5 021 0595 09449 10
989 9 81.8 24 1 05 07 921 178A 15
990 9 81.8 24 1 05 07 921 178A 17
991 9 81.8 24 1 05 07 794 288D 32
992 9 81.8 24 1 05 07 794 288D 32
993 9 81.8 24 1 05 07 794 288D 32
994 9 81.8 24 1 05 07 794 288D 32
995 9 81.8 24 1 05 07 794 288D 32
996 9 81.8 24 1 05 08 444 198 1
997 9 81.8 24 1 05 08 444 198 1
998 9 81.8 24 1 05 08 444 198 1
999 9 81.8 24 1 05 08 444 198 1
1000 9 81.8 24 1 05 08 444 198 1

ALIGNMENTS

RESULT 1
US-08-470-847-7
Sequence 7, Application US/09470947
Patent No. 5800811
GENERAL INFORMATION:
APPLICANT: Nimmi, Marcel E.
APPLICANT: Hall, Frederick L.
APPLICANT: Tuan, Tai-Lan
APPLICANT: Wu, Lingtao
APPLICANT: Cheung, David T.
TITLE OF INVENTION: Transforming Growth Factor B Fusion
TITLE OF INVENTION: and
TITLE OF INVENTION: Their Use in Wound Healing
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 11150 Santa Monica Boulevard, Suite 400
CITY: Los Angeles
STATE: California
COUNTRY: USA
ZIP: 90255-3395
COMPIER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.20
CURRENT APPLICATION DATA: US/98/470-847
FILING DATE:
CLASSIFICATION: 4.24
ATTORNEY/AGENT INFORMATION:
NAME: Shapiro, Janice A.
REGISTRATION NUMBER: 34,051
REFERENCE/AGENT NUMBER: 66630-10501
TELECOMMUNICATION INFORMATION:
TELEPHONE: 410-445-1140
TELEFAX: 410-445-9031
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 3 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: peptide

US-08-470-847-7
Query Match 81.8%; Score 9; BH 4; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LXR 3
DB 1 LXR 3
RESULT 2
US-08-868-452-7
Sequence 7, Application US/09684527
Patent No. 672972
GENERAL INFORMATION:
APPLICANT: Marcell E. Nimmi
APPLICANT: Frederick L. Hall
APPLICANT: Lingtao Wu
APPLICANT: Bo Han
APPLICANT: Edwin Shors
TITLE OF INVENTION: BONE REGENERATION PROMOTING AND THEIR
TITLE OF INVENTION: USE IN BONE GROWTH
FILE REFERENCE: 17972-11
CURRENT APPLICATION NUMBER: US/98/868-4520
CURRENT FILING DATE: 1997-06-04
REMARK OF SEQ ID NO: 51
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO: 7
LENGTH: 3
TYPE: PRT
REMARK: Human
US-08-868-452-7
Query Match 81.8%; Score 9; BH 4; Length 3;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 LXR 3
DB 1 LXR 3
RESULT 3
US-08-288-405A-4
Sequence 4, Application US/98288405A
Patent No. 5556009
GENERAL INFORMATION:
APPLICANT: Chandy, Kaniathara G.
APPLICANT: Kaiman, Katalin
APPLICANT: Chandy, Gyuscha
APPLICANT: Gutman, George A.
TITLE OF INVENTION: A No. 5556009-1 Voltage Gated Potassium Channel
TITLE OF INVENTION: Gene
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Ficht, Holbach, Test, Albritton & Herbert
STREET: 4 Embarcadero Center, Suite 4000
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPIER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/288-405A
FILING DATE: 10-AUG-1994
CLASSIFICATION: 4.45
PRIOR APPLICATION DATA:

1 APPLICATION NUMBER: US 08/207,431
 2 FILING DATE: 04-MAR-1994
 3 ATTORNEY/AGENT INFORMATION:
 4 NAME: Dreger, Walter H.
 5 REGISTRATION NUMBER: 24,190
 6 REFERENCE/POCKET NUMBER: A-56844-1/WHD
 7 TELECOMMUNICATION INFORMATION:
 8 TELEPHONE: (415) 781-1989
 9 TELEFAX: (415) 498-3249
 10 TELEX: 910 277299
 11 INFORMATION FOR SEQ ID NO: 4:
 12 SEQUENCE CHARACTERISTICS:
 13 LENGTH: 4 amino acids
 14 TYPE: amino acid
 15 TOPOLOGY: linear
 16 MOLECULE TYPE: protein
 17 US-08-288-405A-4

Query Match 81.8%; Score 9; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 1 1
 DB 2 LAR 4

1 RESULT 4
 2 US-08-336-443A-36
 3 Sequence 36; Application US/0833643A
 4 Patent No. 5677144
 5 GENERAL INFORMATION:
 6 APPLICANT: Ulrich, Axel
 7 APPLICANT: Altes, Frank
 8 TITLE OF INVENTION: CCK-2, A No. 5677144-el Receptor Tyrosine Kinase
 9 NUMBER OF SEQUENCES: 43
 10 CORRESPONDENCE ADDRESSES:
 11 ADDRESSEE: Pennie & Edmonds
 12 STREET: 1155 Avenue of the Americas
 13 CITY: New York
 14 STATE: New York
 15 COUNTRY: U.S.A.
 16 ZIP: 10036-2711
 17 COMPUTER READABLE FORM:
 18 MEDIUM TYPE: Floppy disk
 19 COMPUTER: IBM PC compatible
 20 OPERATING SYSTEM: PC-DOS/MS-DOS
 21 SOFTWARE: Patent Release #1.0, Version #1.30
 22 CURRENT APPLICATION DATA:
 23 APPLICATION NUMBER: US/08/336,443A
 24 FILING DATE: 08-NOV-1994
 25 CLASSIFICATION: 435
 26 ATTORNEY/AGENT INFORMATION:
 27 NAME: Coruzzi, Laura A.
 28 REGISTRATION NUMBER: 30,742
 29 REFERENCE/POCKET NUMBER: 769; 065
 30 TELECOMMUNICATION INFORMATION:
 31 TELEPHONE: (212) 769-6090
 32 TELEFAX: (212) 969 9741/8864
 33 TELEX: 66141 PENNIE
 34 INFORMATION FOR SEQ ID NO: 36:
 35 SEQUENCE CHARACTERISTICS:
 36 LENGTH: 4 amino acids
 37 TYPE: amino acid
 38 TOPOLOGY: unknown
 39 MOLECULE TYPE: peptide
 40 US-08-336-443A-36

Query Match 81.8%; Score 9; DB 1; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 2 LSR 4

1 RESULT 5
 2 US-09-142-078-19
 3 Sequence 19; Application US/09142078
 4 Patent No. 6172641
 5 GENERAL INFORMATION:
 6 APPLICANT: Matsuo, R. Tyler
 7 APPLICANT: Zhou, Li-Ming
 8 APPLICANT: Layer, Richard L.
 9 TITLE OF INVENTION: Use of Conantokins
 10 NUMBER OF SEQUENCES: 71
 11 CORRESPONDENCE ADDRESSES:
 12 ADDRESSEE: Rothwell, Fluid, Ernst & Kutz, P.C.
 13 STREET: 555 Thirteenth Street, N.W., Suite 701-E
 14 CITY: Washington
 15 STATE: D.C.
 16 COUNTRY: USA
 17 ZIP: 20004
 18 COMPUTER READABLE FORM:
 19 MEDIUM TYPE: Floppy disk
 20 COMPUTER: IBM PC compatible
 21 OPERATING SYSTEM: PC-DOS/MS-DOS
 22 SOFTWARE: Patent Release #1.0, Version #1.30
 23 CURRENT APPLICATION DATA:
 24 APPLICATION NUMBER: US/09/142,078
 25 FILING DATE: 10-FEB-1999
 26 PRIOR APPLICATION DATA:
 27 APPLICATION NUMBER: W0 US97/12652
 28 FILING DATE: 21-JUL-1997
 29 PRIOR APPLICATION DATA:
 30 APPLICATION NUMBER: US 08/762,077
 31 FILING DATE: 06-DEC-1996
 32 PRIOR APPLICATION DATA:
 33 APPLICATION NUMBER: US 08/684,750
 34 FILING DATE: 22-JUL-1996
 35 ATTORNEY/AGENT INFORMATION:
 36 NAME: Thuen, Jeffrey L.
 37 REGISTRATION NUMBER: 28,957
 38 REFERENCE/POCKET NUMBER: 2414-135.A
 39 TELECOMMUNICATION INFORMATION:
 40 TELEPHONE: 202 793-6040
 41 TELEFAX: 202-783-6041
 42 INFORMATION FOR SEQ ID NO: 19:
 43 SEQUENCE CHARACTERISTICS:
 44 LENGTH: 4 amino acids
 45 TYPE: amino acid
 46 STRANDEDNESS:
 47 TOPOLOGY: linear
 48 MOLECULE TYPE: peptide
 49 FRAGMENT TYPE: internal
 50 FEATURE:
 51 NAME: Key, Modified site
 52 LOCATION: 4
 53 OTHER INFORMATION: Note "Xaa is
 54 OTHER INFORMATION: gamma-carboxyglutamic acid"
 55 US-09-142-078-19

Query Match 81.8%; Score 9; DB 4; Length 4;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 1 1
 DB 1 LAR 4

1 RESULT 6
 2 US-09-357-141-19
 3 Sequence 19; Application US/09457141
 4 Patent No. 627825

```

: GENERAL INFORMATION:
: APPLICANT: Olivera, Baldomero M.
: APPLICANT: McIntosh, J. Michael
: APPLICANT: McCabe, R. Tyler
: APPLICANT: Layer, Richard L.
: APPLICANT: Zhou, Li-Ming
: TITLE OF INVENTION: Use of Cytokotkins for Treating Pain
: FILE REFERENCE: 2314-171
: CURRENT APPLICATION NUMBER: US/09/357,141
: PRIOR FILING DATE: 1999-07-20
: PRIOR APPLICATION NUMBER: US 09/283,277
: PRIOR FILING DATE: 1999-04-01
: PRIOR APPLICATION NUMBER: US 09/142,078
: PRIOR FILING DATE: 1999-02-10
: PRIOR APPLICATION NUMBER: W/ US97/12552
: PRIOR FILING DATE: 1997-07-21
: PRIOR APPLICATION NUMBER: US 08/762,377
: PRIOR FILING DATE: 1996-12-06
: PRIOR APPLICATION NUMBER: US 08/694,752
: PRIOR FILING DATE: 1996-07-22
: NUMBER OF SEQ ID NOS: 71
: SOFTWARE: Patent In Vet. 2.0
: SEQ ID NO 19
: LENGTH: 4
: TYPE: PRT
: ORGANISM: Coccus radiatus
: FEATURE:
: NAME/KEY: PEPTIDE
: LOCATION: (4)
: OTHER INFORMATION: Xaa is gamma-carboxyglutamic acid.
: US-09-457-141-19

Query Match 81.8%; Score 9; DB 4; Length 4;
Best Local Similarity 66.7%; Prod No 1 9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 1 LAR 3

RESULT 7
US-09-533-889-19
: Sequence 19, Application US/09/533889
: Patent No. 6499574
: GENERAL INFORMATION:
: APPLICANT: McCabe, R. Tyler
: APPLICANT: Zhou, Li-Ming
: APPLICANT: Layer, Richard L.
: APPLICANT: Olivera, Baldomero M.
: APPLICANT: McIntosh, J. Michael
: TITLE OF INVENTION: Use of Cytokotkins
: NUMBER OF SEQUENCES: 71
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Potlwell, FIVE, Street & Kara, F.O.
: STREET: 555 Thirtieth Street, N.W., Suite 701 E
: CITY: Washington
: STATE: D.C.
: COUNTRY: USA
: ZIP: 20004
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC-IBM/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.20
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 09/357,141
: FILING DATE: 23 MAR 2000
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 09/142,078
: FILING DATE: 10-FEB-1999
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: W/ US97/12552

```

```

: FILING DATE: 21 JUL 1997
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/762,427
: FILING DATE: 06-DEC-1996
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 08/684,750
: FILING DATE: 22-JUL-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Thind, Jeffrey L.
: REGISTRATION NUMBER: 28,957
: EXPIRATION DATE: 2011-12-31
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 202-783-6040
: TELEFAX: 202-783-6041
: INFORMATION FOR SEQ ID NO: 19:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 4 amino acids
: TYPE: amino acid
: SOURCE: UNKNOWN
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: FRAGMENT TYPE: internal
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 4
: OTHER INFORMATION: Xaa is gamma-carboxyglutamic acid"
: US-09-533-889-19

Query Match 81.8%; Score 9; DB 4; Length 4;
Best Local Similarity 66.7%; Prod No 1 9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
Db 1 LAR 3

RESULT 8
US-07-626-923A-12
: Sequence 12, Application US/07/626923A
: GENERAL INFORMATION:
: APPLICANT: Yoshimura, Akihiko
: APPLICANT: Lombardi, Gregory D.
: APPLICANT: Ledish, Harvey
: TITLE OF INVENTION: MUTANT HIV REVERSE TRANSCRIPTASE
: TITLE OF INVENTION: THEREFOR
: NUMBER OF SEQUENCES: 14
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: HAMILTON, HOOK, SMITH & REYNOLDS, P.C.
: STREET: Two Millia Drive
: CITY: Lexington
: STATE: Massachusetts
: COUNTRY: U.S.A.
: ZIP: 02174
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-IBM/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 07/626,923A
: FILING DATE: 13 December 1990
: CLASSIFICATION:
: ATTORNEY/AGENT INFORMATION:
: NAME: Gaudreau, Patricia
: REGISTRATION NUMBER: 22,227
: EXPIRATION DATE: 2011-12-31
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (617) 861-2400
: TELEFAX: (617) 861-9540
: INFORMATION FOR SEQ ID NO: 12:
: SEQUENCE CHARACTERISTICS:

```


LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-07-526-923A-12

Query Match 81.8%; Score 9; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservation 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 1 1
 Db 1 LXR 3

RESULT 9
 US-08-357-264 5
 Sequence 5; Application US/08357264
 Patent No. 5541077
 GENERAL INFORMATION:
 APPLICANT: BURNIE MR., James P.
 APPLICANT: MATTHEWS MS., Ruth C.
 TITLE OF INVENTION: FUNGAL STRESS PROTEINS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cushman, Darby & Cushman
 STREET: 1100 New York Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3918

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/357,264
 FILING DATE:
 CLASSIFICATION: 435

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/152669
 FILING DATE: 16-NOV-1993
 APPLICATION NUMBER: US 663897
 FILING DATE: 14-MAR-1991
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, Paul N.
 REGISTRATION NUMBER: 16773
 TELETYPE: 202-861-3000
 TELEPHONE: 202-861-3000
 TELEFAX: 202-922-0944
 TELEX: 5714627 CUSH
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-357-264-5

Query Match 81.8%; Score 9; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.9e+05;
 Matches 2; Conservation 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 1 1
 Db 1 LXR 3

RESULT 10
 US-08-456-840-48
 Sequence 38; Application US/08456840

Patent No. 5597908
 GENERAL INFORMATION:
 APPLICANT: Label-Peters, W. C.
 APPLICANT: Butler, Sandra M.
 TITLE OF INVENTION: Immunoreactive Peptides of Apo(a)
 NUMBER OF SEQUENCES: 48
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: AVE No. 5597908e1
 STREET: 122 Pinedale Drive
 CITY: Rockville
 STATE: Maryland
 COUNTRY: US
 ZIP: 20850
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/456,840
 FILING DATE: 01 JUN-1995
 CLASSIFICATION: 536
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/266,407
 FILING DATE: 27 JUN-1994
 APPLICATION NUMBER: US 08/172,461
 FILING DATE: 21-DEC-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: GIMLEY, Mary E.
 REGISTRATION NUMBER: 34,409
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 301-258-5200
 TELEFAX: 301-977 0847
 INFORMATION FOR SEQ ID NO: 38:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-456-840-48

Query Match 31.8%; Score 9; DB 1; Length 5;
 Best Local Similarity 56.7%; Pred. No. 1.9e+05;
 Matches 2; Conservation 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 1 1
 Db 1 LXR 3

RESULT 11
 US 08 672-514-5
 Sequence 5; Application US/98672514
 Patent No. 5686248
 GENERAL INFORMATION:
 APPLICANT: BURNIE MR., James P.
 APPLICANT: MATTHEWS MS., Ruth C.
 TITLE OF INVENTION: FUNGAL STRESS PROTEINS
 NUMBER OF SEQUENCES: 10
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Cushman, Darby & Cushman
 STREET: 1100 New York Avenue, N.W.
 CITY: Washington
 STATE: DC
 COUNTRY: USA
 ZIP: 20005-3918
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/98/672,514

FILING DATE: 28-JUN-1996
 CLASSIFICATION: 445
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/152,669
 FILING DATE: 16-NOV-1993
 APPLICATION NUMBER: US 08/152,669
 FILING DATE: 16-NOV-1993
 APPLICATION NUMBER: US 66,4897
 FILING DATE: 14-MAR-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16773
 REFERENCE TO PRIOR NUMBER: 08/152,669
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202 861-4000
 TELEFAX: 202 922-0944
 TELEX: 6714627 CUSH
 INFORMATION FOR SEQ ID NO: 5:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-672-514-5

Query Match 81.8% Score 9; DB 1; Length 5;
 Best Local Similarity 66.7% Pred. No. 1,9e+05;
 Matches 2; Conservative 0; Mismatches 1; Gaps 0;

QY 1 LXR 3
 1 1
 DB 1 LXR 3

RESULT 12
 US-07-295-184-174
 Sequence 174, Application US/07789184
 Patent No. 5688768
 GENERAL INFORMATION:
 APPLICANT: CURELIN, SHAWN R.
 TITLE OF INVENTION: RESPERANT THROMBIN RESISTOR AND
 TITLE OF INVENTION: RELATED PHARMACEUTICALS
 NUMBER OF SEQUENCES: 223
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MORRIS & FORSTER
 STREET: 755 Page Mill Road
 CITY: Palo Alto
 STATE: California
 COUNTRY: USA
 ZIP: 94024 1018
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07789184
 FILING DATE: 19911107
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: MIRASHIGE, KATE H.
 REGISTRATION NUMBER: 29,069
 REFERENCE TO PRIOR NUMBER: 08/000-20609 20
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 814-5600
 TELEFAX: (415) 494-0792
 TELEX: 44-0154
 INFORMATION FOR SEQ ID NO: 174:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: single

TOPOLOGY: linear
 FEATURE:
 NAME/KEY: Modified site
 LOCATION: 5
 OTHER INFORMATION: Note "this position is R NZL."
 US-07-789-184-174

Query Match 81.8% Score 9; DB 1; Length 5;
 Best Local Similarity 66.7% Pred. No. 1,9e+05;
 Matches 2; Conservative 0; Mismatches 1; Gaps 0;

QY 1 LXR 3
 1 1
 DB 3 LAR 5

RESULT 13
 US-08-406-192-12
 Sequence 12, Application US/08406192
 Patent No. 5749287
 GENERAL INFORMATION:
 APPLICANT: Wilbur, D. Scott
 APPLICANT: Prathare, Pradip M
 TITLE OF INVENTION: Biotinylated Cobalamins
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Christensen, O'Connor, Johnson and Kindness
 STREET: 1420 Fifth Avenue, Suite 2800
 CITY: Seattle
 STATE: Washington
 COUNTRY: U.S.A.
 ZIP: WA 98101-2333
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.40
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08406192
 FILING DATE: 16-MAR-1995
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/224,831
 FILING DATE: 08-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Reznick, George E.
 REGISTRATION NUMBER: 47,919
 REFERENCE/AGENT NUMBER: RECI18947
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682 8100
 TELEFAX: (206) 224 0779
 TELEX: 4948024
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-406-192-12

Query Match 81.8% Score 9; DB 1; Length 5;
 Best Local Similarity 66.7% Pred. No. 1,9e+05;
 Matches 2; Conservative 0; Mismatches 1; Gaps 0;

QY 1 LXR 3
 1 1
 DB 3 LAR 5

RESULT 14
 US-08-460-343B-37
 Sequence 37, Application US/08403430

```

1 Patent No. 5741664
2 GENERAL INFORMATION:
3 APPLICANT: Marcus D. Ballinger and James A. Wells
4 TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CHANGING
5 TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
6 NUMBER OF SEQUENCES: 74
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: Genentech, Inc.
9 STREET: 1 DNA Way
10 CITY: South San Francisco
11 STATE: California
12 COUNTRY: USA
13 ZIP: 94080
14 COMPUTER READABLE FORM:
15 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
16 COMPUTER: IBM PC compatible
17 OPERATING SYSTEM: PC-DOS/MS-DOS
18 SOFTWARE: Winpatin (Genentech)
19 CURRENT APPLICATION DATA:
20 APPLICATION NUMBER: US/08/460,343B
21 FILING DATE: 01-Jun-1995
22 CLASSIFICATION: 435
23 PRIOR APPLICATION DATA:
24 APPLICATION NUMBER: 08/398028
25 FILING DATE: 03-mar-1995
26 ATTORNEY/AGENT INFORMATION:
27 NAME: Kubinec, Jeffrey S.
28 REGISTRATION NUMBER: 46,575
29 REFERENCE/DOCKET NUMBER: 6094601
30 TELEPHONE: 650/225-8228
31 TELEFAX: 650/225-9881
32 INFORMATION FOR SEQ ID NO: 37:
33 SEQUENCE CHARACTERISTICS:
34 LENGTH: 5 amino acids
35 TYPE: Amino Acid
36 TOPOLOGY: Linear
37 US-08-460-343B-37

```

```

Query Match      81.8%  Score 9;  DB 1;  Length 5;
Best Local Similarity 66.7%  Pred. No. 1.9e-05;
Matches 2;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0.

```

```

QY 1 LXR 3
DB 1 LXR 3

```

```

1 RESULT 15
2 US-08-460-343B-38
3 Sequence 38, Application US/08460343B
4 Patent No. 5741664
5 GENERAL INFORMATION:
6 APPLICANT: Marcus D. Ballinger and James A. Wells
7 TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CHANGING
8 TITLE OF INVENTION: SUBSTRATES CONTAINING DIBASIC RESIDUES
9 NUMBER OF SEQUENCES: 74
10 CORRESPONDENCE ADDRESS:
11 ADDRESSEE: Genentech, Inc.
12 STREET: 1 DNA Way
13 CITY: South San Francisco
14 STATE: California
15 COUNTRY: USA
16 ZIP: 94080
17 COMPUTER READABLE FORM:
18 MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
19 COMPUTER: IBM PC compatible
20 OPERATING SYSTEM: PC-DOS/MS-DOS
21 SOFTWARE: Winpatin (Genentech)
22 CURRENT APPLICATION DATA:
23 APPLICATION NUMBER: US/08/460,343B
24 FILING DATE: 01-Jun-1995
25 CLASSIFICATION: 435

```

```

1 PRIOR APPLICATION DATA:
2 APPLICATION NUMBER: 08/398028
3 FILING DATE: 03-mar-1995
4 ATTORNEY/AGENT INFORMATION:
5 NAME: Kubinec, Jeffrey S.
6 REGISTRATION NUMBER: 46,575
7 REFERENCE/DOCKET NUMBER: 6094601
8 TELECOMMUNICATION INFORMATION:
9 TELEPHONE: 650/225-8228
10 TELEFAX: 650/225-9881
11 INFORMATION FOR SEQ ID NO: 48:
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 5 amino acids
14 TYPE: Amino Acid
15 TOPOLOGY: Linear
16 US-08-460-343B-38

```

```

Query Match      81.8%  Score 9;  DB 1;  Length 5;
Best Local Similarity 66.7%  Pred. No. 1.9e-05;
Matches 2;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0.

```

```

QY 1 LXR 3
DB 2 LXR 4

```

```

1 RESULT 16
2 US-08-475-263-173
3 Sequence 173, Application US/08475263
4 Patent No. 5756994
5 GENERAL INFORMATION:
6 APPLICANT: COACHING, SHAWN K.
7 APPLICANT: SCARBROUGH, ROBERT M.
8 TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
9 TITLE OF INVENTION: RELATED PHARMACEUTICALS
10 NUMBER OF SEQUENCES: 223
11 CORRESPONDENCE ADDRESS:
12 ADDRESSEE: MORRISON & FORSTER
13 STREET: 2000 Pennsylvania Ave., NW
14 CITY: Washington
15 STATE: DC
16 COUNTRY: USA
17 ZIP: 20006-1812
18 COMPUTER READABLE FORM:
19 MEDIUM TYPE: Floppy disk
20 COMPUTER: IBM PC compatible
21 OPERATING SYSTEM: PC-DOS/MS-DOS
22 SOFTWARE: Patent in Release #1.0, Version #1.25
23 CURRENT APPLICATION DATA:
24 APPLICATION NUMBER: US/08/475,263
25 FILING DATE: 07-JUN-1995
26 CLASSIFICATION: 424
27 ATTORNEY/AGENT INFORMATION:
28 NAME: MORASHIGE, KATE H.
29 REGISTRATION NUMBER: 29,459
30 REFERENCE/DOCKET NUMBER: 22000 20502.03
31 TELECOMMUNICATION INFORMATION:
32 TELEPHONE: (202) 887-1500
33 TELEFAX: (202) 887-0763
34 TELEX: 90-4030
35 INFORMATION FOR SEQ ID NO: 174:
36 SEQUENCE CHARACTERISTICS:
37 LENGTH: 5 amino acids
38 TYPE: amino acid
39 STRANDEDNESS: single
40 TOPOLOGY: linear
41 FEATURE:
42 NAME/KEY: Modified site
43 LOCATION: 5
44 OTHER INFORMATION: /note "This position is R NOT."
45 US-08-475-263-173

```

```

Query Match      81.8%  Score 9;  DB 1;  Length 5;

```

Best Local Similarity 66.7%; Pred. No. 1,96,005;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
1b 3 LXR 5

RESULT 17

US-08-498-028B-47
Sequence 47, Application US/08/498/028B
Patent No. 5786295
GENERAL INFORMATION:
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING DIASIS RESIDUES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: WinEdit (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/498/028B
FILING DATE: 03-Mar-1995
CLASSIFICATION: 4.45
ATTORNEY/AGENT INFORMATION:
NAME: Kubinco, Jeffrey S.
REGISTRATION NUMBER: 46,575
REFERENCE/DESK NUMBER: 13946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-9229
TELEFAX: 650/225-9229
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-498-028B-47

Query Match 81.8%; Score 9; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1,96,005;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
1b 1 LXR 3

RESULT 18

US-08-498-028B-48
Sequence 48, Application US/08/498/028B
Patent No. 5786295
GENERAL INFORMATION:
APPLICANT: Marcus D. Ballinger and James A. Wells
TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
TITLE OF INVENTION: SUBSTRATES CONTAINING DIASIS RESIDUES
NUMBER OF SEQUENCES: 74
CORRESPONDENCE ADDRESS:
ADDRESS: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: WinEdit (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/498/028B
FILING DATE: 03-Mar-1995
CLASSIFICATION: 4.45
ATTORNEY/AGENT INFORMATION:
NAME: Kubinco, Jeffrey S.
REGISTRATION NUMBER: 46,575
REFERENCE/DESK NUMBER: 13946
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-9229
TELEFAX: 650/225-9229
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-498-028B-48

Query Match 81.8%; Score 9; DB 1; Length 5;
Best Local Similarity 66.7%; Pred. No. 1,96,005;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
1b 2 LXR 4

RESULT 19

US-08-266-407A-48
Sequence 48, Application US/08/266/407A
Patent No. 5786156
GENERAL INFORMATION:
APPLICANT: Laddell-Peters, W. R.
APPLICANT: Butler, Sandra M.
TITLE OF INVENTION: Immunoreactive peptides of Apo(a)
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESS: ARZO NO. 5786156d
STREET: 1340 Piccard Drive
CITY: Rockville
STATE: Maryland
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266/407A
FILING DATE: 27-JUN-1994
CLASSIFICATION: 4.45
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/172,461
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary F.
REGISTRATION NUMBER: 44,409
TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-238-9200
TELEFAX: 301-977-0847
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: Linear
MOLECULE TYPE: protein
US-08-266-407A-48

Query Match 81.8%; Score 9; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.9e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

Qy 1 LXR 3
 | |
 Db 1 LSR 3

RESULT 20

US-08-485-886-173
 : Sequence 173, Application US/0804prog
 : Patent No. 5788248
 : GENERAL INFORMATION:
 : APPLICANT: COUGHLIN, SHAUN R.
 : TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
 : TITLE OF INVENTION: RELATED PHARMACEUTICALS
 : NUMBER OF SEQUENCES: 22
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: MOPPISON & FORSTER
 : STREET: 755 Page Mill Road
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94304-1012
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patent In Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/485,886
 : FILING DATE: 07-JUN-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 07/789,164
 : FILING DATE: 07-NOV-1991
 : ATTORNEY/AGENT INFORMATION:
 : NAME: MUKASHIGE, KATE H.
 : REGISTRATION NUMBER: 29,959
 : REFERENCE/AGENT NUMBER: 22009-20502.20
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (415) 813-5600
 : TELEFAX: (415) 494-0792
 : TELEX: 34-0154
 : INFORMATION FOR SEQ ID NO: 173.
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear
 : FEATURE:
 : NAME/KEY: Modified-site
 : LOCATION: 5
 : OTHER INFORMATION: /note= "this position is R NH2."
 : US-08-485-886-173

Query Match 81.8%; Score 9; DB 1; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.9e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

Qy 1 LXR 3
 | |
 Db 3 LAR 5

RESULT 21

US-08-504-265B-37
 : Sequence 37, Application US/08504265B
 : Patent No. 5837516
 : GENERAL INFORMATION:
 : APPLICANT: Marcus D. Ballinger and James A. Wells

: TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
 : TITLE OF INVENTION: SUBSTITUTES CONTAINING BASIC RESIDUES
 : NUMBER OF SEQUENCES: 90
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genotech, Inc.
 : STREET: 1 DNA Way
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch, 1.44 M floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: WinPolin (Genotech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/504,265B
 : FILING DATE: 19-Jul-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 09/308928
 : FILING DATE: 03-MAR-1995
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Kuldinec, Jeffrey S.
 : REGISTRATION NUMBER: 36,575
 : REFERENCE/AGENT NUMBER: 10936PJ
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 650/225-8228
 : TELEFAX: 650/952-9881
 : INFORMATION FOR SEQ ID NO: 37:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 5 amino acids
 : TYPE: Amino Acid
 : TOPOLOGY: Linear
 : US-08-504-265B-37

Query Match 81.8%; Score 9; DB 2; Length 5;
 Best Local Similarity 66.7%; Pred. No. 1.9e-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

Qy 1 LXR 3
 | |
 Db 1 LTR 3

RESULT 22

US-08-504-265B-38
 : Sequence 38, Application US/08504265B
 : Patent No. 5837516
 : GENERAL INFORMATION:
 : APPLICANT: Marcus D. Ballinger and James A. Wells
 : TITLE OF INVENTION: SUBSTITUTED VARIANTS CAPABLE OF CLEAVING
 : TITLE OF INVENTION: SUBSTITUTES CONTAINING BASIC RESIDUES
 : NUMBER OF SEQUENCES: 90
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Genotech, Inc.
 : STREET: 1 DNA Way
 : CITY: South San Francisco
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94080
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: 3.5 inch, 1.44 M floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: WinPolin (Genotech)
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/504,265B
 : FILING DATE: 19-Jul-1995
 : CLASSIFICATION: 435
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 09/308928
 : FILING DATE: 03-MAR-1995

ATTORNEY/AGENT INFORMATION:
 NAME: Kubinek, Jeffrey S.
 REGISTRATION NUMBER: 50,675
 REFERENCE/DECKET NUMBER: PG946P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 650/225-8229
 TELEFAX: 650/952-0881
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: Amino Acid
 TOPOLOGY: Linear
 US-08 504-265B-38

Query Match 81.8% Score 9; DB 2; Length 5;
 Best Local Similarity 66.7% Prod. No. 1.9c-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0.

QY 1 LXR 3
 1 1
 DB 2 LXR 4

RESULT 24
 US-08 545-151-12
 Sequence 12, Application US/08545151
 Patent No. 5840712
 GENERAL INFORMATION:
 APPLICANT: Morton, Jr., A. Charles
 APPLICANT: Whitby, D. Scott
 APPLICANT: Pruthi, Pradip M
 TITLE OF INVENTION: Water Soluble Vitamin B12 Receptor
 TITLE OF INVENTION: Modulating Agents and Methods Related Thereto
 NUMBER OF SEQUENCES: 47
 CORRESPONDENCE ADDRESS:
 ADDRESS: Christopher C. Connor, Johnson & Kindness PLLC
 STREET: 1120 Fifth Avenue, Suite 2500
 CITY: Seattle
 STATE: Washington
 COUNTRY: U.S.A.
 ZIP: WA 98101 2434
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/545,151
 FILING DATE: 19-Oct-1995
 CLASSIFICATION: C14
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: PCI/US95/04404
 FILING DATE: 07-APR-1995
 APPLICATION NUMBER: US 08/406,192
 FILING DATE: 16-MAR-1995
 APPLICATION NUMBER: US 08/406,194
 FILING DATE: 16-MAR-1995
 APPLICATION NUMBER: US 08/406,191
 FILING DATE: 16-MAR-1995
 APPLICATION NUMBER: US 08/224,831
 FILING DATE: 08-APR-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Renzoni, George E.
 REGISTRATION NUMBER: 37,919
 REFERENCE/DECKET NUMBER: PECT19479
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (206) 682 8100
 TELEFAX: (206) 224 0779
 TELEX: 4948023
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid

STANDARDNESS: Single
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 US-08-545-151-12

Query Match 81.8% Score 9; DB 2; Length 5;
 Best Local Similarity 66.7% Prod. No. 1.9c-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 1 1
 DB 3 LXR 5

RESULT 24
 US-08-392-973A-7
 Sequence 7, Application US/08392973A
 Patent No. 5844453
 GENERAL INFORMATION:
 APPLICANT: Holder, Andrew T.
 APPLICANT: Reathie, James
 TITLE OF INVENTION: GROWTH INHIBITOR POTENTIATING MOLECULES
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESS: HALE AND DERR LLP
 STREET: 60 State Street
 CITY: Boston
 STATE: MA
 COUNTRY: United States of America
 ZIP: 02109
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 SOFTWARE: Patent in Release #1.0, Version #1.30
 CURRENT APPLICATION DATA: US/08/392,973A
 APPLICATION NUMBER: US/08/392,973A
 FILING DATE: 25-APR-1995
 CLASSIFICATION: 424
 ATTORNEY/AGENT INFORMATION:
 NAME: BAKER, Hollie L.
 REGISTRATION NUMBER: 41,321
 REFERENCE/DECKET NUMBER: 102286,401
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 617-526-6000
 TELEFAX: 617-526-5000
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 5 amino acids
 TYPE: amino acid
 TOPOLOGY: Linear
 MOLECULE TYPE: peptide
 FRAGMENT TYPE: Internal
 FEATURE:
 NAME/KEY: Peptide
 LOCATION: 1-5
 OTHER INFORMATION: 56.5% "91 95 RESIDUE DIFFERENCE"
 OTHER INFORMATION: "91 95 RESIDUE DIFFERENCE"
 US-08-392-973A-7

Query Match 81.8% Score 9; DB 2; Length 5;
 Best Local Similarity 66.7% Prod. No. 1.9c-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
 1 1
 DB 3 LXR 5

RESULT 25
 US-08-392-973A-8
 Sequence 8, Application US/08392973A
 Patent No. 5844453

GROWTH

```

1 GENERAL INFORMATION:
2 APPLICANT: HOLDER, Andrew T.
3 TITLE OF INVENTION: GROWTH HORMONE POTENTIATING MOLECULES
4 NUMBER OF SEQUENCES: 37
5 CORRESPONDENCE ADDRESS:
6 ADDRESSEE: HALE AND DORR LLP
7 STREET: 60 State Street
8 CITY: Boston
9 STATE: MA
10 COUNTRY: United States of America
11 ZIP: 02109
12 COMPUTER READABLE FORM:
13 MEDIUM TYPE: Floppy disk
14 COMPUTER: IBM PC compatible
15 OPERATING SYSTEM: PC-DOS/MS-DOS
16 SOFTWARE: PatentIn Release #1.0, Version #1.30
17 CURRENT APPLICATION DATA:
18 APPLICATION NUMBER: US 09/498-556c-357A
19 FILING DATE: 25-APR-1995
20 CLASSIFICATION: 424
21 ATTORNEY/AGENT INFORMATION:
22 NAME: BAKER, HOLLE L.
23 REGISTRATION NUMBER: 31,321
24 REFERENCE TO PCT NUMBER: 199286 301
25 TELECOMMUNICATION INFORMATION:
26 TELEPHONE: 617-526-6000
27 TELEFAX: 617-526-5000
28 INFORMATION FOR SEQ ID NO: 8:
29 SEQUENCE CHARACTERISTICS:
30 LENGTH: 5 amino acids
31 TYPE: amino acid
32 TOPOLOGY: linear
33 MOLECULE TYPE: peptide
34 FRAGMENT TYPE: internal
35 FEATURE:
36 NAME/KEY: Peptide
37 LOCATION: 1..5
38 OTHER INFORMATION: "92 96 REGION OF AVINE"
39 OTHER INFORMATION: HORMONE"
40 US-08-392-973A-8
41
42 Query Match: 91.9% Score 9: 98 2: Length 5:
43 Best Local Similarity 66.7% Prod. No. 1.9e+05;
44 Matches 2: Conservative 0, Mismatches 1, Indels 0, Gaps 0.
45
46 QY 1 LXR 4
47 DB 2 LXR 4
48
49 RESULT 26
50 US-08-392-973A-9
51 Sequence 9, Application US/09498556c-357A
52 Patent No. 5843453
53 GENERAL INFORMATION:
54 APPLICANT: HOLDER, Andrew T.
55 ADDRESSEE: HALE AND DORR LLP
56 STREET: 60 State Street
57 CITY: Boston
58 STATE: MA
59 COUNTRY: United States of America
60 ZIP: 02109
61 COMPUTER READABLE FORM:
62 MEDIUM TYPE: Floppy disk
63 COMPUTER: IBM PC compatible
64 OPERATING SYSTEM: PC-DOS/MS-DOS
65 SOFTWARE: PatentIn Release #1.0, Version #1.30
66 CURRENT APPLICATION DATA:

```

```

APPLICATION NUMBER: US/09498556c-357A
FILING DATE: 25-APR-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: BAKER, HOLLE L.
REGISTRATION NUMBER: 31,321
REFERENCE TO PCT NUMBER: 199286 301
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-526-6000
TELEFAX: 617-526-5000
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..5
OTHER INFORMATION: "94 97 REGION OF AVINE"
OTHER INFORMATION: HORMONE"
US-08-392-973A-9
Query Match: 91.9% Score 9: 98 2: Length 5:
Best Local Similarity 66.7% Prod. No. 1.9e+05;
Matches 2: Conservative 0, Mismatches 1, Indels 0, Gaps 0.
QY 1 LXR 4
DB 1 LXR 4
RESULT 27
US-08-477-362-173
Sequence 174, Application US/08477462
Patent No. 5849507
GENERAL INFORMATION:
APPLICANT: STABOROUGH, ROBERT M.
TITLE OF INVENTION: RECOMBINANT THROMBIN RECEPTOR AND
NUMBER OF SEQUENCES: 223
REFERENCE ADDRESS:
ADDRESS: MERRISON & FAJES
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
FILING DATE: 07-JUN-1995
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08477462
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,059
REFERENCE TO PCT NUMBER: 1990 2650120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 814-5600
TELEFAX: (415) 494-0792
TELEX: 34-0154
INFORMATION FOR SEQ ID NO: 174:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids

```

1 TYPE: amino acid
2 STRANDEDNESS: single
3 TOPOLOGY: linear
4 FEATURE:
5 NAME/KEY: Modified site
6 LOCATION: 5
7 OTHER INFORMATION: /note: "This position is R-NH2."
8 US 08-477-134-173

Query Match 81.8%; Score 9; 09 2; Length 5;
Best Local Similarity 66.7%; Prod. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
Db 3 LXR 5

RESULT 28
US 08-477-134-173
Sequence 173, Application US/08477134
Patent No. 5856448
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: EPIMETHYL THEOPHYLLINE AND
TITLE OF INVENTION: EPIMETHYL THEOPHYLLINE AND
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: MERRISON & PIERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/477-173
FILING DATE: 07-JUN-1995
CLASSIFICATION: 546
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/789,184
FILING DATE: 07-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/AGENT NUMBER: 22000-20502.20
TELEPHONE: (415) 814-5600
TELEFAX: (415) 494-0792
TELEX: 44-0154

SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
FEATURE:
NAME/KEY: Modified site
LOCATION: 5
OTHER INFORMATION: /note: "This position is R-NH2."
US 08-477-134-173

Query Match 81.8%; Score 9; 09 2; Length 5;
Best Local Similarity 66.7%; Prod. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1

Db 3 LXR 5
RESULT 29
US 08-892-544-48
Sequence 48, Application US/08892544
Patent No. 5874544
GENERAL INFORMATION:
APPLICANT: Laddai Peters, W. C.
TITLE OF INVENTION: Immunoactive Peptides of Apo(a)
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: AKZO No. 5874544-1
STREET: 1330 Piccard Drive
CITY: Rockville
STATE: Maryland
COUNTRY: US
ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: PC-DOS/MS-DOS
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 08/892-544
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/892-544
FILING DATE: 27-JUN-1994
APPLICATION NUMBER: 08/172,461
FILING DATE: 21-DEC-1993
ATTORNEY/AGENT INFORMATION:
NAME: Gormley, Mary E.
REGISTRATION NUMBER: 44,409

TELECOMMUNICATION INFORMATION:
TELEPHONE: 301-258-5200
TELEFAX: 301-577-0847
INFORMATION FOR SEQ ID NO: 48:
SEQUENCE CHARACTERISTICS:
LENGTH: 4 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-892-544-48

Query Match 81.8%; Score 9; 09 2; Length 5;
Best Local Similarity 66.7%; Prod. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
Db 1 LXR 3

RESULT 30
US 08-473-469A-173
Sequence 173, Application US/08473469A
Patent No. 6024936
GENERAL INFORMATION:
APPLICANT: COUGHLIN, SHAUN R.
TITLE OF INVENTION: EPIMETHYL THEOPHYLLINE AND
TITLE OF INVENTION: EPIMETHYL THEOPHYLLINE AND
NUMBER OF SEQUENCES: 224
CORRESPONDENCE ADDRESS:
ADDRESSEE: MERRISON & PIERSTER
STREET: 755 Page Mill Road
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1018


```

: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: OPERATING SYSTEM: PC DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/09/498-556c
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US/07/789,184
: FILING DATE: 1991-11-07
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE CHARACTERISTICS:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: INFORMATION FOR SEQ ID NO: 173:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /note- "this position is R H22."
:
: Query Match 81.8% Score 9: DB 3: Length 5;
: Best Local Similarity 66.7% Pred. No. 1.9e-05;
: Matches 2: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
:
: QY 1 LXR 3
: Db 3 LAR 5
:
: RESULT 31
: US-08-485-695-173
: Sequence 173, Application US/08485695
: Patent No. 6124191
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THERMOLABILE PROTEIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FORSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/485-695
: FILING DATE: 07-JUN-1995
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE CHARACTERISTICS:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: INFORMATION FOR SEQ ID NO: 173:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /note- "this position is R H22."

```

```

: REFERENCE CHARACTERISTICS:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: INFORMATION FOR SEQ ID NO: 173:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /note- "this position is R H22."
:
: Query Match 81.8% Score 9: DB 3: Length 5;
: Best Local Similarity 66.7% Pred. No. 1.9e-05;
: Matches 2: Conservative 0; Mismatches 1; Indels 0; Gaps 0;
:
: QY 1 LXR 3
: Db 3 LAR 5
:
: RESULT 32
: US-08-018-760-174
: Sequence 174, Application US/08018760
: Patent No. 6197541
: GENERAL INFORMATION:
: APPLICANT: COUGHLIN, SHAUN R.
: APPLICANT: SCARBOROUGH, ROBERT M.
: TITLE OF INVENTION: RECOMBINANT THERMOLABILE PROTEIN RECEPTOR AND
: TITLE OF INVENTION: RELATED PHARMACEUTICALS
: NUMBER OF SEQUENCES: 223
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: MORRISON & FORSTER
: STREET: 755 Page Mill Road
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1018
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patent In Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/018-760
: FILING DATE: 17-FEB-1994
: CLASSIFICATION: 435
: PRIORITY APPLICATION DATA:
: APPLICATION NUMBER: US 07/789,184
: FILING DATE: 07-NOV-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: MURASHIGE, KATE H.
: REGISTRATION NUMBER: 29,959
: REFERENCE CHARACTERISTICS:
: TELEPHONE: (415) 813-5600
: TELEFAX: (415) 494-0792
: INFORMATION FOR SEQ ID NO: 174:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 5 amino acids
: TYPE: amino acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: FEATURE:
: NAME/KEY: Modified-site
: LOCATION: 5
: OTHER INFORMATION: /note- "this position is R H22."

```

US 09-018 760-174

Query Match 81.8% Score 9; DB 4; Length 5;
Best Local Similarity 66.7% Pred No. 1,960,05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
1 1
DB 4 LXR 5

RESULT 44

US-09-246-500B-17
Sequence 17, Application US/09246500B

Patent No. 6245494

GENERAL INFORMATION:

APPLICANT: Hough, Tony E.
TITLE OF INVENTION: Substrates for Assessing Mannan-Binding
TITLE OF INVENTION: Protein Associated Serine Protease Activity and Methods
TITLE OF INVENTION: Using the Substrates
FILE REFERENCE: 24730-2204
CURRENT APPLICATION NUMBER: US/09/246,500B
CURRENT FILING DATE: 1999-02-08
NUMBER OF SEQ ID NOS: 19
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 5
TYPE: ORF
ORGANISM: MASP substrate

US 09-246-500B-17

Query Match 81.8% Score 9; DB 4; Length 5;
Best Local Similarity 66.7% Pred No. 1,960,05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
1 1
DB 4 LXR 5

RESULT 45

5464756-42

Patent No. 5469943

APPLICANT: ANDERSON, DAVID C.; MORGAN, CHARLES JR.; FRITZBERG,
JALAN R.; NICHOLS, EVERETT J.
TITLE OF INVENTION: CAVALENTLY-LINKED COMPLEXES AND METHODS
FOR ENHANCED CYTOTOXICITY AND IMAGING

NUMBER OF SEQUENCES: 45

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/97/490,241

FILING DATE: 07-AUG-1989

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 242,447

FILING DATE: 15-AUG-1989

SEQ ID NO: 16;

LENGTH: 5

5469944-16

Query Match 81.8% Score 9; DB 6; Length 5;
Best Local Similarity 66.7% Pred No. 1,960,05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
1 1
DB 4 LXR 5

RESULT 46

5464756-42

Patent No. 5464756

APPLICANT: HENNER, PIERRE L.; VANDER, FLORENCE L.; WILKINS,
JAMES A.; YANISURA, DANIEL G.

TITLE OF INVENTION: PEPTIDES AND COMPOSITIONS FOR THE

ISOLATION HUMAN RELAXIN

NUMBER OF SEQUENCES: 42

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/97/299,266

FILING DATE: 01-JUL-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 447,550

FILING DATE: 04-MAY-1989

SEQ ID NO: 42;

LENGTH: 5

5464756-42

Query Match

Best Local Similarity 81.8% Score 9; DB 6; Length 5;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4

1 1

DB 1 LXR 4

RESULT 46

US-08-246-427-11

Sequence 11, Application US/08246427

Patent No. 5641310

GENERAL INFORMATION:

APPLICANT: Ward, Eric

APPLICANT: Volrath, Sandra

APPLICANT: Kotzumi, Saito-ichi

APPLICANT: Tada, Sachio

APPLICANT: Mori, Ichiro

APPLICANT: Iwasaki, Genji

TITLE OF INVENTION: Herbicide Resistant Plants

NUMBER OF SEQUENCES: 12

CORRESPONDENCE ADDRESS:

ADDRESSEE: CHA-GEIJO Corporation

STREET: 7 Skyline Drive

CITY: Hawthorne

STATE: New York

COUNTRY: USA

ZIP: 10532

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC DOS/MS DOS

SOFTWARE: Patent Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/96/246,427

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/95/061,644

FILING DATE: 13 MAY 1993

ATTORNEY/AGENT INFORMATION:

NAME: Spruill, W. Murray

REGISTRATION NUMBER: 32,944

TELEPHONE: 919 541-8615

TELEFAX: 919 541-8615

TELECOMMUNICATION INFORMATION:

TELEPHONE: 919 541-8615

TELEFAX: 919 541-8615

INFORMATION PER SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 6 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

HYPOTHETICAL: N

FRAGMENT TYPE: internal

FEATURE:

NAME: Peptide

LOCATION: 1-6

OTHER INFORMATION: Note: "Sequence for internal

Patent No. 5541310
OTHER INFORMATION: peptide #2 of purified IGDP"

Query Match 81.8% Score 9; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3
DB 3 LSR 5

RESULT 47

US-07-923-724-35
Sequence 35, Application: US/07022724
Patent No. 698292
GENERAL INFORMATION:
APPLICANT: Novalainen, Helena K.M.
APPLICANT: Paloheimo, Marja T.
APPLICANT: Miettinen-Oinonen, Arja S.K.
APPLICANT: Torkkeli, Tuula K.
APPLICANT: Cantrell, Michael
APPLICANT: Piddington, Christopher S.
APPLICANT: Rambosek, John A.
APPLICANT: Turunen, Marja K.
APPLICANT: Fahrström, Richard B.
TITLE OF INVENTION: Production of Phytase-Extruded Emulsions
TITLE OF INVENTION: in Trichoderma
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 500
CITY: Washington
STATE: D.C. U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/923,724
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Cimbatu, Michele A.
REGISTRATION NUMBER: 33,851
REFERENCE/DOCKET NUMBER: 1050,0240004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
TOPOLOGY: both

US-07-923-724-35
Query Match 81.8% Score 9; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 4
DB 4 LSR 6

RESULT 48

US-09-498-556c-357.ra1
Sequence 3, Application: US/09498556c-357
Patent No. 5811094
GENERAL INFORMATION:
APPLICANT: MERRILL, Carl R.
APPLICANT: CARLSON, Richard H.
APPLICANT: ADHYA, Sankar L.
TITLE OF INVENTION: ANTIBACTERIAL LIBRARY WITH BACTERIOPHAGE
TITLE OF INVENTION: GENETICALLY MODIFIED TO DELAY INACTIVATION BY THE HOST
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nikaido, Marmelstein, Murray & Gram LLP
STREET: 655 Fifteenth Street, N.W., Suite 330
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005 5701
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
APPLICATION: 357, 357, 357, 357, 357, 357
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/498,556c-357
FILING DATE: 12 APR 1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/222,956
FILING DATE: 05-APR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/593,269
FILING DATE: 29 JAN 1996
ATTORNEY/AGENT INFORMATION:
NAME: KILTS, Monica C.
REGISTRATION NUMBER: 36,105
REFERENCE/DOCKET NUMBER: 10026-6002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 648-5000
TELEFAX: (202) 648-4810
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-09-498-556c-357.ra1

Query Match 81.8% Score 9; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 4
DB 1 LAR 4

RESULT 49

US-08-806-203-2
Sequence 2, Application: US/08806203-2
Patent No. 5830434
GENERAL INFORMATION:
APPLICANT: TAYLOR, IAN L.
APPLICANT: GUTTSY, IRMAS
TITLE OF INVENTION: METHODS OF TREATING DMN INSULIN
TITLE OF INVENTION: DEPTHWISE MEASURES WITH PARACRYSTALLIC POLYPEPTIDE


```

: Sequence 5, Application US/08856203
: Patent No. 5830434
: GENERAL INFORMATION:
: APPLICANT: TAYLOR, IAN L.
: APPLICANT: GETTYS, THOMAS
: TITLE OF INVENTION: METHODS OF TREATING NON INSULIN
: DEPENDENT DIABETIS MELLITUS WITH PANCREATIC POLYPEPTIDE
: NUMBER OF SEQUENCES: 5
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: NEEDLE & ROSENBERG, P.C.
: STREET: Suite 1200, 127 Peachtree Street
: CITY: Atlanta
: STATE: Georgia
: COUNTRY: USA
: ZIP: 30303
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.30
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 09-498-556
: FILING DATE:
: CLASSIFICATION: 514
: ATTORNEY/AGENT INFORMATION:
: NAME: Spratt, Woodruff D.
: REGISTRATION NUMBER: 36,016
: REFERENCE/CKET NUMBER: 36,016
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 404/688-0770
: TELEFAX: 404/688-6440
: INFORMATION FOR SEQ ID NO. 5:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: STRANDEDNESS: not relevant
: TOPOLOGY: linear
: MOLECULE TYPE: peptide
: US-08-805-203-5

```

```

Query Match 81.8% Score 9; DB 2; Length 6;
Best Local Similarity 66.7% Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
   1 1
DB 1 LIR 3

```

```

RESULT 43
US-08-609-426A-35
: Sequence 25, Application US/03609126
: Patent No. 5830733
: GENERAL INFORMATION:
: APPLICANT: Nevalainen, Helena K.M.
: APPLICANT: Paloheimo, Marja T.
: APPLICANT: Miettinen-Oinonen, Arja S.K.
: APPLICANT: Terkkeli, Tuula K.
: APPLICANT: Cantrell, Michael
: APPLICANT: Piddington, Christopher S.
: APPLICANT: Pambossek, John A.
: APPLICANT: Turunen, Marja K.
: APPLICANT: Fagerström, Richard B.
: APPLICANT: Houston, Christine S.
: TITLE OF INVENTION: Production of Phytase Inactivating Enzymes
: TITLE OF INVENTION: in Trichoderma
: NUMBER OF SEQUENCES: 69
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Sterne, Kessler, Goldstein & Fox
: STREET: 1100 New York Avenue, Suite 600
: CITY: Washington
: STATE: D.C.
: COUNTRY: U.S.A.

```

```

: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US 09-498-556
: FILING DATE: 01-MAR-1996
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/920,724
: FILING DATE: 31-JUL-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/496,155
: FILING DATE: 19-MAR-1990
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/934,877
: FILING DATE: 29-APR-1987
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: UK 8610600
: FILING DATE: 31-MAR-1986
: ATTORNEY/AGENT INFORMATION:
: NAME: Reed, Grant E.
: REGISTRATION NUMBER: F 41,264
: REFERENCE/CKET NUMBER: 1050,0080001
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 433-2600
: TELEFAX: (202) 371-2540
: INFORMATION FOR SEQ ID NO. 45:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 6 amino acids
: TYPE: amino acid
: STRANDEDNESS: both
: TOPOLOGY: both
: US-08-609-426A-35

```

```

Query Match 81.8% Score 9; DB 2; Length 6;
Best Local Similarity 66.7% Pred. No. 1.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
   1 1
DB 4 LIR 5

```

```

RESULT 44
US-08-374-6520-25
: Sequence 25, Application US/984746520
: Patent No. 5834286
: GENERAL INFORMATION:
: APPLICANT: NEVALAINEN, HELENA K.M.
: APPLICANT: PALOHEIMO, MARJA T.
: APPLICANT: FAGERSTRÖM, RICHARD B.
: APPLICANT: MIETTINEN-OINONEN, ARJA S.
: APPLICANT: TERKKELI, TUULA K.
: APPLICANT: KARKASEK, JOHN A.
: APPLICANT: PIDDINGTON, CHRISTOPHER S.
: APPLICANT: GANTRELL, MICHAEL A.
: TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
: VECTORS AND METHODS FOR EXPRESSING PHYTASE DEGRADING
: ENZYMES IN DESIRED HOSTS
: NUMBER OF SEQUENCES: 94
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
: STREET: 1100 NEW YORK AVENUE, SUITE 600
: CITY: WASHINGTON
: STATE: DC
: COUNTRY: USA
: ZIP: 20005
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

```

```

1 OPERATING SYSTEM: PC-IPUS/MS-DOS
2 SOFTWARE: Patent In Release #1.0, Version #1.40
3 CURRENT APPLICATION DATA:
4 APPLICATION NUMBER: US/08/474,552C
5 FILING DATE: 24 MAY-1995
6 CLASSIFICATION: 435
7 PRIOR APPLICATION DATA:
8 APPLICATION NUMBER: PC/08/47058
9 FILING DATE: 27 JUL-1994
10 CLASSIFICATION: 435
11 PRIOR APPLICATION DATA:
12 APPLICATION NUMBER: US 07/925,401
13 FILING DATE: 31-JUL-1992
14 CLASSIFICATION: 435
15 ATTORNEY/AGENT INFORMATION:
16 NAME: REED, GRANT E.
17 REGISTRATION NUMBER: 41,264
18 REPRESENTATIVE NUMBER: 1050,071001
19 TELECOMMUNICATION INFORMATION:
20 TELEPHONE: 202-371-2540
21 TELEFAX: 202-371-2540
22 INFORMATION FOR SEQ ID NO. 25:
23 SEQUENCE CHARACTERISTICS:
24 LENGTH: 6 amino acids
25 TYPE: amino acid
26 STRANDEDNESS: single
27 TOPOLOGY: not relevant
28 MOLECULE TYPE: peptide
29 US-08-474-552C-25

```

```

Query Match      81.8%, Score 9,  Db 2, Length 6;
Best Local Similarity 66.7%, Prod. No. 1.5e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

27 1 LXR 4
   | |
Db 4 LTR 6

```

```

RESULT 45
US-08-492-973A-15
1 Sequence 15, Application US/0832973A
2 Patent No. 5843453
3 GENERAL INFORMATION:
4 APPLICANT: HOLDER, Andrew T.
5 APPLICANT: HEATHIE, James
6 TITLE OF INVENTION: GROWTH HORMONE POTENTIATING MOLECULES
7 NUMBER OF SEQUENCES: 37
8 CORRESPONDENCE ADDRESS:
9 ADDRESSEE: HALE AND DORR LLP
10 STREET: 60 State Street
11 CITY: Boston
12 STATE: MA
13 COUNTRY: United States of America
14 ZIP: 02109
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-IPUS/MS-DOS
19 SOFTWARE: Patent In Release #1.0, Version #1.40
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/492,973A
22 FILING DATE: 25 APR-1995
23 CLASSIFICATION: 424
24 ATTORNEY/AGENT INFORMATION:
25 NAME: BAKER, Hollie L.
26 REGISTRATION NUMBER: 41,421
27 REFERENCE/SEQUENCE SHEET: 152286,301
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 617-526-6000
30 TELEFAX: 617-526-5000
31 INFORMATION FOR SEQ ID NO. 15:
32 SEQUENCE CHARACTERISTICS:

```

```

1 LENGTH: 6 amino acids
2 TYPE: amino acid
3 TOPOLOGY: linear
4 MOLECULE TYPE: peptide
5 FRAGMENT TYPE: internal
6 FEATURE:
7 NAME/KEY: Peptide
8 LOCATION: 1-6
9 OTHER INFORMATION: Zide "91-90 RITTER HORMONE"
10 OTHER INFORMATION: GROWTH HORMONE
11 US-08-492-973A-15
12 Query Match      81.8%, Score 9,  Db 2, Length 6;
13 Best Local Similarity 66.7%, Prod. No. 1.5e+05;
14 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
15 QY 1 LXR 4
16 | |
17 Db 3 LXR 5
18
19 Search completed: April 30, 2003, 13:47:28
20 Job time : 19.7273 secs

```



```

969      9 81.8 7 9 US-09-990-186-1474
970      9 81.8 7 9 US-09-990-186-1475
971      9 81.8 7 9 US-09-990-186-1476
972      9 81.8 7 9 US-09-990-186-1479
973      9 81.8 7 9 US-09-990-186-1480
974      9 81.8 7 9 US-09-990-186-1482
975      9 81.8 7 9 US-09-990-186-1483
976      9 81.8 7 9 US-09-990-186-1485
977      9 81.8 7 9 US-09-990-186-1486
978      9 81.8 7 9 US-09-990-186-1488
979      9 81.8 7 9 US-09-990-186-1490
980      9 81.8 7 9 US-09-990-186-1493
981      9 81.8 7 9 US-09-990-186-1497
982      9 81.8 7 9 US-09-990-186-1498
983      9 81.8 7 9 US-09-990-186-1499
984      9 81.8 7 9 US-09-990-186-1502
985      9 81.8 7 9 US-09-990-186-1503
986      9 81.8 7 9 US-09-990-186-1508
987      9 81.8 7 9 US-09-990-186-1510
988      9 81.8 7 9 US-09-990-186-1515
989      9 81.8 7 9 US-09-990-186-1519
990      9 81.8 7 9 US-09-990-186-1522
991      9 81.8 7 9 US-09-990-186-1525
992      9 81.8 7 9 US-09-990-186-1527
993      9 81.8 7 9 US-09-990-186-1529
994      9 81.8 7 9 US-09-990-186-1530
995      9 81.8 7 9 US-09-990-186-1531
996      9 81.8 7 9 US-09-990-186-1547
997      9 81.8 7 9 US-09-990-186-1541
998      9 81.8 7 9 US-09-990-186-1544
999      9 81.8 7 9 US-09-990-186-1546
1000     9 81.8 7 10 US-09-845-224-25

```

ALIGNMENTS

```

RESULT 1
US-09-249-159-2
Sequence 2, Applicant: us-09-00249.rapb
Patent No. US2002015478A1
GENERAL INFORMATION:
APPLICANT: Yuan, Zhenduo
APPLICANT: Chen, Zhenduo
TITLE OF INVENTION: Direct Adsorption Scintillation Assay
TITLE OF INVENTION: for Measuring Enzyme Activity and Assaying Biochemical
TITLE OF INVENTION: Processes
FILE REFERENCE: 342412000600
CURRENT APPLICATION NUMBER: US-09-074-15a
PRIOR FILING DATE: 1999-02-09
PRIOR FILING DATE: 1999-02-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 2
LENGTH: 4
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-249-159-2

```

```

Query Match      81.8%  Score 9, DB 10, Length 4,
Best Local Similarity 66.7%  Prod. No. 2,30-05,
Matches 2, Conservative 9, Mismatches 1, Indels 0, Gaps 0;

```

```

QY 1 LXR 4
   1 1
DB 2 LXR 4

```

```

RESULT 2
US-09-818-656A-8

```

```

Sequence 8, Applicant: US-09-818-656A
Patent No. US20020142361A1
GENERAL INFORMATION:
APPLICANT: GONG, Fancheang et al.
TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION: NOVELLY ACTIVE MOLECULES INHIBITING HUMAN TRANSPORTER PROTEINS,
TITLE OF INVENTION, AND USES THEREOF
FILE REFERENCE: C000191
CURRENT APPLICATION NUMBER: US-09-818-656A
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 104
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 8
LENGTH: 4
TYPE: PRT
ORGANISM: Homo sapiens
US-09-818-656A-8
Query Match      81.8%  Score 9, DB 10, Length 4,
Best Local Similarity 66.7%  Prod. No. 2,30-05,
Matches 2, Conservative 9, Mismatches 1, Indels 0, Gaps 0;

```

```

QY 1 LXR 4
   1 1
DB 2 LXR 4

```

```

RESULT 4
US-10-006-557-7
Sequence 7, Applicant: US-10006557
Patent No. US20020173464A1
GENERAL INFORMATION:
APPLICANT: Kind, George L.
APPLICANT: Abrahamson, Susan
APPLICANT: Ptasley, Michael
TITLE OF INVENTION: Modulation of Pericyte Proliferation
FILE REFERENCE: 2712936789A
CURRENT APPLICATION NUMBER: US-10-006-557
CURRENT FILING DATE: 2001-12-04
PRIOR APPLICATION NUMBER: 09/250,142
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PatentIn version 4.1
SEQ ID NO 7
LENGTH: 5
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: 4-SC-FUADDFE
OTHER INFORMATION: XMP.711
NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: Position 1 is derivatized at the alpha-amino group with
OTHER INFORMATION: 4 biphenyl carbonyl
NAME/KEY: SITE
LOCATION: (4)..(4)
OTHER INFORMATION: Position 4 is substituted with 4 biphenyl ala
NAME/KEY: SITE
LOCATION: (1)..(2)
OTHER INFORMATION: Positions 1-2 are L amino acids
NAME/KEY: SITE
LOCATION: (1)..(1)
OTHER INFORMATION: Position 1 is L amino acid
NAME/KEY: SITE
LOCATION: (4)..(5)
OTHER INFORMATION: Positions 4-5 are L amino acids
NAME/KEY: SITE
LOCATION: (5)..(5)
OTHER INFORMATION: AMINATE-N-Terminals is Amidated
US-10-006-557-7

```

```

Query Match      81.8%  Score 9, DB 9, Length 5,
Best Local Similarity 66.7%  Prod. No. 2,30-05,

```

Matches	2;	Conservative	0;	Mismatches	1;	Indels	0;	Gaps	0;
---------	----	--------------	----	------------	----	--------	----	------	----

Qy	1	1XR	3
		—	
Db	2	1AR	4

RESULT 4

```

US-09-486-734A-17
: Sequence 17, Application US/09486734A
: Patent No. US20020164732A1
: GENERAL INFORMATION:
: APPLICANT: Chopin, Marie-Christine
: APPLICANT: Clier, Florence
: APPLICANT: Erlich, S. Dusko
: APPLICANT: Gautier, Michel
: APPLICANT: Schouler, Catherine
: APPLICANT: Institut National de la Recherche Aeronomique
: TITLE OF INVENTION: Reconstitue Medium for L Type EHEC
: TITLE OF INVENTION: Bacteriophages of Lactice Acid Bacteria
: FILE REFERENCE: 33359746048
: CURRENT APPLICATION NUMBER: US/09/486-734A
: CURRENT FILING DATE: 2000-05-03
: PRIOR APPLICATION NUMBER: FR 970401873
: PRIOR FILING DATE: 1998-09-01
: PRIOR APPLICATION NUMBER: EP 9710385
: PRIOR FILING DATE: 1997-09-02
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 17
: LENGTH: 6
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Hsdr submit
US-09-486-734A-17

```

Query Match 81.88; Score 9; DB 9; Length 6;
Best Local Similarity 55.78; Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels

Qy	1	LXR	3
		1	1
Lub	3	LAP	5

5 1 11123456

```

1  US-09-486-734A-27
2  : Sequence 27, Application US/00486734A
3  : Patent No. US202016737A1
4  : GENERAL INFORMATION:
5  :
6  : APPLICANT: Chopin, Marie-Christine
7  : APPLICANT: Clier, Florence
8  : APPLICANT: Erlich, S. Dushko
9  : APPLICANT: Gauthier, Michel
10 : APPLICANT: Institut National de la Recherche Agronomique
11 :
12 : TITLE OF INVENTION: Pesticides Mechanisms for IG Type P/M
13 :
14 : TITLE OF INVENTION: Bacterial Mechanisms of Lanthic Acid Production
15 :
16 : FILE REFERENCE: 43330/196048
17 :
18 : CURRENT APPLICATION NUMBER: 2008-08-03 734A
19 :
20 : PRIOR FILING DATE: 2008-08-03 734A
21 :
22 : PRIOR FILING DATE: 1998-09-01
23 :
24 : PRIOR APPLICATION NUMBER: FR 97-03496
25 :
26 : PRIOR FILING DATE: 1997-09-02
27 :
28 : NUMBER OF SEQ ID NOS: 40
29 :
30 : SOFTWARE: FastSPQ for Windows Version 4.0
31 :
32 : SEQ ID NO: 27
33 :
34 : LENGTH: 6
35 :
36 : TYPE: PRI
37 :
38 : ORGANISM: Artificial Sequence
39 :
40 : FEATURE:

```

US-09-486-734A-27

Query Match 81.8%; Score 9; DB 9; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.9e+05;
Matches 2; Conservative 0; Mismatches 1; Index

1 LXR 3

25

```

US-09-770-102A-17
: Sequence ID: Application US/99770102A
: Publication No. US2002077406A1
: GENERAL INFORMATION:
: APPLICANT: CYCLOPS
: INVENTOR: INVENTOR'S Information and Methods for Identification
: TITLE OF INVENTION: Independent Binding Further Polypeptides
: FILING DATE: 1999/10/22
: SEQ. NO.: 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97, 98, 99, 100, 101, 102, 103, 104, 105, 106, 107, 108, 109, 110, 111, 112, 113, 114, 115, 116, 117, 118, 119, 120, 121, 122, 123, 124, 125, 126, 127, 128, 129, 130, 131, 132, 133, 134, 135, 136, 137, 138, 139, 140, 141, 142, 143, 144, 145, 146, 147, 148, 149, 150, 151, 152, 153, 154, 155, 156, 157, 158, 159, 160, 161, 162, 163, 164, 165, 166, 167, 168, 169, 170, 171, 172, 173, 174, 175, 176, 177, 178, 179, 180, 181, 182, 183, 184, 185, 186, 187, 188, 189, 190, 191, 192, 193, 194, 195, 196, 197, 198, 199, 200, 201, 202, 203, 204, 205, 206, 207, 208, 209, 210, 211, 212, 213, 214, 215, 216, 217, 218, 219, 220, 221, 222, 223, 224, 225, 226, 227, 228, 229, 230, 231, 232, 233, 234, 235, 236, 237, 238, 239, 240, 241, 242, 243, 244, 245, 246, 247, 248, 249, 250, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 81
```

Query Match: 81.88; Score: 9; DB: 9; Length: 6;
Post local similarity: 61.79; Pct. No. 2.9e-05;
Matches: 2; Conservative: 9; Mismatches: 1; Index:

1 LXX 3
1 — 5
3 LSP 5

1262111 7 7

RESOL: 05-09-846-512A-9
1 5-10-96 9, Application, 1509966512A
2 Publication No. US20030054954A1
3 GENERAL INFORMATION:
4 APPLICANT: Meade, Thomas J
5 TITLE OF INVENTION: Magnetic Resonance Imaging
6 TITLE OF INVENTION: Acoustic
7 FILE REFERENCE: A 58634 7
8 CURRENT APPLICATION NUMBER: 05-09966512A
9 CURRENT FILING DATE: 2001-05-24
10 PRIORITY APPLICATION NUMBER: 05-02897419
11 PRIORITY DATE: 2001-05-26
12 PRIORITY DATE: 2001-05-26
13 PRIORITY DATE: 1997-06-02
14 PRIORITY DATE: 1997-06-02
15 PRIORITY DATE: 1995-06-07
16 PRIORITY DATE: 1995-06-07
17 PRIORITY DATE: 1997-11-17
18 PRIORITY DATE: 1997-11-17
19 PRIORITY DATE: 1999-08-13
20 PRIORITY DATE: 1999-08-13
21 PRIORITY DATE: 2001-05-24
22 PRIORITY DATE: 2001-05-24
23 PRIORITY DATE: 1999-09-27
24 PRIORITY DATE: 1999-09-27
25 PRIORITY DATE: 2001-05-24

? PRIOR FILING DATE: 1997-12-27
 ? NUMBER OF SEQ ID NOS: 17
 ? SOFTWARE: Patent In version 3.1
 ? SEQ ID NO 9
 ? LENGTH: 6
 ? TYPE: PRI
 ? ORGANISM: Unknown
 ? FEATURE:
 ? OTHER INFORMATION: could be from any mammal.
 US-09-866-512A 9

Query Match 81.8%; Score 9; DB 9; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2 9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 1 1
 4 LXR 6

RESULT 8
 US-09-500-700 73
 ? Sequence 73; Application US/09500700
 ? Publication No. US20030059767A1
 ? GENERAL INFORMATION:
 ? APPLICANT: THE SCRIPPS RESEARCH INSTITUTE
 ? APPLICANT: BARBAS III, Carlos F.
 ? APPLICANT: GOTTFELD, Joel M.
 ? APPLICANT: WRIGHT, Peter F.
 ? TITLE OF INVENTION: 2122 FINGER PROTEIN DERIVATIVES AND METHODS THEREFOR
 ? FILE REFERENCE: SCRIPT160-4
 ? CURRENT APPLICATION NUMBER: US/09500700
 ? PRIOR FILING DATE: 2003-01-10
 ? PRIOR APPLICATION NUMBER: US 08/863,813
 ? PRIOR FILING DATE: 1997-05-27
 ? PRIOR APPLICATION NUMBER: US 08/676,318
 ? PRIOR FILING DATE: 1996-12-30
 ? PRIOR APPLICATION NUMBER: 09170895/20029
 ? PRIOR FILING DATE: 1995-01-18
 ? PRIOR APPLICATION NUMBER: US 08/112,604
 ? PRIOR FILING DATE: 1994-09-26
 ? PRIOR APPLICATION NUMBER: US 08/193,119
 ? PRIOR FILING DATE: 1994-01-18
 ? NUMBER OF SEQ ID NOS: 127
 ? SOFTWARE: Patent In version 3.1
 ? SEQ ID NO 73
 ? LENGTH: 6
 ? TYPE: PRI
 ? ORGANISM: Artificial sequence
 ? FEATURE:
 ? OTHER INFORMATION: Modified sequence of finger 1 of 211248

Query Match 81.8%; Score 9; DB 9; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2 9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 1 1
 4 LXR 6

RESULT 9
 US-09-795-903A 26
 ? Sequence 26; Application US/09795903A
 ? Patent No. US20020164760A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Lin, Xindi
 ? APPLICANT: Lin, Xindi
 ? APPLICANT: Kopsch, Gerald
 ? TITLE OF INVENTION: Catalytically Active Peptidyl Metapsin and Methods
 ? FILE REFERENCE: 0MR 179

? CURRENT APPLICATION NUMBER: US/09795903A
 ? CURRENT FILING DATE: 2001-02-28
 ? PRIOR APPLICATION NUMBER: 09/604,608
 ? PRIOR FILING DATE: 2000-06-27
 ? PRIOR APPLICATION NUMBER: 60/166,060
 ? PRIOR FILING DATE: 1999-11-30
 ? PRIOR APPLICATION NUMBER: 60/177,846
 ? PRIOR FILING DATE: 2000-01-26
 ? PRIOR APPLICATION NUMBER: 60/178,368
 ? PRIOR FILING DATE: 2000-01-27
 ? PRIOR APPLICATION NUMBER: 60/210,292
 ? PRIOR FILING DATE: 2000-06-08
 ? NUMBER OF SEQ ID NOS: 31
 ? SOFTWARE: Patent In Ver. 2.1
 ? SEQ ID NO 26
 ? LENGTH: 7
 ? TYPE: PRI
 ? ORGANISM: Artificial Sequence
 ? FEATURE:
 ? OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ? OTHER INFORMATION: Peptide
 US-09-795-903A 26

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2 9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 1 1
 4 LXR 6

RESULT 10
 US-09-826-290-370
 ? Sequence 370; Application US/09826290
 ? Patent No. US2002014969A1
 ? GENERAL INFORMATION:
 ? APPLICANT: Barham, L. Kathryn
 ? APPLICANT: Friedman, David L.
 ? APPLICANT: Herath, Henath Mudiyanselage Athula Chandrasiri
 ? APPLICANT: Kimmel, Linda R.
 ? APPLICANT: Parakk, Rajesh Bhikhu
 ? APPLICANT: Potter, David M.
 ? APPLICANT: Rohini, Christian
 ? APPLICANT: Silber, R. Michael
 ? APPLICANT: Stiller, Thomas R.
 ? APPLICANT: Sunderland, P. Troy
 ? APPLICANT: Townsend, Robert Reid
 ? APPLICANT: White, Frost
 ? APPLICANT: Williams, Stephen A.
 ? TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
 ? TITLE OF INVENTION: Uses Thereof, Including Diagnosis and Treatment of
 ? FILE REFERENCE: 2572-1-001 N2
 ? CURRENT APPLICATION NUMBER: US/09826290
 ? CURRENT FILING DATE: 2001-04-30
 ? PRIOR APPLICATION NUMBER: US 60/194,504
 ? PRIOR FILING DATE: 2000-04-03
 ? PRIOR APPLICATION NUMBER: US 60/253,647
 ? PRIOR FILING DATE: 2000-11-28
 ? NUMBER OF SEQ ID NOS: 492
 ? SOFTWARE: FASTSEQ for Windows Version 4.0
 ? SEQ ID NO 370
 ? LENGTH: 7
 ? TYPE: PRI
 ? ORGANISM: homo sapien
 US-09-826-290-370

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2 9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

db 1 1
5 LSR 7

RESULT 11

US-09-468-561A-273
Sequence 50, Application US/09468561A
Patent No. US2002016462A1
GENERAL INFORMATION:
APPLICANT: Tomlinson, Ian M
TITLE OF INVENTION: Method to Screen Plate Display Libraries with Efficient Ligands
FILE FILING DATE: 2001-10-01
CURRENT APPLICATION NUMBER: US/09468561A
PRIOR FILING DATE: 1997-10-20
PRIOR APPLICATION NUMBER: US 60/065,248
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: US 60/066,729
PRIOR FILING DATE: 1997-11-21
PRIOR APPLICATION NUMBER: PCT/09468/03135
PRIOR FILING DATE: 1998-10-20
PRIOR APPLICATION NUMBER: US 09/411,939
PRIOR FILING DATE: 2000-02-24
NUMBER OF SEQ ID NOS: 350
SOFTWARE: PatentIn version 3.1
SEQ ID NO 273
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-468-561A-273

Query Match 81.8%; Score 9; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 2
1 1
db 2 LSR 4

RESULT 12

US-09-498-909-7
Sequence 7, Application US/09498909
Patent No. US2002016464A1
GENERAL INFORMATION:
APPLICANT: Blavatny, Jehu
TITLE OF INVENTION: Detection and Treatment of Prostate Cancer
FILE REFERENCE: MTP-027
CURRENT APPLICATION NUMBER: US/09498909
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: US 60/250,294
PRIOR FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn version 3.0
SEQ ID NO 7
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-498-909-7

Query Match 81.8%; Score 9; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 3
1 1
db 5 LSR 7

RESULT 13

US-10-080-100-50
Sequence 50, Application US/10080100
Patent No. US20020165356A1
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos
TITLE OF INVENTION: Zinc Finger Binding Domains for
TITLE OF INVENTION: Nucleotide Sequence ARR
FILE REFERENCE: ISRI 760.0
CURRENT APPLICATION NUMBER: US/10080100
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 92/057,791.106
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 50
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetized
US-10-080-100-50

Query Match 81.8%; Score 9; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
db 5 LSR 7

RESULT 14

US-10-080-100-51
Sequence 51, Application US/10080100
Patent No. US20020165356A1
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos
TITLE OF INVENTION: Zinc Finger Binding Domains for
FILE REFERENCE: ISRI 760.0
CURRENT APPLICATION NUMBER: US/10080100
CURRENT FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 92/057,791.106
PRIOR FILING DATE: 2001-02-21
NUMBER OF SEQ ID NOS: 114
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 51
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetized
US-10-080-100-51

Query Match 81.8%; Score 9; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
1 1
db 5 LSR 7

RESULT 15

US-10-080-100-82
Sequence 82, Application US/10080100
Patent No. US20020165356A1
GENERAL INFORMATION:
APPLICANT: Barbas, Carlos
TITLE OF INVENTION: Zinc Finger Binding Domains for

```

1 TITLE OF INVENTION: Nucleotide Sequence ANN
2 FILE REFERENCE: US94 760.0
3 CURRENT APPLICATION NUMBER: US799/999,100
4 CURRENT FILING DATE: 2002-02-21
5 PRIOR APPLICATION NUMBER: US699,791,106
6 PRIOR FILING DATE: 2001-02-21
7 NUMBER OF SEQ ID NOS: 113
8 SOFTWARE: FASTSEQ for Windows Version 4.0
9 SEQ ID NO 92
10 LENGTH: 7
11 TYPE: PRI
12 ORGANISM: Artificial Sequence
13 FEATURE:
14 OTHER INFORMATION: synthesized
15 US-10-080-100-92

```

```

Query Match
Best Local Similarity 81.8%; Score 9; DB 9; Length 7;
Matches 2; Conservativeness 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
DB 5 LXR 7

```

```

RESULT 16
US-10-080-100-97
1 Sequence 97 Application: us-09-498-556c-357
2 Publication No. US2002/0165466A1
3 GENERAL INFORMATION:
4 APPLICANT: Barbas, Carlos
5 APPLICANT: Dreier, Birgit
6 TITLE OF INVENTION: Zinc Finger Binding Domains for
7 FILE REFERENCE: US94 760.0
8 CURRENT APPLICATION NUMBER: US799/999,100
9 PRIOR FILING DATE: 2002-02-21
10 PRIOR APPLICATION NUMBER: US699,791,106
11 PRIOR FILING DATE: 2001-02-21
12 NUMBER OF SEQ ID NOS: 113
13 SOFTWARE: FASTSEQ for Windows Version 4.0
14 SEQ ID NO 97
15 LENGTH: 7
16 TYPE: PRI
17 ORGANISM: Artificial Sequence
18 FEATURE:
19 OTHER INFORMATION: synthesized
20 US-10-080-100-97

```

```

Query Match
Best Local Similarity 81.8%; Score 9; DB 9; Length 7;
Matches 2; Conservativeness 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
DB 5 LXR 7

```

```

RESULT 17
US-10-080-100-112
1 Sequence 112 Application: us-09-498-556c-357
2 Publication No. US2002/0165466A1
3 GENERAL INFORMATION:
4 APPLICANT: Barbas, Carlos
5 APPLICANT: Dreier, Birgit
6 TITLE OF INVENTION: Zinc Finger Binding Domains for
7 FILE REFERENCE: US94 760.0
8 CURRENT APPLICATION NUMBER: US799/999,100
9 PRIOR FILING DATE: 2002-02-21
10 PRIOR APPLICATION NUMBER: US699,791,106
11 PRIOR FILING DATE: 2001-02-21
12 NUMBER OF SEQ ID NOS: 113

```

```

1 SOFTWARE: FASTSEQ for Windows Version 4.0
2 SEQ ID NO 112
3 LENGTH: 7
4 TYPE: PRI
5 ORGANISM: Artificial Sequence
6 FEATURE:
7 OTHER INFORMATION: synthesized
8 US-10-080-100-112

```

```

Query Match
Best Local Similarity 81.8%; Score 9; DB 9; Length 7;
Matches 2; Conservativeness 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
DB 5 LXR 7

```

```

RESULT 18
US-09-995-973-16
1 Sequence 16 Application: US/0995973
2 Publication No. US2003/0024006A1
3 GENERAL INFORMATION:
4 APPLICANT: CHOO, Yoon
5 APPLICANT: ULLMAN, Christopher G.
6 TITLE OF INVENTION: GENE SWITCHES
7 FILE REFERENCE: 9,425-2003 / 67 US1
8 CURRENT APPLICATION NUMBER: US/0995973
9 CURRENT FILING DATE: 2002-03-19
10 NUMBER OF SEQ ID NOS: 59
11 SOFTWARE: Patent In Ver. 2.0
12 SEQ ID NO 16
13 LENGTH: 7
14 TYPE: PRI
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence; Zinc Finger
18 OTHER INFORMATION: binding domain
19 US-09-995-973-16

```

```

Query Match
Best Local Similarity 81.8%; Score 9; DB 9; Length 7;
Matches 2; Conservativeness 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
DB 5 LXR 7

```

```

RESULT 19
US-09-995-973-50
1 Sequence 50 Application: US/0995973
2 Publication No. US2003/0024006A1
3 GENERAL INFORMATION:
4 APPLICANT: CHOO, Yoon
5 APPLICANT: ULLMAN, Christopher G.
6 TITLE OF INVENTION: GENE SWITCHES
7 FILE REFERENCE: 9,425-2003 / 67 US1
8 CURRENT APPLICATION NUMBER: US/0995973
9 CURRENT FILING DATE: 2002-03-19
10 NUMBER OF SEQ ID NOS: 59
11 SOFTWARE: Patent In Ver. 2.0
12 SEQ ID NO 50
13 LENGTH: 7
14 TYPE: PRI
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: Description of Artificial Sequence; Zinc Finger
18 OTHER INFORMATION: binding domain
19 US-09-995-973-50

```

```

Query Match
Best Local Similarity 81.8%; Score 9; DB 9; Length 7;
Matches 2; Conservativeness 0; Mismatches 1; Indels 0; Gaps 0;

```

Matches 2: Conservative 0: Mismatches 1: Indels 3: Caps 0:

QY 1 LXR 4
1 1
Db 5 LSR 7

RESULT 20

US-10-006-069A-30

: Sequence 30, Application US/1000069A

: Publication No. US20030021776A1

: GENERAL INFORMATION:

: APPLICANT: Rebar, Edward

: APPLICANT: Jamieson, Andrew

: APPLICANT: Liu, Qiang

: APPLICANT: Liu, Pei-Qi

: APPLICANT: Wolfe, Alan

: APPLICANT: Eisenberg, Stephen P.

: APPLICANT: Jarvis, Eric

: APPLICANT: Sandamo Biosciences, Inc.

: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc

: FILE REFERENCE: 019496-0058300S

: CURRENT APPLICATION NUMBER: US/1000069A

: PRIOR FILING DATE: 2001-12-17

: PRIOR APPLICATION NUMBER: US 09/733,604

: PRIOR FILING DATE: 2000-12-07

: PRIOR APPLICATION NUMBER: US 09/736,083

: PRIOR FILING DATE: 2000-12-12

: PRIOR APPLICATION NUMBER: US 09/846,033

: PRIOR FILING DATE: 2001-04-30

: NUMBER OF SEQ ID NOS: 252

: SOFTWARE: FASTSEQ for Windows Version 3.0

: SEQ ID NO 30

: LENGTH: 7

: TYPE: PRT

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: finger

US-10-006-069A-30

Query Match

Best Local Similarity 81.8%; Score 9; DB 9; Length 7;

Matches 2: Conservative 0: Mismatches 1: Indels 0: Caps 0:

QY 1 LXR 3
1 1
Db 5 LSR 7

RESULT 21

US-10-006-069A-34

: Sequence 34, Application US/1000069A

: Publication No. US20030021776A1

: GENERAL INFORMATION:

: APPLICANT: Rebar, Edward

: APPLICANT: Jamieson, Andrew

: APPLICANT: Liu, Qiang

: APPLICANT: Liu, Pei-Qi

: APPLICANT: Wolfe, Alan

: APPLICANT: Eisenberg, Stephen P.

: APPLICANT: Jarvis, Eric

: APPLICANT: Sandamo Biosciences, Inc.

: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc

: FILE REFERENCE: 019496-0058300S

: CURRENT APPLICATION NUMBER: US/1000069A

: PRIOR FILING DATE: 2001-12-17

: PRIOR APPLICATION NUMBER: US 09/733,604

: PRIOR FILING DATE: 2000-12-07

: PRIOR APPLICATION NUMBER: US 09/736,083

: PRIOR FILING DATE: 2000-12-12

: PRIOR APPLICATION NUMBER: US 09/846,033

: FILE REFERENCE: US/1000069A-40

: NUMBER OF SEQ ID NOS: 252

: SOFTWARE: FASTSEQ for Windows Version 3.0

: SEQ ID NO 44

: LENGTH: 7

: TYPE: PRT

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: finger

US-10-006-069A-44

Query Match

Best Local Similarity 61.6%; Score 9; DB 9; Length 7;

Matches 2: Conservative 0: Mismatches 1: Indels 0: Caps 0:

QY 1 LXR 4
1 1
Db 5 LSR 7

RESULT 22

US-10-006-069A-45

: Sequence 35, Application US/1000069A

: Publication No. US20030021776A1

: GENERAL INFORMATION:

: APPLICANT: Rebar, Edward

: APPLICANT: Jamieson, Andrew

: APPLICANT: Liu, Qiang

: APPLICANT: Liu, Pei-Qi

: APPLICANT: Wolfe, Alan

: APPLICANT: Eisenberg, Stephen P.

: APPLICANT: Jarvis, Eric

: APPLICANT: Sandamo Biosciences, Inc.

: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc

: FILE REFERENCE: 019496-0058300S

: CURRENT APPLICATION NUMBER: US/1000069A

: PRIOR FILING DATE: 2001-12-17

: PRIOR APPLICATION NUMBER: US 09/733,604

: PRIOR FILING DATE: 2000-12-07

: PRIOR APPLICATION NUMBER: US 09/736,083

: PRIOR FILING DATE: 2000-12-12

: PRIOR APPLICATION NUMBER: US 09/846,033

: PRIOR FILING DATE: 2001-04-30

: NUMBER OF SEQ ID NOS: 252

: SOFTWARE: FASTSEQ for Windows Version 3.0

: SEQ ID NO 45

: LENGTH: 7

: TYPE: PRT

: ORGANISM: Artificial Sequence

: FEATURE:

: OTHER INFORMATION: finger

US-10-006-069A-45

Query Match

Best Local Similarity 81.8%; Score 9; DB 9; Length 7;

Matches 2: Conservative 0: Mismatches 1: Indels 0: Caps 0:

QY 1 LXR 4
1 1
Db 5 LSR 7

RESULT 23

US-10-006-069A-46

: Sequence 36, Application US/1000069A

: Publication No. US20030021776A1

: GENERAL INFORMATION:

: APPLICANT: Rebar, Edward

: APPLICANT: Jamieson, Andrew

: APPLICANT: Liu, Qiang

: APPLICANT: Liu, Pei-Qi

: APPLICANT: Wolfe, Alan

```

1 APPLICANT: Eisenberg, Stephen P.
2 APPLICANT: Jarvis, Eric
3 APPLICANT: Sandamo Biosciences, Inc.
4 TITLE OF INVENTION: Regulation of Androgenesis With Zinc
5 FILE REFERENCE: 019496-0058400S
6 CURRENT APPLICATION NUMBER: US/10/006,069A
7 PRIOR FILING DATE: 2001-12-17
8 PRIOR APPLICATION NUMBER: US 09/743,604
9 PRIOR FILING DATE: 2000-12-07
10 PRIOR FILING DATE: 2000-12-12
11 PRIOR APPLICATION NUMBER: US 09/845,033
12 PRIOR FILING DATE: 2001-04-30
13 NUMBER OF SEQ ID NOS: 252
14 SOFTWARE: FastSeq for Windows Version 4.0
15 SEQ ID NO 49
16 LENGTH: 7
17 TYPE: PRT
18 ORGANISM: Artificial Sequence
19 FEATURE:
20 OTHER INFORMATION: Finger
US-10-006,069A-46

```

```

Query Match      81.8%  Score 9; DB 9; Length 7;
Best Local Similarity 66.7%  Pref. No. 2,9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

```

```

QY 1 LXR 3
1 1
DB 5 LXR 7

```

```

RESULT 24
US-10-006,069A-48
1 Sequence 36, Application US/10006069A
2 Publication No. US2003021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolfe, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sandamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Androgenesis With Zinc
13 FILE REFERENCE: 019496-0058400S
14 CURRENT FILING DATE: 2001-12-17
15 PRIOR APPLICATION NUMBER: US 09/743,604
16 PRIOR FILING DATE: 2000-12-07
17 PRIOR FILING DATE: 2000-12-12
18 PRIOR APPLICATION NUMBER: US 09/746,083
19 PRIOR FILING DATE: 2000-12-12
20 PRIOR APPLICATION NUMBER: US 09/845,033
21 PRIOR FILING DATE: 2001-04-30
22 NUMBER OF SEQ ID NOS: 252
23 SOFTWARE: FastSeq for Windows Version 4.0
24 SEQ ID NO 49
25 LENGTH: 7
26 TYPE: PRT
27 ORGANISM: Artificial Sequence
28 FEATURE:
29 OTHER INFORMATION: Finger
US-10-006,069A-48

```

```

Query Match      81.8%  Score 9; DB 9; Length 7;
Best Local Similarity 66.7%  Pref. No. 2,9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

```

```

QY 1 LXR 3
1 1

```

```

DB 5 LXR 7

RESULT 25
US-10-006,069A-49
1 Sequence 39, Application US/10006069A
2 Publication No. US2003021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolfe, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sandamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Androgenesis With Zinc
13 FILE REFERENCE: 019496-0058400S
14 CURRENT FILING DATE: 2001-12-17
15 PRIOR APPLICATION NUMBER: US 09/743,604
16 PRIOR FILING DATE: 2000-12-07
17 PRIOR APPLICATION NUMBER: US 09/746,083
18 PRIOR FILING DATE: 2000-12-12
19 PRIOR APPLICATION NUMBER: US 09/845,033
20 PRIOR FILING DATE: 2001-04-30
21 NUMBER OF SEQ ID NOS: 252
22 SOFTWARE: FastSeq for Windows Version 4.0
23 SEQ ID NO 49
24 LENGTH: 7
25 TYPE: PRT
26 ORGANISM: Artificial Sequence
27 FEATURE:
28 OTHER INFORMATION: Finger
US-10-006,069A-49

```

```

Query Match      81.8%  Score 9; DB 9; Length 7;
Best Local Similarity 66.7%  Pref. No. 2,9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0;

```

```

QY 1 LXR 3
1 1
DB 5 LXR 7

```

```

RESULT 26
US-10-006,069A-40
1 Sequence 40, Application US/10006069A
2 Publication No. US2003021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolfe, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sandamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Androgenesis With Zinc
13 FILE REFERENCE: 019496-0058400S
14 CURRENT FILING DATE: 2001-12-17
15 PRIOR APPLICATION NUMBER: US 09/743,604
16 PRIOR FILING DATE: 2000-12-07
17 PRIOR FILING DATE: 2000-12-12
18 PRIOR APPLICATION NUMBER: US 09/746,083
19 PRIOR FILING DATE: 2000-12-12
20 PRIOR APPLICATION NUMBER: US 09/845,033
21 PRIOR FILING DATE: 2001-04-30
22 NUMBER OF SEQ ID NOS: 252
23 SOFTWARE: FastSeq for Windows Version 4.0
24 SEQ ID NO 40

```

```

: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-40

Query Match      81.9%; Score 9; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
   1 1
Db 5 LAR 7

RESULT 27
US-10-006-069A-41
: Sequence 41, Application US/09/09/069A
: Publication No. US20030021776A1
: GENERAL INFORMATION:
: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Pei-Qi
: APPLICANT: Wolfe, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo BioSciences, Inc.
: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
: FILE REFERENCE: 019496-005830US
: CURRENT FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,083
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/846,033
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 352
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 41
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-41

Query Match      81.9%; Score 9; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
   1 1
Db 5 LAR 7

RESULT 28
US-10-006-069A-42
: Sequence 42, Application US/09/09/069A
: Publication No. US20030021776A1
: GENERAL INFORMATION:
: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Pei-Qi
: APPLICANT: Wolfe, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo BioSciences, Inc.
: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc

```

```

: TITLE OF INVENTION: Finger Proteins
: FILE REFERENCE: 019496-005830US
: CURRENT FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,083
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/846,033
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 352
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 42
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-42

Query Match      81.9%; Score 9; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
   1 1
Db 5 LAR 7

RESULT 29
US-10-006-069A-46
: Sequence 45, Application US/10/09/069A
: Publication No. US20030021776A1
: GENERAL INFORMATION:
: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Liu, Pei-Qi
: APPLICANT: Wolfe, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo BioSciences, Inc.
: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
: FILE REFERENCE: 019496-005830US
: CURRENT FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,083
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/846,033
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 352
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 46
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-46

Query Match      81.8%; Score 9; DB 9; Length 7;
Best Local Similarity 66.7%; Pred. No. 2.9e-05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
   1 1
Db 5 LAR 7

RESULT 30

```



```

: PRIOR APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,083
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/946,043
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 252
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 52
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-52

```

```

Query Match      81.8%  Score 9;  DB 9;  Length 7;
Best Local Similarity 56.7%  Pct. Id. 2.9e-05;
Matches 2;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

```

```

QY      1 LXR 3
      |
Db      5 LTR 7

```

RESULT 44

```

US-10-006-069A-54
: Sequence 54; Application: US/10006069A
: Publication No: US20030021776A1
: GENERAL INFORMATION:

```

```

: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Wolfe, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo Biosciences, Inc.

```

```

: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
: FILE REFERENCE: 019496-005840S

```

```

: CURRENT APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 09/736,083
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/946,043
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 252
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 54
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-54

```

```

Query Match      81.8%  Score 9;  DB 9;  Length 7;
Best Local Similarity 56.7%  Pct. Id. 2.9e-05;
Matches 2;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

```

```

QY      1 LXR 3
      |
Db      5 LTR 7

```

RESULT 45

```

US-10-006-069A-55
: Sequence 55; Application: US/10006069A
: Publication No: US20030021776A1
: GENERAL INFORMATION:

```

```

: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Wolfe, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo Biosciences, Inc.
: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
: FILE REFERENCE: 019496-005840S
: CURRENT APPLICATION NUMBER: US/10/006,069A
: CURRENT FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,083
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/946,043
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 252
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 55
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-55

```

```

Query Match      81.8%  Score 9;  DB 9;  Length 7;
Best Local Similarity 56.7%  Pct. Id. 2.9e-05;
Matches 2;  Conservative 0;  Mismatches 1;  Indels 0;  Gaps 0;

```

```

QY      1 LXR 3
      |
Db      5 LTR 7

```

RESULT 46

```

US-10-006-069A-56
: Sequence 56; Application: US/10006069A
: Publication No: US20030021776A1
: GENERAL INFORMATION:

```

```

: APPLICANT: Rebar, Edward
: APPLICANT: Jamieson, Andrew
: APPLICANT: Liu, Qiang
: APPLICANT: Wolfe, Alan
: APPLICANT: Eisenberg, Stephen P.
: APPLICANT: Jarvis, Eric
: APPLICANT: Sangamo Biosciences, Inc.

```

```

: TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
: FILE REFERENCE: 019496-005840S
: CURRENT APPLICATION NUMBER: US/10/006,069A
: CURRENT FILING DATE: 2001-12-17
: PRIOR APPLICATION NUMBER: US 09/733,604
: PRIOR FILING DATE: 2000-12-07
: PRIOR APPLICATION NUMBER: US 09/736,083
: PRIOR FILING DATE: 2000-12-12
: PRIOR APPLICATION NUMBER: US 09/946,043
: PRIOR FILING DATE: 2001-04-30
: NUMBER OF SEQ ID NOS: 252
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 56
: LENGTH: 7
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: finger
US-10-006-069A-56

```

```

Query Match      81.8%  Score 9;  DB 9;  Length 7;

```

Best Local Similarity 66.7%, Score 9, DB 9, Length 7;
Matches 2: Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 1 LXR 3
1 1
1b 5 LTR 7

RESULT 47

US-10-006-069A-57
Sequence 57, Application US/10006069A
Publication No. US20030021776A1

GENERAL INFORMATION:

APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi
APPLICANT: Wolffe, Alan
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Autophagosome With Zinc
TITLE OF INVENTION: Fingert Proteins
FILE REFERENCE: 019496-0058300S
CURRENT APPLICATION NUMBER: US/09/733,604
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 09/846,033
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 57
LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: finger

US-10-006-069A-57

Query Match 81.8%, Score 9, DB 9, Length 7;
Best Local Similarity 66.7%, Score 9, DB 9, Length 7;
Matches 2: Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 1 LXR 3
1 1
1b 5 LTR 7

RESULT 48

US-10-006-069A-59

Sequence 59, Application US/10006069A
Publication No. US20030021776A1

GENERAL INFORMATION:

APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi
APPLICANT: Wolffe, Alan
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Autophagosome With Zinc
TITLE OF INVENTION: Fingert Proteins
FILE REFERENCE: 019496-0058300S
CURRENT APPLICATION NUMBER: US/09/733,604
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/846,083
PRIOR FILING DATE: 2000-12-12

PRIOR APPLICATION NUMBER: US 09/846,044
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 59
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: finger

US-10-006-069A-59

Query Match 81.8%, Score 9, DB 9, Length 7;
Best Local Similarity 66.7%, Score 9, DB 9, Length 7;
Matches 2: Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 1 LXR 3
1 1
1b 5 LTR 7

RESULT 49

US-10-006-069A-60

Sequence 60, Application US/10006069A
Publication No. US20030021776A1

GENERAL INFORMATION:

APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi
APPLICANT: Wolffe, Alan
APPLICANT: Eisenberg, Stephen P.
APPLICANT: Jarvis, Eric
APPLICANT: Sangamo Biosciences, Inc.
TITLE OF INVENTION: Regulation of Autophagosome With Zinc
TITLE OF INVENTION: Fingert Proteins
FILE REFERENCE: 019496-0058300S
CURRENT APPLICATION NUMBER: US/09/733,604
PRIOR APPLICATION NUMBER: US 09/733,604
PRIOR FILING DATE: 2000-12-07
PRIOR APPLICATION NUMBER: US 09/736,083
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: US 09/846,044
PRIOR FILING DATE: 2001-04-30
NUMBER OF SEQ ID NOS: 252
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 60
LENGTH: 7

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: finger

US-10-006-069A-60

Query Match 81.8%, Score 9, DB 9, Length 7;
Best Local Similarity 66.7%, Score 9, DB 9, Length 7;
Matches 2: Conservative 0, Mismatches 1, Indels 0, Gaps 0;

QY 1 LXR 3
1 1
1b 5 LTR 7

RESULT 40

US-10-006-069A-61

Sequence 61, Application US/10006069A
Publication No. US20030021776A1

GENERAL INFORMATION:

APPLICANT: Rebar, Edward
APPLICANT: Jamieson, Andrew
APPLICANT: Liu, Qiang
APPLICANT: Liu, Pei-Qi


```

1 APPLICANT: Wolffe, Alan
2 APPLICANT: Eisenberg, Stephen P.
3 APPLICANT: Jarvis, Eric
4 APPLICANT: Sangamo Biosciences, Inc.
5 TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
6 FILE REFERENCE: 019496-00584008
7 CURRENT APPLICATION NUMBER: US 09/744,604
8 PRIOR FILING DATE: 2001-12-17
9 PRIOR APPLICATION NUMBER: US 09/744,604
10 PRIOR FILING DATE: 2000-12-07
11 PRIOR APPLICATION NUMBER: US 09/746,023
12 PRIOR FILING DATE: 2000-12-12
13 PRIOR APPLICATION NUMBER: US 09/846,033
14 PRIOR FILING DATE: 2001-04-30
15 NUMBER OF SEQ ID NOS: 252
16 SOFTWARE: FastSeq for Windows Version 3.0
17 SEQ ID NO 61
18 LENGTH: 7
19 TYPE: PRT
20 ORGANISM: Artificial Sequence
21 FEATURE:
22 OTHER INFORMATION: Finger
23 US-10-006-069A-61

```

```

Query Match      81.8%  Score 9; DB 9; Length 7;
Best Local Similarity 66.7%  Pred. No. 2.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
   | |
DB 5 LXR 7

```

```

RESULT 41
US-10-006-069A-64
1 Sequence 64, Application US/160606069A
2 Publication No. US20030021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolffe, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sangamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
13 FILE REFERENCE: 019496-00584008
14 CURRENT APPLICATION NUMBER: US 09/744,604
15 PRIOR FILING DATE: 2001-12-17
16 PRIOR APPLICATION NUMBER: US 09/744,604
17 PRIOR FILING DATE: 2000-12-07
18 PRIOR APPLICATION NUMBER: US 09/746,023
19 PRIOR FILING DATE: 2000-12-12
20 PRIOR APPLICATION NUMBER: US 09/846,033
21 NUMBER OF SEQ ID NOS: 252
22 SOFTWARE: FastSeq for Windows Version 3.0
23 SEQ ID NO 64
24 LENGTH: 7
25 TYPE: PRT
26 ORGANISM: Artificial Sequence
27 FEATURE:
28 OTHER INFORMATION: Finger
29 US-10-006-069A-64

```

```

Query Match      91.8%  Score 9; DB 9; Length 7;
Best Local Similarity 66.7%  Pred. No. 2.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3

```

```

Db 5 LXR 7
| |
RESULT 42
US-10-006-069A-65
1 Sequence 65, Application US/160606069A
2 Publication No. US20030021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolffe, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sangamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
13 FILE REFERENCE: 019496-00584008
14 CURRENT APPLICATION NUMBER: US 09/744,604
15 PRIOR FILING DATE: 2001-12-17
16 PRIOR APPLICATION NUMBER: US 09/744,604
17 PRIOR FILING DATE: 2000-12-07
18 PRIOR APPLICATION NUMBER: US 09/746,023
19 PRIOR FILING DATE: 2000-12-12
20 PRIOR APPLICATION NUMBER: US 09/846,033
21 NUMBER OF SEQ ID NOS: 252
22 SOFTWARE: FastSeq for Windows Version 3.0
23 SEQ ID NO 65
24 LENGTH: 7
25 TYPE: PRT
26 ORGANISM: Artificial Sequence
27 FEATURE:
28 OTHER INFORMATION: Finger
29 US-10-006-069A-65

```

```

Query Match      81.8%  Score 9; DB 9; Length 7;
Best Local Similarity 66.7%  Pred. No. 2.9e+05;
Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 1 LXR 3
   | |
DB 5 LXR 7

```

```

RESULT 43
US-10-006-069A-66
1 Sequence 66, Application US/160606069A
2 Publication No. US20030021776A1
3 GENERAL INFORMATION:
4 APPLICANT: Rebar, Edward
5 APPLICANT: Jamieson, Andrew
6 APPLICANT: Liu, Qiang
7 APPLICANT: Liu, Pei-Qi
8 APPLICANT: Wolffe, Alan
9 APPLICANT: Eisenberg, Stephen P.
10 APPLICANT: Jarvis, Eric
11 APPLICANT: Sangamo Biosciences, Inc.
12 TITLE OF INVENTION: Regulation of Angiogenesis With Zinc
13 FILE REFERENCE: 019496-00584008
14 CURRENT APPLICATION NUMBER: US 09/744,604
15 PRIOR FILING DATE: 2001-12-17
16 PRIOR APPLICATION NUMBER: US 09/744,604
17 PRIOR FILING DATE: 2000-12-07
18 PRIOR APPLICATION NUMBER: US 09/746,023
19 PRIOR FILING DATE: 2000-12-12
20 PRIOR APPLICATION NUMBER: US 09/846,033
21 NUMBER OF SEQ ID NOS: 252
22 SOFTWARE: FastSeq for Windows Version 3.0

```

; SEQ ID NO 64
 ; LENGTH: 7
 ; TYPE: PRI
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: finger
 US 10-006-069A-66

Query Match 91.8%; Score 9; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 1 1
 DB 5 LXR 7

RESULT 44

US-10-006-069A-67
 ; Sequence 67; Application US/10006069A
 ; Publication No. US20030921776A1

; GENERAL INFORMATION:
 ; APPLICANT: Rebar, Edward
 ; APPLICANT: Jamieson, Andrew
 ; APPLICANT: Liu, Qiang
 ; APPLICANT: Liu, Pei-Qi
 ; APPLICANT: Wollie, Alan
 ; APPLICANT: Eisenberg, Stephen P.
 ; APPLICANT: Jarvis, Eric
 ; APPLICANT: Sanquamo Biosciences, Inc.

; TITLE OF INVENTION: Regulation of Androgenesis With Zinc
 ; FILE REFERENCE: 019496-005830US

; CURRENT APPLICATION NUMBER: US/10/006,069A
 ; CURRENT FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: US 09/733,664
 ; PRIOR FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: US 09/736,083
 ; PRIOR FILING DATE: 2000-12-12
 ; PRIOR APPLICATION NUMBER: US 09/846,033
 ; PRIOR FILING DATE: 2001-04-30
 ; NUMBER OF SEQ ID NOS: 252

; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 67
 ; LENGTH: 7
 ; TYPE: PRI
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: finger
 US 10-006-069A-67

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

QY 1 LXR 4
 1 1
 DB 5 LXR 7

RESULT 45

US-10-006-069A-68
 ; Sequence 68; Application US/10006069A
 ; Publication No. US20030021776A1

; GENERAL INFORMATION:
 ; APPLICANT: Rebar, Edward
 ; APPLICANT: Jamieson, Andrew
 ; APPLICANT: Liu, Qiang
 ; APPLICANT: Liu, Pei-Qi
 ; APPLICANT: Wollie, Alan
 ; APPLICANT: Eisenberg, Stephen P.
 ; APPLICANT: Jarvis, Eric
 ; APPLICANT: Sanquamo Biosciences, Inc.

; TITLE OF INVENTION: Regulation of Androgenesis With Zinc
 ; FILE REFERENCE: 019496-005830US

; CURRENT APPLICATION NUMBER: US/10/006,069A
 ; CURRENT FILING DATE: 2001-12-17
 ; PRIOR APPLICATION NUMBER: US 09/733,664
 ; PRIOR FILING DATE: 2000-12-07
 ; PRIOR APPLICATION NUMBER: US 09/736,083
 ; PRIOR FILING DATE: 2000-12-12
 ; PRIOR APPLICATION NUMBER: US 09/846,033
 ; PRIOR FILING DATE: 2001-04-30
 ; NUMBER OF SEQ ID NOS: 252

; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 68
 ; LENGTH: 7
 ; TYPE: PRI
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: finger
 US-10-006-069A-68

Query Match 81.8%; Score 9; DB 9; Length 7;
 Best Local Similarity 66.7%; Pred. No. 2.9e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 1 1
 DB 5 LXR 7

Search completed: April 30, 2004, 14:45:01
 Job time : 22.7273 secs

27	94.1	195	17	AAH51767	AcrAP25, Anacylos	26	81.2	249	23	AAH19417	Human protein scqu	
27	84.4	105	17	AAH91708	ArMAP44, Anacylos	158	81.2	270	22	AAH92750	Human secreted pro	
27	84.4	195	20	AAH30406	Rematode extracted	159	25	275	22	AAH11756	Human protein scqu	
27	84.4	195	20	AAH30406	Rematode extracted	160	26	275	22	AAH79728	Lactococcus lactis	
27	84.4	195	17	AAH91706	ArMAP24, Anacylos	161	26	81.2	291	34	AAH54908	Arbitidopsis thalia
27	84.4	195	20	AAH30406	Rematode extracted	162	26	81.2	295	31	AAH42467	Human secreted pro
27	84.4	197	17	AAH91705	ArMAP23, Anacylos	163	26	81.2	345	23	AAH25965	Human secreted pro
27	84.4	168	20	AAH64304	Rematode extracted	164	25	81.2	721	23	AAH53166	Paratuberculo abyssal
27	84.4	117	22	AAH10467	Human polypeptide	165	26	81.2	437	22	AAH63779	Paratuberculo abyssal
27	84.4	173	21	AAH58517	Lung cancer associ	166	26	81.2	445	22	AAH62671	Paratuberculo abyssal
27	84.4	197	22	AAH382305	S. epidermidis cpe	167	26	81.2	1242	22	AAH63779	Paratuberculo abyssal
27	84.4	199	20	AAH14465	Parthol amino acid	168	26	81.2	1247	22	AAH62792	Paratuberculo abyssal
27	84.4	199	20	AAH93245	Arbitidopsis thalia	169	26	81.2	1742	22	AAH63467	Paratuberculo abyssal
27	84.4	201	23	AAH52590	Lactococcus lactis	170	26	81.2	1954	21	AAH59197	Paratuberculo abyssal
27	84.4	226	21	AAH82152	S. epidermidis cpe	171	25	78.1	5	17	AAH91120	Paratuberculo abyssal
27	84.4	231	23	AAH105048	Staphylococcus efi	172	25	78.1	5	20	AAH10139	Paratuberculo abyssal
27	84.4	234	22	AAH99243	Grylla salivary prote	173	25	78.1	5	21	AAH15324	Paratuberculo abyssal
27	84.4	338	20	AAH97911	Phlebotomus leish	174	25	79.1	7	17	AAH53729	Paratuberculo abyssal
27	84.4	342	20	AAH47618	Human inactive tri	175	25	78.1	7	23	AAH30448	Paratuberculo abyssal
27	84.4	392	23	AAH13494	Human inactive tri	176	25	79.1	11	16	AAH72897	Paratuberculo abyssal
27	84.4	401	22	AAH239123	Novel human diapo	177	25	78.1	11	16	AAH72897	Paratuberculo abyssal
27	84.4	415	22	AAH47617	Human superoxide tr	178	25	78.1	11	16	AAH72897	Paratuberculo abyssal
27	84.4	415	22	AAH13493	Human superoxide tr	179	25	78.1	11	16	AAH72897	Paratuberculo abyssal
27	84.4	437	22	AAH47616	Human mini triptop	180	25	78.1	20	16	AAH72897	Paratuberculo abyssal
27	84.4	437	23	AAH13492	Human mini triptop	181	25	78.1	20	16	AAH72897	Paratuberculo abyssal
27	84.4	439	22	AAH95547	Mouse prorepressi	182	25	78.1	47	19	AAH92742	Paratuberculo abyssal
27	84.4	471	29	AAH955374	Human HCMV integr	183	25	78.1	47	21	AAH91614	Paratuberculo abyssal
27	84.4	475	21	AAH58240	Human HCMV integr	184	25	78.1	47	21	AAH72956	Paratuberculo abyssal
27	81.1	482	22	AAH69968	Protophila melano	185	25	78.1	44	16	AAH72912	Paratuberculo abyssal
27	84.4	484	22	AAH47615	Human full-length	186	25	78.1	59	23	AAH97297	Paratuberculo abyssal
27	84.4	481	23	AAH13491	Human triptophan1	187	25	78.1	63	22	AAH30486	Paratuberculo abyssal
27	84.4	492	17	AAH95582	Mouse prorepressi	188	25	78.1	60	22	AAH72958	Paratuberculo abyssal
27	84.4	506	17	AAH89146	Chondroitinase B p	189	25	78.1	63	22	AAH72958	Paratuberculo abyssal
27	84.4	533	23	AAH53284	Human polypeptide	190	25	78.1	60	22	AAH71867	Paratuberculo abyssal
27	84.4	543	22	AAH66608	Protophila melano	191	25	7				

230	25	78.1	166	19	AAW67469	E. coli mutant per	302	78.1	514	23	AAW48134	Human specific pro
231	25	78.1	166	19	AAW67465	E. coli periplasm	304	78.1	515	23	AAW41761	Human periplasm
232	25	78.1	166	19	AAW67466	E. coli mutant per	305	78.1	516	23	AAW44257	Human periplasm (HNR)
233	25	78.1	166	19	AAW67467	E. coli mutant per	306	78.1	517	23	AAW57462	Arabidopsis thalia
234	25	78.1	166	22	AAW01676	Human gene 5 unseq	307	78.1	518	23	AAW61132	Arabidopsis thalia
235	25	78.1	166	22	AAW01707	Human gene 5 unseq	308	78.1	519	23	AAW29061	Human pro polypept
236	25	78.1	166	23	AAW63949	Human albumin fus	309	78.1	520	23	AAW07592	elypeptin 5 llo
237	25	78.1	166	23	AAW53560	Human albumin fus	310	78.1	521	23	AAW57592	elypeptin 5 llo
238	25	78.1	168	22	AAW69478	Protophylla melonog	311	78.1	522	23	AAW57592	elypeptin 5 llo
239	25	78.1	171	21	AAW94221	Cytoplasmic melonog	312	78.1	523	23	AAW57592	elypeptin 5 llo
240	25	78.1	191	21	AAW63227	Cytoplasmic melonog	313	78.1	524	23	AAW57592	elypeptin 5 llo
241	25	78.1	241	20	AAW59671	Protophylla melonog	314	78.1	525	23	AAW57592	elypeptin 5 llo
242	25	78.1	191	21	AAW59671	Protophylla melonog	315	78.1	526	23	AAW57592	elypeptin 5 llo
243	25	78.1	214	23	AAW53566	Protophylla melonog	316	78.1	527	23	AAW57592	elypeptin 5 llo
244	25	78.1	215	23	AAW53566	Protophylla melonog	317	78.1	528	23	AAW57592	elypeptin 5 llo
245	25	78.1	216	23	AAW53566	Protophylla melonog	318	78.1	529	23	AAW57592	elypeptin 5 llo
246	25	78.1	227	19	AAW85918	Protophylla melonog	319	78.1	530	23	AAW57592	elypeptin 5 llo
247	25	78.1	227	23	AAW83940	Protophylla melonog	320	78.1	531	23	AAW57592	elypeptin 5 llo
248	25	78.1	239	22	AAW33856	Protophylla melonog	321	78.1	532	23	AAW57592	elypeptin 5 llo
249	25	78.1	249	24	AAW75486	Protophylla melonog	322	78.1	533	23	AAW57592	elypeptin 5 llo
250	25	78.1	244	21	AAW49214	Protophylla melonog	323	78.1	534	23	AAW57592	elypeptin 5 llo
251	25	78.1	244	21	AAW49214	Protophylla melonog	324	78.1	535	23	AAW57592	elypeptin 5 llo
252	25	78.1	246	22	AAW529473	Protophylla melonog	325	78.1	536	23	AAW57592	elypeptin 5 llo
253	25	78.1	251	21	AAW14810	Protophylla melonog	326	78.1	537	23	AAW57592	elypeptin 5 llo
254	25	78.1	251	21	AAW59671	Protophylla melonog	327	78.1	538	23	AAW57592	elypeptin 5 llo
255	25	78.1	251	23	AAW51176	Protophylla melonog	328	78.1	539	23	AAW57592	elypeptin 5 llo
256	25	78.1	253	23	AAW36695	Protophylla melonog	329	78.1	540	23	AAW57592	elypeptin 5 llo
257	25	78.1	256	23	AAW54641	Protophylla melonog	330	78.1	541	23	AAW57592	elypeptin 5 llo
258	25	78.1	260	21	AAW44419	Protophylla melonog	331	78.1	542	23	AAW57592	elypeptin 5 llo
259	25	78.1	274	9	AAW81277	Protophylla melonog	332	78.1	543	23	AAW57592	elypeptin 5 llo
260	25	78.1	296	21	AAW14809	Protophylla melonog	333	78.1	544	23	AAW57592	elypeptin 5 llo
261	25	78.1	296	21	AAW57574	Protophylla melonog	334	78.1	545	23	AAW57592	elypeptin 5 llo
262	25	78.1	289	21	AAW19421	Protophylla melonog	335	78.1	546	23	AAW57592	elypeptin 5 llo
263	25	78.1	292	23	AAW82860	Protophylla melonog	336	78.1	547	23	AAW57592	elypeptin 5 llo
264	25	78.1	292	22	AAW82970	Protophylla melonog	337	78.1	548	23	AAW57592	elypeptin 5 llo
265	25	78.1	296	21	AAW94613	Protophylla melonog	338	78.1	549	23	AAW57592	elypeptin 5 llo
266	25	78.1	296	21	AAW94613	Protophylla melonog	339	78.1	550	23	AAW57592	elypeptin 5 llo
267	25	78.1	313	19	AAW57574	Protophylla melonog	340	78.1	551	23	AAW57592	elypeptin 5 llo
268	25	78.1	317	22	AAW52736	Protophylla melonog	341	78.1	552	23	AAW57592	elypeptin 5 llo
269	25	78.1	318	21	AAW56711	Protophylla melonog	342	78.1	553	23	AAW57592	elypeptin 5 llo
270	25	78.1	318	22	AAW571018	Protophylla melonog	343	78.1	554	23	AAW57592	elypeptin 5 llo
271	25	78.1	318	21	AAW571018	Protophylla melonog	344	78.1	555	23	AAW57592	elypeptin 5 llo
272	25	78.1	318	21	AAW571018	Protophylla melonog	345	78.1	556	23	AAW57592	elypeptin 5 llo
273	25	78.1	318	21	AAW571018	Protophylla melonog	346	78.1	557	23	AAW57592	elypeptin 5 llo
274	25	78.1	319	22	AAW59564	Protophylla melonog	347	78.1	558	23	AAW57592	elypeptin 5 llo
275	25	78.1	356	23	AAW38563	Protophylla melonog	348	78.1	559	23	AAW57592	elypeptin 5 llo
276	25	78.1	372	23	AAW52966	Protophylla melonog	349	78.1	560	23	AAW57592	elypeptin 5 llo
277	25	78.1	372	23	AAW52966	Protophylla melonog	350	78.1	561	23	AAW57592	elypeptin 5 llo
278	25	78.1	372	23	AAW52966	Protophylla melonog	351	78.1	562	23	AAW57592	elypeptin 5 llo
279	25	78.1	381	23	AAW48456	Protophylla melonog	352	78.1	563	23	AAW57592	elypeptin 5 llo
280	25	78.1	381	23	AAW48456	Protophylla melonog	353	78.1	564	23	AAW57592	elypeptin 5 llo
281	25	78.1	381	23	AAW48456	Protophylla melonog	354	78.1	565	23	AAW57592	elypeptin 5 llo
282	25	78.1	381	23	AAW48456	Protophylla melonog	355	78.1	566	23	AAW57592	elypeptin 5 llo
283	25	78.1	381	23	AAW48456	Protophylla melonog	356	78.1	567	23	AAW57592	elypeptin 5 llo
284	25	78.1	411	22	AAW14834	Protophylla melonog	357	78.1	568	23	AAW57592	elypeptin 5 llo
285	25	78.1	411	22	AAW14834	Protophylla melonog	358	78.1	569	23	AAW57592	elypeptin 5 llo
286	25	78.1	411	22	AAW14834	Protophylla melonog	359	78.1	570	23	AAW57592	elypeptin 5 llo
287	25	78.1	411	22	AAW14834	Protophylla melonog	360	78.1	571	23	AAW57592	elypeptin 5 llo
288	25	78.1	411	22	AAW14834	Protophylla melonog	361	78.1	572	23	AAW57592	elypeptin 5 llo
289	25	78.1	411	22	AAW14834	Protophylla melonog	362	78.1	573	23	AAW57592	elypeptin 5 llo
290	25	78.1	411	22	AAW14834	Protophylla melonog	363	78.1	574	23	AAW57592	elypeptin 5 llo
291	25	78.1	411	22	AAW14834	Protophylla melonog	364	78.1	575	23	AAW57592	elypeptin 5 llo
292	25	78.1	411	22	AAW14834	Protophylla melonog	365	78.1	576	23	AAW57592	elypeptin 5 llo
293	25	78.1	411	22	AAW14834	Protophylla melonog	366	78.1	577	23	AAW57592	elypeptin 5 llo
294	25	78.1	411	22	AAW14834	Protophylla melonog	367	78.1	578	23	AAW57592	elypeptin 5 llo
295	25	78.1	411	22	AAW14834	Protophylla melonog	368	78.1	579	23	AAW57592	elypeptin 5 llo
296	25	78.1	411	22	AAW14834	Protophylla melonog	369	78.1	580	23	AAW57592	elypeptin 5 llo
297	25	78.1	411	22	AAW14834	Protophylla melonog	370	78.1	581	23	AAW57592	elypeptin 5 llo
298	25	78.1	411	22	AAW14834	Protophylla melonog	371	78.1	582	23	AAW57592	elypeptin 5 llo
299	25	78.1	411	22	AAW14834	Protophylla melonog	372	78.1	583	23	AAW57592	elypeptin 5 llo
300	25	78.1	411	22	AAW14834	Protophylla melonog	373	78.1	584	23	AAW57592	elypeptin 5 llo
301	25	78.1	411	22	AAW14834	Protophylla melonog	374	78.1	585	23	AAW57592	elypeptin 5 llo
302	25	78.1	411	22	AAW14834	Protophylla melonog	375	78.1	586	23	AAW57592	elypeptin 5 llo

522	24	75.0	58	18	RAN28441	Staphylococcus ant	595	164	22	AAW52826	Human thymocyte
523	24	75.0	58	21	RAN27011	Arabidopsis thaliana	596	165	21	AAW54387	Arabidopsis thaliana
524	24	75.0	58	23	AAW50251	Human cAMP protein	597	166	24	AAW51149	Human cAMP protein
525	24	75.0	59	22	AAW00877	Human excretory re	598	167	22	AAW51112	Human prostate spe
526	24	75.0	59	23	AAW13676	Human bladder anti	599	168	23	AAW50765	Human prostate dise
527	24	75.0	59	23	AAW33592	Human prostate anti	600	169	23	AAW50765	Human prostate dise
528	24	75.0	60	22	AAW06647	Human prostate anti	601	170	22	AAW50765	Human prostate dise
529	24	75.0	61	22	AAW15289	Human prostate anti	602	171	22	AAW17328	Human prostate anti
530	24	75.0	61	22	AAW29529	Human prostate anti	603	172	22	AAW17328	Human prostate anti
531	24	75.0	61	22	AAW08896	Human prostate anti	604	173	22	AAW08896	Human prostate anti
532	24	75.0	62	22	AAW09945	Human prostate anti	605	174	22	AAW09945	Human prostate anti
533	24	75.0	62	23	AAW38487	Human prostate anti	606	175	23	AAW1641	Human prostate anti
534	24	75.0	63	20	AAW36130	Human prostate anti	607	176	20	AAW5255	Human prostate anti
535	24	75.0	64	22	AAW09167	Human prostate anti	608	177	22	AAW17328	Human prostate anti
536	24	75.0	64	22	AAW04584	Human prostate anti	609	178	22	AAW17328	Human prostate anti
537	24	75.0	65	21	AAW12127	Human prostate anti	610	179	21	AAW17328	Human prostate anti
538	24	75.0	65	22	AAW16162	Human prostate anti	611	180	22	AAW16162	Human prostate anti
539	24	75.0	65	22	AAW09700	Human prostate anti	612	181	22	AAW09700	Human prostate anti
540	24	75.0	66	22	AAW17639	Human prostate anti	613	182	22	AAW17639	Human prostate anti
541	24	75.0	66	22	AAW15615	Human prostate anti	614	183	22	AAW15615	Human prostate anti
542	24	75.0	68	21	AAW43683	Human prostate anti	615	184	21	AAW43683	Human prostate anti
543	24	75.0	68	21	AAW50713	Human prostate anti	616	185	21	AAW50713	Human prostate anti
544	24	75.0	68	22	AAW88630	Human prostate anti	617	186	22	AAW88630	Human prostate anti
545	24	75.0	69	22	AAW52529	Human prostate anti	618	187	22	AAW52529	Human prostate anti
546	24	75.0	70	22	AAW66894	Human prostate anti	619	188	22	AAW66894	Human prostate anti
547	24	75.0	70	22	AAW67859	Human prostate anti	620	189	22	AAW67859	Human prostate anti
548	24	75.0	71	19	AAW38743	Human prostate anti	621	190	19	AAW38743	Human prostate anti
549	24	75.0	72	21	AAW21547	Human prostate anti	622	191	21	AAW21547	Human prostate anti
550	24	75.0	72	21	AAW42467	Human prostate anti	623	192	21	AAW42467	Human prostate anti
551	24	75.0	72	22	AAW08644	Human prostate anti	624	193	22	AAW08644	Human prostate anti
552	24	75.0	72	22	AAW16283	Human prostate anti	625	194	22	AAW16283	Human prostate anti
553	24	75.0	75	23	AAW09690	Human prostate anti	626	195	23	AAW09690	Human prostate anti
554	24	75.0	76	21	AAW21546	Human prostate anti	627	196	21	AAW21546	Human prostate anti
555	24	75.0	76	21	AAW42466	Human prostate anti	628	197	21	AAW42466	Human prostate anti
556	24	75.0	78	16	AAW71257	Human prostate anti	629	198	16	AAW71257	Human prostate anti
557	24	75.0	78	16	AAW71245	Human prostate anti	630	199	16	AAW71245	Human prostate anti
558	24	75.0	78	19	AAW50011	Human prostate anti	631	200	19	AAW50011	Human prostate anti
559	24	75.0	78	19	AAW50012	Human prostate anti	632	201	19	AAW50012	Human prostate anti
560	24	75.0	78	22	AAW05913	Human prostate anti	633	202	22	AAW05913	Human prostate anti
561	24	75.0	79	9	AAW80468	Human prostate anti	634	203	9	AAW80468	Human prostate anti
562	24	75.0	80	9	AAW80469	Human prostate anti	635	204	9	AAW80469	Human prostate anti
563	24	75.0	80	9	AAW80470	Human prostate anti	636	205	9	AAW80470	Human prostate anti
564	24	75.0	81	22	AAW74104	Human prostate anti	637	206	22	AAW74104	Human prostate anti
565	24	75.0	82	22	AAW36323	Human prostate anti	638	207	22	AAW36323	Human prostate anti
566	24	75.0	84	22	AAW74719	Human prostate anti	639	208	22	AAW74719	Human prostate anti
567	24	75.0	85	22	AAW64165	Human prostate anti	640	209	22	AAW64165	Human prostate anti
568	24	75.0	85	22	AAW58556	Human prostate anti	641	210	22	AAW58556	Human prostate anti
569	24	75.0	85	22	AAW49749	Human prostate anti	642	211	22	AAW49749	Human prostate anti
570	24	75.0	85	22	AAW53264	Human prostate anti	643	212	22	AAW53264	Human prostate anti
571	24	75.0	85	22	AAW71919	Human prostate anti	644	213	22	AAW71919	Human prostate anti
572	24	75.0	85	22	AAW32200	Human prostate anti	645	214	22	AAW32200	Human prostate anti
573	24	75.0	85	23	AAW41733	Human prostate anti	646	215	23	AAW41733	Human prostate anti
574	24	75.0	88	23	AAW60766	Human prostate anti	647	216	23	AAW60766	Human prostate anti
575	24	75.0	88	23	AAW60766	Human prostate anti	648	217	23	AAW60766	Human prostate anti
576	24	75.0	88	23	AAW60766	Human prostate anti	649	218	23	AAW60766	Human prostate anti
577	24	75.0	88	23	AAW60766	Human prostate anti	650	219	23	AAW60766	Human prostate anti
578	24	75.0	89	21	AAW322776	Human prostate anti	651	220	21	AAW322776	Human prostate anti
579	24	75.0	90	21	AAW322776	Human prostate anti	652	221	21	AAW322776	Human prostate anti
580	24	75.0	91	19	AAW11221	Human prostate anti	653	222	19	AAW11221	Human prostate anti
581	24	75.0	92	22	AAW05045	Human prostate anti	654	223	22	AAW05045	Human prostate anti
582	24	75.0	93	21	AAW56523	Human prostate anti	655	224	21	AAW56523	Human prostate anti
583	24	75.0	94	21	AAW11226	Human prostate anti	656	225	21	AAW11226	Human prostate anti
584	24	75.0	94	21	AAW22606	Human prostate anti	657	226	21	AAW22606	Human prostate anti
585	24	75.0	94	21	AAW35872	Human prostate anti	658	227	21	AAW35872	Human prostate anti
586	24	75.0	95	21	AAW35872	Human prostate anti	659	228	21	AAW35872	Human prostate anti
587	24	75.0	98	20	AAW35873	Human prostate anti	660	229	20	AAW35873	Human prostate anti
588	24	75.0	99	22	AAW86411	Human prostate anti	661	230	22	AAW86411	Human prostate anti
589	24	75.0	101	22	AAW44628	Human prostate anti	662	231	22	AAW44628	Human prostate anti
590	24	75.0	101	23	AAW08506	Human prostate anti	663	232	23	AAW08506	Human prostate anti
591	24	75.0	102	19	AAW00650	Human prostate anti	664	233	19	AAW00650	Human prostate anti
592	24	75.0	102	21	AAW32261	Human prostate anti	665	234	21	AAW32261	Human prostate anti
593	24	75.0	103	21	AAW75304	Human prostate anti	666	235	21	AAW75304	Human prostate anti
594	24	75.0	103	21	AAW75305	Human prostate anti	667	236	21	AAW75305	Human prostate anti

668	24	75.0	142	22	AA047076	Filin protein, rim	741	24	75.0	163	22	AA023484	Neel human diamo
669	24	76.0	143	22	AA022812	Bacterial type 1 p	742	24	75.0	163	22	AA096122	putative isoprop
670	24	76.0	144	23	AA033136	Bacillus glyphosat	743	24	75.0	164	21	AA025006	Arabidopsis thalia
671	24	76.0	145	23	AA033138	Bacillus glyphosat	744	24	75.0	164	21	AA037068	Arabidopsis thalia
672	24	76.0	146	23	AA033139	Bacillus glyphosat	745	24	75.0	164	22	AA096259	putative isoprop
673	24	76.0	147	23	AA033140	Bacillus glyphosat	746	24	75.0	165	22	AA024249	human EST encoded
674	24	75.0	148	23	AA033141	Bacillus glyphosat	747	24	75.0	167	21	AA015940	E. coli proliferat
675	24	75.0	149	23	AA033142	Bacillus glyphosat	748	24	75.0	167	21	AA016309	E. coli proliferat
676	24	76.0	150	23	AA033143	Bacillus glyphosat	749	24	75.0	169	23	AA069540	human polypeptide
677	24	75.0	151	23	AA033144	Bacillus glyphosat	750	24	75.0	170	21	AA022961	Arabidopsis thalia
678	24	75.0	152	23	AA033145	Bacillus glyphosat	751	24	75.0	170	22	AA015496	Neel human diamo
679	24	75.0	153	23	AA033146	Bacillus glyphosat	752	24	75.0	172	23	AA029414	putative poly
680	24	75.0	154	23	AA033147	Bacillus glyphosat	753	24	75.0	172	21	AA059121	Arabidopsis thalia
681	24	75.0	155	23	AA033148	Bacillus glyphosat	754	24	75.0	172	21	AA036058	Arabidopsis thalia
682	24	75.0	156	23	AA033149	Bacillus glyphosat	755	24	75.0	173	21	AA036009	zein may protein f
683	24	75.0	157	23	AA033150	Bacillus glyphosat	756	24	75.0	173	21	AA031889	Arabidopsis thalia
684	24	76.0	158	23	AA033151	Bacillus glyphosat	757	24	75.0	173	22	AA022959	Neel human diamo
685	24	76.0	159	23	AA033152	Bacillus glyphosat	758	24	75.0	173	22	AA022959	Neel human diamo
686	24	75.0	160	23	AA033153	Bacillus glyphosat	759	24	75.0	173	23	AA042789	human ovarian anti
687	24	75.0	161	23	AA033154	Bacillus glyphosat	760	24	75.0	174	21	AA032337	putative protein
688	24	76.0	162	23	AA033155	Bacillus glyphosat	761	24	75.0	174	22	AA051936	Arabidopsis thalia
689	24	75.0	163	23	AA033156	Bacillus glyphosat	762	24	75.0	176	23	AA064864	Leptococcus lactis
690	24	75.0	164	23	AA033157	Bacillus glyphosat	763	24	75.0	179	22	AA064528	Protein factorium
691	24	75.0	165	23	AA033158	Bacillus glyphosat	764	24	75.0	181	22	AA032296	Neel human diamo
692	24	75.0	166	23	AA033159	Bacillus glyphosat	765	24	75.0	182	21	AA051088	Arabidopsis thalia
693	24	75.0	167	23	AA033160	Bacillus glyphosat	766	24	75.0	182	21	AA051088	Arabidopsis thalia
694	24	75.0	168	23	AA033161	Bacillus glyphosat	767	24	75.0	183	22	AA062955	Protein factorium
695	24	75.0	169	23	AA033162	Bacillus glyphosat	768	24	75.0	187	22	AA025415	human protein sequ
696	24	75.0	170	23	AA033163	Bacillus glyphosat	769	24	75.0	188	20	AA045109	Amino acid sequen
697	24	75.0	171	23	AA033164	Bacillus glyphosat	770	24	75.0	189	22	AA031237	putative protein
698	24	75.0	172	23	AA033165	Bacillus glyphosat	771	24	75.0	189	22	AA067877	Arabidopsis thalia
699	24	75.0	173	23	AA033166	Bacillus glyphosat	772	24	75.0	190	19	AA050014	human hyaluronan s
700	24	75.0	174	23	AA033167	Bacillus glyphosat	773	24	75.0	191	19	AA050014	S. pneumoniae deri
701	24	75.0	175	23	AA033168	Bacillus glyphosat	774	24	75.0	191	21	AA022960	Arabidopsis thalia
702	24	75.0	176	23	AA033169	Bacillus glyphosat	775	24	75.0	192	21	AA022960	Arabidopsis thalia
703	24	75.0	177	23	AA033170	Bacillus glyphosat	776	24	75.0	193	21	AA022960	Arabidopsis thalia
704	24	75.0	178	23	AA033171	Bacillus glyphosat	777	24	75.0	194	22	AA036567	Bumex tumour thoma
705	24	75.0	179	23	AA033172	Bacillus glyphosat	778	24	75.0	194	22	AA036567	Bumex tumour thoma
706	24	75.0	180	23	AA033173	Bacillus glyphosat	779	24	75.0	194	22	AA036567	Bumex tumour thoma
707	24	75.0	181	23	AA033174	Bacillus glyphosat	780	24	75.0	194	22	AA036567	Bumex tumour thoma
708	24	75.0	182	23	AA033175	Bacillus glyphosat	781	24	75.0	194	22	AA036567	Bumex tumour thoma
709	24	75.0	183	23	AA033176	Bacillus glyphosat	782	24	75.0	194	22	AA036567	Bumex tumour thoma
710	24	75.0	184	23	AA033177	Bacillus glyphosat	783	24	75.0	194	22	AA036567	Bumex tumour thoma
711	24	75.0	185	23	AA033178	Bacillus glyphosat	784	24	75.0	194	22	AA036567	Bumex tumour thoma
712	24	75.0	186	23	AA033179	Bacillus glyphosat	785	24	75.0	194	22	AA036567	Bumex tumour thoma
713	24	75.0	187	23	AA033180	Bacillus glyphosat	786	24	75.0	194	22	AA036567	Bumex tumour thoma
714	24	75.0	188	23	AA033181	Bacillus glyphosat	787	24	75.0	194	22	AA036567	Bumex tumour thoma
715	24	75.0	189	23	AA033182	Bacillus glyphosat	788	24	75.0	194	22	AA036567	Bumex tumour thoma
716	24	75.0	190	23	AA033183	Bacillus glyphosat	789	24	75.0	194	22	AA036567	Bumex tumour thoma
717	24	75.0	191	23	AA033184	Bacillus glyphosat	790	24	75.0	194	22	AA036567	Bumex tumour thoma
718	24	75.0	192	23	AA033185	Bacillus glyphosat	791	24	75.0	194	22	AA036567	Bumex tumour thoma
719	24	75.0	193	23	AA033186	Bacillus glyphosat	792	24	75.0	194	22	AA036567	Bumex tumour thoma
720	24	75.0	194	23	AA033187	Bacillus glyphosat	793	24	75.0	194	22	AA036567	Bumex tumour thoma
721	24	75.0	195	23	AA033188	Bacillus glyphosat	794	24	75.0	194	22	AA036567	Bumex tumour thoma
722	24	75.0	196	23	AA033189	Bacillus glyphosat	795	24	75.0	194	22	AA036567	Bumex tumour thoma
723	24	75.0	197	23	AA033190	Bacillus glyphosat	796	24	75.0	194	22	AA036567	Bumex tumour thoma
724	24	75.0	198	23	AA033191	Bacillus glyphosat	797	24	75.0	194	22	AA036567	Bumex tumour thoma
725	24	75.0	199	23	AA033192	Bacillus glyphosat	798	24	75.0	194	22	AA036567	Bumex tumour thoma
726	24	75.0	200	23	AA033193	Bacillus glyphosat	799	24	75.0	194	22	AA036567	Bumex tumour thoma
727	24	75.0	201	23	AA033194	Bacillus glyphosat	800	24	75.0	194	22	AA036567	Bumex tumour thoma
728	24	75.0	202	23	AA033195	Bacillus glyphosat	801	24	75.0	194	22	AA036567	Bumex tumour thoma
729	24	75.0	203	23	AA033196	Bacillus glyphosat	802	24	75.0	194	22	AA036567	Bumex tumour thoma
730	24	75.0	204	23	AA033197	Bacillus glyphosat	803	24	75.0	194	22	AA036567	Bumex tumour thoma
731	24	75.0	205	23	AA033198	Bacillus glyphosat	804	24	75.0	194	22	AA036567	Bumex tumour thoma
732	24	75.0	206	23	AA033199	Bacillus glyphosat	805	24	75.0	194	22	AA036567	Bumex tumour thoma
733	24	75.0	207	23	AA033200	Bacillus glyphosat	806	24	75.0	194	22	AA036567	Bumex tumour thoma
734	24	75.0	208	23	AA033201	Bacillus glyphosat	807	24	75.0	194	22	AA036567	Bumex tumour thoma
735	24	75.0	209	23	AA033202	Bacillus glyphosat	808	24	75.0	194	22	AA036567	Bumex tumour thoma
736	24	75.0	210	23	AA033203	Bacillus glyphosat	809	24	75.0	194	22	AA036567	Bumex tumour thoma
737	24	75.0	211	23	AA033204	Bacillus glyphosat	810	24	75.0	194	22	AA036567	Bumex tumour thoma
738	24	75.0	212	23	AA033205	Bacillus glyphosat	811	24	75.0	194	22	AA036567	Bumex tumour thoma
739	24	75.0	213	23	AA033206	Bacillus glyphosat	812	24	75.0	194	22	AA036567	Bumex tumour thoma
740	24	75.0	214	23	AA033207	Bacillus glyphosat	813	24	75.0	194	22	AA036567	Bumex tumour thoma

814	24	75.0	214	20	AAW93590	Mouse MARV4 alpha	897	24	75.0	264	21	AAW52011	Arabidopsis thaliana
815	24	75.0	214	21	XAB23438	Marine diatom prote	898	24	75.0	265	22	AAW52011	Streptococcus epid
816	24	75.0	214	22	XAB23438	Amino acid sequence	899	24	75.0	266	23	AAW52011	Arabidopsis thaliana
817	24	75.0	215	21	AAW09757	YFP5 5' amino acid	900	24	75.0	267	24	AAW52011	Arabidopsis thaliana
818	24	75.0	215	22	ABG22523	Recombinant diatom	901	24	75.0	268	25	AAW52011	Amino acid sequence
819	24	75.0	216	21	AAW09757	Regulin like protein	902	24	75.0	269	26	AAW52011	Arabidopsis thaliana
820	24	75.0	216	22	AAW09757	Recombinant diatom	903	24	75.0	270	27	AAW52011	Arabidopsis thaliana
821	24	75.0	217	21	AAW36355	Recombinant diatom	904	24	75.0	271	28	AAW52011	Arabidopsis thaliana
822	24	75.0	217	22	AAW36355	Arabidopsis thaliana	905	24	75.0	272	29	AAW52011	Arabidopsis thaliana
823	24	75.0	219	21	ABF40797	Epidermal cell wall	906	24	75.0	273	30	AAW52011	Arabidopsis thaliana
824	24	75.0	219	22	ABF40797	Streptococcus epid	907	24	75.0	274	31	AAW52011	Arabidopsis thaliana
825	24	75.0	222	21	ABF42803	Listeria monocytogenes	908	24	75.0	275	32	AAW52011	Arabidopsis thaliana
826	24	75.0	222	22	ABF42803	Human ovarian anti	909	24	75.0	276	33	AAW52011	Arabidopsis thaliana
827	24	75.0	223	21	ABF43101	Human ovarian anti	910	24	75.0	277	34	AAW52011	Arabidopsis thaliana
828	24	75.0	223	22	AAW09757	Recombinant diatom	911	24	75.0	278	35	AAW52011	Arabidopsis thaliana
829	24	75.0	224	21	AAW09757	Streptococcus epid	912	24	75.0	279	36	AAW52011	Arabidopsis thaliana
830	24	75.0	224	22	AAW09757	Arabidopsis thaliana	913	24	75.0	280	37	AAW52011	Arabidopsis thaliana
831	24	75.0	226	21	AAW36355	Arabidopsis thaliana	914	24	75.0	281	38	AAW52011	Arabidopsis thaliana
832	24	75.0	226	22	AAW36355	Arabidopsis thaliana	915	24	75.0	282	39	AAW52011	Arabidopsis thaliana
833	24	75.0	227	21	ABF42803	Human protein SEQ	916	24	75.0	283	40	AAW52011	Arabidopsis thaliana
834	24	75.0	227	22	ABF42803	Arabidopsis thaliana	917	24	75.0	284	41	AAW52011	Arabidopsis thaliana
835	24	75.0	229	21	AAW36355	Arabidopsis thaliana	918	24	75.0	285	42	AAW52011	Arabidopsis thaliana
836	24	75.0	229	22	AAW36355	Arabidopsis thaliana	919	24	75.0	286	43	AAW52011	Arabidopsis thaliana
837	24	75.0	231	21	AAW09757	Recombinant diatom	920	24	75.0	287	44	AAW52011	Arabidopsis thaliana
838	24	75.0	231	22	AAW09757	Arabidopsis thaliana	921	24	75.0	288	45	AAW52011	Arabidopsis thaliana
839	24	75.0	231	23	AAW09757	Arabidopsis thaliana	922	24	75.0	289	46	AAW52011	Arabidopsis thaliana
840	24	75.0	231	24	AAW09757	Arabidopsis thaliana	923	24	75.0	290	47	AAW52011	Arabidopsis thaliana
841	24	75.0	231	25	AAW09757	Arabidopsis thaliana	924	24	75.0	291	48	AAW52011	Arabidopsis thaliana
842	24	75.0	231	26	AAW09757	Arabidopsis thaliana	925	24	75.0	292	49	AAW52011	Arabidopsis thaliana
843	24	75.0	231	27	AAW09757	Arabidopsis thaliana	926	24	75.0	293	50	AAW52011	Arabidopsis thaliana
844	24	75.0	231	28	AAW09757	Arabidopsis thaliana	927	24	75.0	294	51	AAW52011	Arabidopsis thaliana
845	24	75.0	231	29	AAW09757	Arabidopsis thaliana	928	24	75.0	295	52	AAW52011	Arabidopsis thaliana
846	24	75.0	231	30	AAW09757	Arabidopsis thaliana	929	24	75.0	296	53	AAW52011	Arabidopsis thaliana
847	24	75.0	231	31	AAW09757	Arabidopsis thaliana	930	24	75.0	297	54	AAW52011	Arabidopsis thaliana
848	24	75.0	231	32	AAW09757	Arabidopsis thaliana	931	24	75.0	298	55	AAW52011	Arabidopsis thaliana
849	24	75.0	231	33	AAW09757	Arabidopsis thaliana	932	24	75.0	299	56	AAW52011	Arabidopsis thaliana
850	24	75.0	231	34	AAW09757	Arabidopsis thaliana	933	24	75.0	300	57	AAW52011	Arabidopsis thaliana
851	24	75.0	231	35	AAW09757	Arabidopsis thaliana	934	24	75.0	301	58	AAW52011	Arabidopsis thaliana
852	24	75.0	231	36	AAW09757	Arabidopsis thaliana	935	24	75.0	302	59	AAW52011	Arabidopsis thaliana
853	24	75.0	231	37	AAW09757	Arabidopsis thaliana	936	24	75.0	303	60	AAW52011	Arabidopsis thaliana
854	24	75.0	231	38	AAW09757	Arabidopsis thaliana	937	24	75.0	304	61	AAW52011	Arabidopsis thaliana
855	24	75.0	231	39	AAW09757	Arabidopsis thaliana	938	24	75.0	305	62	AAW52011	Arabidopsis thaliana
856	24	75.0	231	40	AAW09757	Arabidopsis thaliana	939	24	75.0	306	63	AAW52011	Arabidopsis thaliana
857	24	75.0	231	41	AAW09757	Arabidopsis thaliana	940	24	75.0	307	64	AAW52011	Arabidopsis thaliana
858	24	75.0	231	42	AAW09757	Arabidopsis thaliana	941	24	75.0	308	65	AAW52011	Arabidopsis thaliana
859	24	75.0	231	43	AAW09757	Arabidopsis thaliana	942	24	75.0	309	66	AAW52011	Arabidopsis thaliana
860	24	75.0	231	44	AAW09757	Arabidopsis thaliana	943	24	75.0	310	67	AAW52011	Arabidopsis thaliana
861	24	75.0	231	45	AAW09757	Arabidopsis thaliana	944	24	75.0	311	68	AAW52011	Arabidopsis thaliana
862	24	75.0	231	46	AAW09757	Arabidopsis thaliana	945	24	75.0	312	69	AAW52011	Arabidopsis thaliana
863	24	75.0	231	47	AAW09757	Arabidopsis thaliana	946	24	75.0	313	70	AAW52011	Arabidopsis thaliana
864	24	75.0	231	48	AAW09757	Arabidopsis thaliana	947	24	75.0	314	71	AAW52011	Arabidopsis thaliana
865	24	75.0	231	49	AAW09757	Arabidopsis thaliana	948	24	75.0	315	72	AAW52011	Arabidopsis thaliana
866	24	75.0	231	50	AAW09757	Arabidopsis thaliana	949	24	75.0	316	73	AAW52011	Arabidopsis thaliana
867	24	75.0	231	51	AAW09757	Arabidopsis thaliana	950	24	75.0	317	74	AAW52011	Arabidopsis thaliana
868	24	75.0	231	52	AAW09757	Arabidopsis thaliana	951	24	75.0	318	75	AAW52011	Arabidopsis thaliana
869	24	75.0	231	53	AAW09757	Arabidopsis thaliana	952	24	75.0	319	76	AAW52011	Arabidopsis thaliana
870	24	75.0	231	54	AAW09757	Arabidopsis thaliana	953	24	75.0	320	77	AAW52011	Arabidopsis thaliana
871	24	75.0	231	55	AAW09757	Arabidopsis thaliana	954	24	75.0	321	78	AAW52011	Arabidopsis thaliana
872	24	75.0	231	56	AAW09757	Arabidopsis thaliana	955	24	75.0	322	79	AAW52011	Arabidopsis thaliana
873	24	75.0	231	57	AAW09757	Arabidopsis thaliana	956	24	75.0	323	80	AAW52011	Arabidopsis thaliana
874	24	75.0	231	58	AAW09757	Arabidopsis thaliana	957	24	75.0	324	81	AAW52011	Arabidopsis thaliana
875	24	75.0	231	59	AAW09757	Arabidopsis thaliana	958	24	75.0	325	82	AAW52011	Arabidopsis thaliana
876	24	75.0	231	60	AAW09757	Arabidopsis thaliana	959	24	75.0	326	83	AAW52011	Arabidopsis thaliana
877	24	75.0	231	61	AAW09757	Arabidopsis thaliana	960	24	75.0	327	84	AAW52011	Arabidopsis thaliana
878	24	75.0	231	62	AAW09757	Arabidopsis thaliana	961	24	75.0	328	85	AAW52011	Arabidopsis thaliana
879	24	75.0	231	63	AAW09757	Arabidopsis thaliana	962	24	75.0	329	86	AAW52011	Arabidopsis thaliana
880	24	75.0	231	64	AAW09757	Arabidopsis thaliana	963	24	75.0	330	87	AAW52011	Arabidopsis thaliana
881	24	75.0	231	65	AAW09757	Arabidopsis thaliana	964	24	75.0	331	88	AAW52011	Arabidopsis thaliana
882	24	75.0	231	66	AAW09757	Arabidopsis thaliana	965	24	75.0	332	89	AAW52011	Arabidopsis thaliana
883	24	75.0	231	67	AAW09757	Arabidopsis thaliana	966	24	75.0	333	90	AAW52011	Arabidopsis thaliana
884	24	75.0	231	68	AAW09757	Arabidopsis thaliana	967	24	75.0	334	91	AAW52011	Arabidopsis thaliana
885	24	75.0	231	69	AAW09757	Arabidopsis thaliana	968	24	75.0	335	92	AAW52011	Arabidopsis thaliana
886	24	75.0	231	70	AAW09757	Arabidopsis thaliana	969	24	75.0	336	93	AAW52011	Arabidopsis thaliana

960 24 75.0 314 21 AAN90783
 961 24 75.0 314 22 AAN90465
 962 24 75.0 314 22 AAM93824
 963 24 75.0 315 22 AAR76736
 964 24 75.0 315 23 ABF60912
 965 24 75.0 315 23 ABF60913
 966 24 75.0 317 15 AAR54718
 967 24 75.0 317 21 AAG37542
 968 24 75.0 318 15 AAR47069
 969 24 75.0 318 15 AAR47071
 970 24 75.0 318 21 AAG45095
 971 24 75.0 318 23 ABP60860
 972 24 75.0 318 23 ABP60943
 973 24 75.0 319 21 AAN201867
 974 24 75.0 319 21 AAG42777
 975 24 75.0 319 21 AAY52215
 976 24 75.0 320 14 AAM41279
 977 24 75.0 320 18 AAM48217
 978 24 75.0 320 23 ABP60878
 979 24 75.0 320 23 ABP61149
 980 24 75.0 321 21 AAB29257
 981 24 75.0 321 21 AAB34747
 982 24 75.0 321 21 AAY72341
 983 24 75.0 321 23 ABP60699
 984 24 75.0 321 23 ABG61541
 985 24 75.0 321 23 AAR50461
 986 24 75.0 322 13 AAR22209
 987 24 75.0 322 23 AAE23133
 988 24 75.0 323 21 AAG22970
 989 24 75.0 323 22 AAB33982
 990 24 75.0 323 23 AAE23135
 991 24 75.0 324 12 AAF12427
 992 24 75.0 324 12 AAR13275
 993 24 75.0 324 13 AAF11833
 994 24 75.0 324 18 AAM31297
 995 24 75.0 324 18 AAM31007
 996 24 75.0 324 20 AAK77731
 997 24 75.0 324 20 AAM21493
 998 24 75.0 324 21 AAN90783
 999 24 75.0 324 23 ABP92876
 1000 24 75.0 325 21 AAG10313

ALIGNMENT

RESULT 1

AAR91721

ID AAR91721 standard; Protein: 5 AA.

XX

AC AAR91721;

XX 17-NOV-1996 (first entry)

XX NAP subsequence.

DE

XX

XX Ac-AARF, Hs-AARF, NaARF, Aa-AARF, Ad-AARF, anti-coagulant,

KW nematode-extracted anti-coagulant protein; serine protease;

KW nematode; thrombosis; parasitic worm.

XX Synthetic.

XX

XX W09612021-A2.

XX

XX 25-APR-1996.

XX

XX 17-OCT-1995; 9505-US14241.

XX

XX 05-JUN-1995; 9505-0486399.

XX 18-OCT-1994; 9505-0326110.

XX 05-JUN-1995; 9505-0463965.

XX 05-JUN-1995; 9505-0465380.

XX 05-JUN-1995; 9505-0486397.

XX (CORV-) CORVAS INT INC.
 PA Berquon PW, Ganssems YGJ, Jaspers IS, Larochie VR;
 XX Lauwereys MJ, Messens JH, Mayle M, Staussens PH;
 FI Vlasak GP;
 XX WFL, 1996, 222067/22.
 DE Proteins with anti-coagulant activity: serine protease inhibitory
 XX activity - isolated from nematodes and useful to inhibit blood
 PT coagulation
 XX Claim 10; Page 144; 243pp; English.
 XX Proteins with anti-coagulant activity: serine protease inhibitory
 CC activity, isolated from nematodes, are useful to inhibit blood
 CC coagulation. The proteins can be added to blood collection tubes
 CC defining the collection of mammalian plasma. They are also useful
 CC to prevent or inhibit thrombosis, and may be given alone or in
 CC combination with other therapeutic or in vivo diagnostic agents.
 CC The proteins can serve as immunogens to raise antibodies for use in
 CC the diagnosis and identification of NAP concn. levels in biological
 CC fluids, e.g. to detect mammalian infection with a parasitic worm.
 CC They can also be used as immunogens in prophylactic and therapeutic
 CC vaccines against parasitic worm infection. The proteins may
 CC double the clotting time of human plasma in thrombin time assays
 CC when present at 10-50 nMol, and double the clotting time of human
 CC plasma in activated partial thrombin time assays when present
 CC at 10-100 nMol.
 CC The anticoagulant proteins are pref. derived from
 CC *Ancylostoma caninum*, *A. ceylanicum*, *A. duodenale*, *Necator*
 CC *americanus* or *Helicostoma* polychaeta.
 CC The proteins pref. have 2 NAP domains and specifically inhibit
 CC the catalytic activity of the factor VIIa/TF complex in the
 CC presence of factor Xa or a catalytically inactive factor Xa derivative.
 CC do not specifically inhibit the activation of factor VIII in the
 CC absence of TF and do not specifically inhibit prothrombinase.
 CC Proteins derived in AAR91720 E91742 are preferred subsequences
 CC of a genetic NAP sequence.
 XX Sequence 5 AA:
 SX

Query Match 93.8%; Score 40; Dk 17; Length 5;

Best local Similarity 100.0%; Pred. No. 7; Res 05;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GFYRN 7

Db 1 GFYRN 5

RESULT 2

AAY30440

ID AAY30440 standard; Peptide: 5 AA.

XX

AC AAY30440;

XX 15-NOV-1999 (first entry)

XX

XX Nematode extracted anticoagulant protein fragment.

DE

XX Nematode extracted anticoagulant protein; NAP, anti-coagulant;

KW serine protease inhibitor; NAP domain; factor VIIa/TF.

XX Unidentified.

XX OS

XX US9505294-A.

XX

XX 21-SEP-1999.

XX

XX 19 APR-1996; 9605-0634641.

XX

PD 25 APR 1996.
 XX
 PF 17-OCT-1995; 95WO-0513231.
 XX
 PR 05 JUN-1995; 950S-0486399.
 PR 18-OCT-1994; 940S-0326110.
 PR 05 JUN-1995; 950S-0461965.
 PR 05 JUN-1995; 950S-0455380.
 PR 05 JUN-1995; 950S-0456397.
 XX
 PA (ORV-) CORVAS INT INC.
 XX
 PF Bertram PM, Ganssmans YGJ, Jaspers LS, Laroché YR;
 P1 Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;
 P1 Vlasuk GP;
 XX
 DR WPI: 1996-222907/22.
 XX
 XX Proteins with anticoagulant and/or serine protease inhibitory
 PT activity - isolated from nematodes and useful to inhibit blood
 PT coagulation
 XX
 PS Claim 26: Page 147; 243pp; English.
 XX
 XX Proteins with anticoagulant and/or serine protease inhibitory
 CC activity, isolated from nematodes, are useful to inhibit blood
 CC coagulation. The proteins can be added to blood collection tubes
 CC defining the collection of mammalian plasma. They are also useful
 CC to prevent or inhibit thrombosis, and may be given alone or in
 CC combination with other therapeutic or in vivo diagnostic agents.
 CC The proteins can serve as immunogens to raise antibodies for use in
 CC the diagnosis and identification of NAP concn. levels in biological
 CC fluids, e.g. to detect mammalian infection with a parasitic agent.
 CC They can also be used as immunogens in prophylactic and therapeutic
 CC vaccines against parasitic worm infection. The proteins may
 CC double the clotting time of human plasma in prothrombin time assays
 CC when present at 10-50 nMol, and double the clotting time of human
 CC plasma in activated partial thromboplastin time assays when present
 CC at 10-100 nMol
 CC The anticoagulant proteins are prot. derived from
 CC Ancylostoma caninum, A. ceylanicum, A. duodenale, Necator
 CC americanus or Heligmosomoides polygyrus.
 CC The proteins prot. have 2 NAP domains and specifically inhibit
 CC the catalytic activity of the factor VIIa/TF complex in the
 CC presence of factor Xa or a catalytically inactive factor Xa deriv.
 CC do not specifically inhibit the activation of factor VIIa in the
 CC absence of TF and do not specifically inhibit prothrombinase.
 CC Proteins given in AAF91729 E91732 are preferred subsequences
 CC of a genetic NAP sequence.

XX Sequence 7 AA:

Query Match 93.8%; Score 40; DB 17; Length 7;
 Best Local Similarity 100.0%; Prod. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GFYRN 7
 D6 3 GFYRN 7

RESULT 5

AAY40449
 ID AAY40449 standard; Peptide: 7 AA.

XX
 AC AAY40449;

XX
 DT 15-NOV-1999 (first entry)

XX Nematode extracted anticoagulant protein fragment.

DE
 XX Nematode extracted anticoagulant protein. NAP: anticoagulant;
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.

XX Unidentified.
 OS
 XX US955294-A.
 PN
 XX 21-SEP-1999.
 PD
 XX 19-APR-1996; 960S-0644641.
 XX
 PR 19 APR-1996; 960S-0644641.
 PR 18-OCT-1994; 940S-0326110.
 PR 05 JUN-1995; 950S-0451965.
 PR 05 JUN-1995; 950S-0455380.
 PR 05 JUN-1995; 950S-0456397.
 PR 05 JUN-1995; 950S-0456399.
 PR 17-OCT-1995; 95WO-0513231.
 XX
 PA (ORV-) CORVAS INT INC.
 XX
 PF Bertram PM, Ganssmans YGJ, Jaspers LS, Laroché YR;
 P1 Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;
 P1 Vlasuk GP;
 XX
 DR WPI: 1999-534569/45.
 XX
 XX Screening an isolated protein for Nematode extracted Anticoagulant
 PT Protein domains
 XX
 PS Disclosure: Volume 166; 167pp; English.
 XX
 XX The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP) fragment. The protein has activity as an anticoagulant
 CC and/or serine protease inhibitor. The protein contains at least one
 CC NAP domain which has a better inhibitory activity for factor VIIa/TF.
 CC The specification describes a method for screening an isolated protein
 CC in a test system for factor VIIa/TF selective inhibitory activity.
 CC The method comprises determining the time to clotting effected by a
 CC concentration of the isolated protein in an *ex vivo* prothrombin time
 CC (PT) assay and an *ex vivo* activated partial thromboplastin time (APTT)
 CC assay; calculating prolongation of clotting effected by the isolated
 CC protein in each of the PT and APTT assays, with respect to a baseline
 CC clotting value for each assay, where prolongation of clotting is
 CC calculated as fold elevation of clotting time relative to a baseline
 CC clotting value, where a doubling of clotting time is deemed a two fold
 CC elevation; and calculating a PT to APTT prolongation ratio, where a
 CC ratio at least one is indicative of factor VIIa/TF inhibitory activity.
 CC The method is useful for determining if a protein has factor VIIa/TF
 CC inhibitory activity.

XX Sequence 7 AA:

Query Match 93.8%; Score 40; DB 20; Length 7;
 Best Local Similarity 100.0%; Prod. No. 7.8e+05;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GFYRN 7
 D6 3 GFYRN 7

RESULT 6

AAR15344
 ID AAR15344 standard; Peptide: 7 AA.

XX
 AC AAR15344;

XX 19-DEC-2000 (first entry)

XX NAP domain fragment #11.

DE
 XX Nematode-extracted anticoagulant protein; NAP domain; blood clotting;
 KW canine hookworm; thrombosis; vaccine.

Unidentified.

OS XX Key Location/Qualifiers
 PH XX Misc-difference 1..2
 FI XX /label= OTHER
 FT XX /note= "one of these two residues must be either
 FT XX Glu or Asp"

XX XX US6087487-A.
 XX XX 11-JUL-2000.
 XX XX 12-FEB-1999; 950S-0249451.
 XX XX 17-OCT-1995; 95WO-0513231.
 XX XX 17-APR-1997; 970S-0809455.
 XX XX 18-OCT-1994; 940S-026110.
 XX XX 05-JUN-1995; 950S-0461965.
 XX XX 05-JUN-1995; 950S-0465390.
 XX XX 05-JUN-1995; 950S-0486397.
 XX XX 05-JUN-1995; 950S-0486399.
 XX XX (CORV-) CORVAS INT INC.

XX XX Lauwereys MJ, Stanssens PEH, Jaspers LS, Ganssemaes VOJ, Moxie M,
 FI Berquim PW, Messens JHL, Laboche YR, Vlasuk GP;
 XX WPI: 2000-531350/48

XX XX New cDNA molecule encoding a protein having factor XIa inhibitory
 PT activity for preventing and treating blood clotting disorders.
 PT comprises nematode-extracted anticoagulant protein domains.

XX XX Claim 4: Column 286; 197pp; English.

XX XX The present sequence is a fragment of the NAP domain (see AAB15347),
 CC which is found in all nematode-extracted anticoagulant proteins (NAPs).
 CC Proteins of this kind have been shown to be effective at preventing
 CC blood clotting without causing excessive bleeding. They can be used in
 CC blood collection tubes to aid the isolation of plasma from the blood, to
 CC prevent thrombosis which may be linked to the rupture of an
 CC atherosclerotic plaque, acute myocardial infarction, angina,
 CC thrombolytic therapy, percutaneous transluminal coronary angioplasty,
 CC disseminated intravascular coagulation, infarcted cancer and septic
 CC shock, and to produce antibodies. In the latter instance, the antibodies
 CC can be raised in order to detect infection by nematodes (the coding
 CC sequences can also be used for this) or as diagnostic tests. The proteins
 CC can also be used as vaccines against nematode parasites.

XX XX Sequence 7 AA:

Query Match 93.8%; Score 30; PP 21; Length 7;
 Best Local Similarity 100.0%; Pred. No. 7; 80-06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GYRN 7
 Dd 3 GYRN 7

RESULT 7
 AAY30420
 ID AAY30420 standard; Protein: 78 AA.
 XX AC AAY30420;
 XX DI 15-NOV-1999 (first entry)
 XX DE Mature nematode extracted anticoagulant protein A-ANAP31.
 XX KW Nematode extracted anticoagulant protein, AANAP31; AANAP42; AANAP46;
 XX FW Serine protease inhibitor, NAP domain; Factor VIIa/TF.
 XX OS Anacylostoma caninum.

OS XX Anacylostoma caninum.
 XX XX US5955294-A.
 XX XX 21-SEP-1999.
 XX XX 19-APR-1995; 960S-0634641.
 XX XX 19-APR-1996; 960S-0634641.
 XX XX 18-OCT-1994; 940S-0426110.
 XX XX 05-JUN-1995; 950S-0461965.
 XX XX 05-JUN-1995; 950S-0465390.
 XX XX 05-JUN-1995; 950S-0486397.
 XX XX 05-JUN-1995; 950S-0486399.
 XX XX 17-OCT-1995; 95WO-0513231.
 XX XX (CORV-) CORVAS INT INC.

XX XX Berquim PW, Ganssemaes VOJ, Jaspers LS, Moxie YR,
 FI Lauwereys MJ, Messens JHL, Moxie M, Stanssens PEH,
 DI Vlasuk GP;
 XX WPI: 1999-590563/45.

XX XX Screening an isolated protein for Nematode extracted Anticoagulant
 PT protein domains
 XX Disclosure: Columns 122-124; 197pp; English.

XX XX The present sequence represents a nematode extracted anti-coagulant
 CC protein (NAP). The protein has activity as an anti-coagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (APTT) assay, calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay, with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.

XX XX Sequence 78 AA:

Query Match 93.8%; Score 30; PP 20; Length 78;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 3 GYRN 7
 Dd 54 GYRN 58

RESULT 8
 AAB15305
 ID AAB15305 standard; Protein: 78 AA.
 XX AC AAB15305;
 XX XX 19-DEC-2000 (first entry)
 XX DE A. caninum nematode-extracted anticoagulant protein A-ANAP31.42.46.
 XX KW Nematode extracted anticoagulant protein, AANAP31; AANAP42; AANAP46;
 XX FW Serine protease inhibitor, NAP domain; Factor VIIa/TF.
 XX OS Anacylostoma caninum.

```

XX PN US6087487-A
XX PR
XX PD 11-JUL 2000.
XX PP
XX PT 12-FEB-1999; 960S-024451.
XX PR 17-OCT-1995; 95W0-US14241.
XX PR 17-APR-1997; 970S-0809455.
XX PR 18-OCT-1994; 940S-0326110.
XX PR 05-JUN-1995; 950S-0461965.
XX PR 05-JUN-1995; 950S-0465480.
XX PR 05-JUN-1995; 950S-0486497.
XX PR 05-JUN-1995; 950S-0486499.
XX PA (CORV-) CORVAS INT INC.
XX PT
XX PR Lauwereys MJ, Stanssens JHL, Jaspers JS, Laroché YP, Meyle M;
XX PR Borquim PW, Messens JHL, Laroché YP, Vlasuk GP;
XX PR WPI: 2000-541359/48.
XX PR N-PSDB: AAY3378.
XX PT New cDNA molecule encoding a protein having factor Xa inhibitory
XX PT activity for preventing and treating blood clotting disorders.
XX PT comprises nematode-extracted anticoagulant protein domains.
XX PR
XX PS Disclosure: Fig 16; 197pp; English.
XX CC The present sequence comprises the Ancylostoma caninum
XX CC nematode-extracted anticoagulant protein AcanAP3, AcanAP4 and
XX CC AcanAP46. Proteins of this kind have been shown to be effective at
XX CC preventing blood clotting without causing excessive bleeding. The
XX CC plasma can be used in blood collection tubes to aid the isolation of
XX CC rupture of an atherosclerotic plaque, atherosclerotic infarction,
XX CC angina, thrombolytic therapy, percutaneous transluminal coronary
XX CC angioplasty, disseminated intravascular coagulopathy, infection, cancer
XX CC and septic shock and to produce antibodies. In the latter instance, the
XX CC antibodies can be raised in order to detect infection by nematodes (the
XX CC coding sequence can also be used for this) or as diagnostic tests. The
XX CC proteins can also be used as a vaccine against nematode parasites.
XX PR
XX SQ Sequence 78 AA;
Query Match 92.9%; Score 40; DB 21; Length 78;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 3 GYRN 7
DB 54 GYRN 58
|||||
RESULT 9
AAY40499
ID AAY40499 standard; Protein: 82 AA.
XX AC
XX AC AAY40499;
XX DI 15-NOV-1999 (first entry)
XX DE
XX DE Nematode extracted anticoagulant protein AcanAP442.
XX PR
XX PR Nematode extracted anticoagulant protein AcanAP442; Nematode extracted
XX PR serine protease inhibitor; NAP domain; factor VIIa/TF.
XX PR
XX PR Ancylostoma caninum.
XX PN US5955294-A.
XX PD 21-SEP-1999.
XX PP

```

```

PE 19-APR-1996; 960S-0644641.
XX PR
XX PR 19-APR-1996; 960S-0644641.
XX PR 18-OCT-1994; 940S-0326110.
XX PR 05-JUN-1995; 950S-0461965.
XX PR 05-JUN-1995; 950S-0465480.
XX PR 05-JUN-1995; 950S-0486497.
XX PR 05-JUN-1995; 950S-0486499.
XX PR 17-OCT-1995; 95W0-US14241.
XX PA (CORV-) CORVAS INT INC.
XX PT
XX PR Borquim PW, Stanssens JHL, Jaspers JS, Laroché YP;
XX PR Lauwereys MJ, Messens JHL, Meyle M, Stanssens JHL;
XX PR Vlasuk GP;
XX PR WPI: 1999-539569/45.
XX PT Screening an isolated protein for nematode extracted Anticoagulant
XX PT Protein domains
XX PR
XX PR Disclosure: Column 111-112; 197pp; English.
XX CC The present sequence represents a nematode extracted anticoagulant
XX CC protein (NAP); the protein has activity as an anticoagulant and/or serine
XX CC protease inhibitor. The protein contains at least one NAP domain which
XX CC has selective inhibitory activity for Factor VIIa/TF. The specification
XX CC describes a method for screening an isolated protein at least one domain
XX CC for factor VIIa/TF selective inhibitory activity. The method comprises:
XX CC determining the time to clotting effected by a concentration of the
XX CC isolated protein in an ex vivo protein in time (PT) assay; and
XX CC activated partial thromboplastin time (APTT) assay; calculating
XX CC prolongation of clotting effected by the isolated protein in each of
XX CC the PT and APTT assay; with respect to a baseline clotting value for
XX CC each assay, where prolongation of clotting is calculated as fold
XX CC extension of clotting time relative to a baseline clotting value, where
XX CC a doubling of clotting time is deemed a two-fold extension; and
XX CC calculating a PT to APTT prolongation ratio, where a ratio of at least
XX CC one is indicative of factor VIIa/TF inhibitory activity. The method is
XX CC useful for determining if a protein has factor VIIa/TF inhibitory
XX CC activity.
XX SQ Sequence 82 AA;
Query Match 93.9%; Score 40; DB 20; Length 82;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Caps 0;
QY 3 GYRN 7
DB 51 GYRN 56
|||||
RESULT 10
AAY30422
ID AAY30422 standard; Protein: 82 AA.
XX AC
XX AC AAY30422;
XX DI 15-NOV-1999 (first entry)
XX DE
XX DE Mature nematode extracted anticoagulant protein AcanAP442.
XX PR
XX PR Nematode extracted anticoagulant protein NAP; NAP domain;
XX PR serine protease inhibitor; NAP domain; factor VIIa/TF.
XX PR
XX PR Ancylostoma caninum.
XX PN US5955294-A.
XX PD 21-SEP-1999.
XX PP
XX PP 19-APR-1996; 960S-0644641.

```

XX 19-APR-1996; 96US-0634641.
 PR 18-OCT-1994; 94US-0326110.
 PR 05-JUN-1995; 95US-0465380.
 PR 05-JUN-1995; 95US-0465380.
 PR 05-JUN-1995; 95US-0486397.
 PR 05-JUN-1995; 95US-0486399.
 PR 17-OCT-1995; 95WO-US13231.
 XX (CORV-) CORVAS INT INC.
 PA Lauwereys MJ, Stanssens PH, Jespers LS, Ganssens YL, Moyle M,
 PI Lauwereys MJ, Messens JIL, Lafache YS, Vlaek GP;
 PL Vlaek GP;
 XX WPI: 1999-531559/45
 DE Screening an isolated protein for Nematode-extracted Anticoagulant
 PT Protein domains
 XX Disclosure: Columns 135-136; 197pp; English.
 XX The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay, with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elongation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX SQ Sequence 82 AA;
 Query Match 93.8%; Score 30; DB 20; Length 82;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GFYRN 7
 Db 51 GFYRN 55
 RESULT 11
 AAB15293
 ID AAB15293 standard; Protein: 82 AA
 XX AAB15293;
 AC AAB15293;
 XX 19-DEC-2000 (first entry)
 XX A. ceylanicum nematode-extracted anticoagulant protein AecNAP432 #1.
 DE Nematode-extracted anticoagulant protein; AecNAP432; blood clotting;
 KW canine hookworm; thrombosis; vaccine.
 KW Ancylostoma ceylanicum.
 OS US6087487-A.
 XX 11-JUL-2000.
 XX 12-FEB-1999; 96US-0249451.
 PR 17-OCT-1995; 95WO-US13231.
 PR 18-OCT-1994; 94US-0326110.
 PR 05-JUN-1995; 95US-0465380.
 PR 05-JUN-1995; 95US-0486397.
 PR 05-JUN-1995; 95US-0486399.
 PR 17-OCT-1995; 95WO-US13231.

PR 17-OCT-1995; 95WO-US13231.
 PR 17-APR-1997; 97US-0809455.
 PR 18-OCT-1994; 94US-0326110.
 PR 05-JUN-1995; 95US-0465380.
 PR 05-JUN-1995; 95US-0465380.
 PR 05-JUN-1995; 95US-0486397.
 PR 05-JUN-1995; 95US-0486399.
 XX (CORV-) CORVAS INT INC.
 PA Lauwereys MJ, Stanssens PH, Jespers LS, Ganssens YL, Moyle M,
 PI Lauwereys MJ, Messens JIL, Lafache YS, Vlaek GP;
 XX WPI: 2000-531559/48.
 XX AEC NARA molecule encoding a protein having factor Xa inhibitory
 PT activity for preventing and treating blood clotting disorders,
 PI comprises nematode-extracted anticoagulant protein domains
 XX Disclosure: Fig 11; 197pp; English.
 XX The present sequence is the Ancylostoma ceylanicum nematode extracted
 CC anticoagulant protein AecNAP432. Proteins of this kind have been shown to
 CC be effective in preventing blood clotting without causing excessive
 CC bleeding. The protein can be used in blood collection tubes to aid the
 CC isolation of plasma from the blood, to prevent thrombosis which may be
 CC linked to the capture of an atherosclerotic plaque, acute myocardial
 CC infarction, angina, thrombolytic therapy, percutaneous transluminal
 CC coronary angioplasty, disseminated intravascular coagulopathy, infection,
 CC cancer and septic shock, and to produce antibodies. In the latter
 CC instance, the antibodies can be raised in order to detect infection by
 CC nematodes or as diagnostic tests. The protein can also be used as a
 CC vaccine against nematode parasites.
 XX Sequence 82 AA;
 Query Match 93.8%; Score 30; Length 82;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GFYRN 7
 Db 51 GFYRN 55
 RESULT 12
 AAB15307
 ID AAB15307 standard; Protein: 82 AA.
 XX AAB15307;
 AC AAB15307;
 XX 19-DEC-2000 (first entry)
 XX A. ceylanicum nematode-extracted anticoagulant protein AecNAP432 #2.
 DE Nematode-extracted anticoagulant protein; AecNAP432; blood clotting;
 KW canine hookworm; thrombosis; vaccine.
 KW Ancylostoma ceylanicum.
 OS US6087487-A.
 XX 11-JUL-2000.
 XX 12-FEB-1999; 96US-0249451.
 PR 17-OCT-1995; 95WO-US13231.
 PR 18-OCT-1994; 94US-0326110.
 PR 05-JUN-1995; 95US-0465380.
 PR 05-JUN-1995; 95US-0486397.
 PR 05-JUN-1995; 95US-0486399.
 PR 17-OCT-1995; 95WO-US13231.

XX PA (CORV-) CORVAS INT INC.
 XX PT Lauwereys MJ, Stammsens PER, Jaspers LS, Gansmans YGL, Moyle M;
 PT Berquim PW, Messens JHL, Latoche YR, Vlasuk GP;
 XX XX WPI: 2000-541559/48.
 XX XX New cDNA molecule encoding a protein having factor Va inhibitory
 PT activity for prevention and treating blood clotting disorders,
 PT comprises nematode-extracted anticoagulant protein domains.
 XX XX Disclousure: Fig 16; 197pp; English.
 XX CC The present sequence is the Ancylostoma caninum nematode extracted
 CC anticoagulant protein AcanAP442. Proteins of this kind have been shown to
 CC be effective at preventing blood clotting without causing excessive
 CC bleeding. The protein can be used in blood collection tubes to aid the
 CC isolation of plasma from the blood, to prevent thrombosis which may be
 CC linked to the rupture of an atherosclerotic plaque, acute myocardial
 CC infarction, angina, thrombolytic therapy, percutaneous transluminal
 CC coronary angioplasty, disseminated intravascular coagulopathy, infection,
 CC cancer and septic shock, and to produce antibodies. In the latter
 CC instances, the antibodies can be raised in order to detect infection by
 CC nematodes or as diagnostic tests. The protein can also be used as a
 CC vaccine against nematode parasites.
 XX XX Sequence 82 AA;

Query Match 93.8%; Score 40; Dk 21; Length 82;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 3 GYRN 7
 II III
 Ib 51 GYRN 55

RESULT 14
 AAY0425
 ID AAY0425 standard; Protein: 83 AA
 XX XX
 AC AAY0425;
 XX XX
 DT 15-NOV-1999 (first entry)
 DE Mature nematode extracted anticoagulant protein AduNAP741.
 XX XX
 KW Nematode extracted anticoagulant protein, NAF, anticoagulant,
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.

XX OS Ancylostoma duodenale,
 XX XX US5955294 A,
 XX XX 21-SEP-1999.
 XX XX 19-APR-1999; 960S-0634641.
 XX XX 19-APR-1999; 960S-0634641.
 XX XX 18-OCT-1994; 940S-0326110.
 XX XX 05-JUN-1995; 950S-0461965.
 XX XX 05-JUN-1995; 950S-0465480.
 XX XX 05-JUN-1995; 950S-0486397.
 XX XX 05-JUN-1995; 950S-0486399.
 XX XX 17-OCT-1995; 95W0-US14241.
 XX XX (CORV-) CORVAS INT INC.

XX XX Berquim PW, Gansmans YGL, Jaspers LS, Latoche YR,
 XX XX Lauwereys MJ, Messens JHL, Moyle M, Stammsens PER,
 XX XX Vlasuk GP;
 XX XX WPI: 2000-541559/48.

DR WPI: 1999-539569/45.
 XX XX Screening an isolated protein for Nematode extracted Anticoagulant
 PT Protein domains
 XX XX Disclousure: Columns 137-148; 197pp; English.
 XX XX The present sequence represents a nematode extracted anticoagulant
 CC protein (NAF). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein of at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an *ex vivo* prothrombin time (PT) assay and activating
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay, with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two-fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX XX Sequence 83 AA;

Query Match 93.8%; Score 40; Dk 20; Length 83;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

UY 3 GYRN 7
 II III
 Ib 55 GYRN 54

RESULT 14
 AAY0423
 ID AAY0423 standard; Protein: 84 AA
 XX XX
 AC AAY0423;
 XX XX
 DT 15-NOV-1999 (first entry)
 DE Mature nematode extracted anticoagulant protein AduNAP45J.
 XX XX
 KW Nematode extracted anticoagulant protein; NAF; anticoagulant;
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.

XX OS Ancylostoma caninum,
 XX XX US5955294-A,
 XX XX 21-SEP-1999.
 XX XX 19-APR-1999; 960S-0634641.
 XX XX 19-APR-1999; 960S-0634641.
 XX XX 18-OCT-1994; 940S-0326110.
 XX XX 05-JUN-1995; 950S-0461965.
 XX XX 05-JUN-1995; 950S-0465480.
 XX XX 05-JUN-1995; 950S-0486397.
 XX XX 05-JUN-1995; 950S-0486399.
 XX XX 17-OCT-1995; 95W0-US14241.
 XX XX (CORV-) CORVAS INT INC.

XX XX Berquim PW, Gansmans YGL, Jaspers LS, Latoche YR,
 XX XX Lauwereys MJ, Messens JHL, Moyle M, Stammsens PER,
 XX XX Vlasuk GP;
 XX XX WPI: 1999-539569/45.

XX Screening an isolated protein for Nematode-extracted Anticoagulant
 PT Protein domains
 XX
 PS Disclosure: Columns 135-136; 197pp; English.
 XX
 CC The present sequence represents a nematode-extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay; with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two-fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.

XX
 SQ Sequence 84 AA;

Query Match 93.8%; Score 30; DP 20; Length 84;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 I I I I I
 DB 56 GYRN 60

RESULT 15
 AAY30424
 ID AAY30424 standard; Protein; 84 AA.
 AC AAY30424;
 XX
 DT 15-NOV-1999 (first entry)
 DE Mature nematode extracted anticoagulant protein AcaNAP47d1.
 DF
 EE Nematode extracted anticoagulant protein. NAP, anticoagulant.
 FW Serine protease inhibitor; NAP domain; factor VIIa/TF.
 KW
 XX Ancylostoma caninum.
 OS
 SS US5955294-A.
 PN
 XX
 PD 21-SEP-1999.
 XX
 PF 19-APR-1996; 960S-0634641.
 XX
 PR 19-APR-1996; 960S-0634641.
 PR 18-OCT-1994; 940S-0426110.
 PR 05-JUN-1995; 950S-0461965.
 PR 05-JUN-1995; 950S-0465360.
 PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 PR 17-OCT-1995; 95W0-US13231.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 XX Berqum PW, Gansmaus YGJ, Jaspers LS, Laroche YR;
 PI Lauwereys MJ, Meessens JHL, Moyle M, Staussens PEH;
 VIasuk GP;
 XX
 DR WPI: 1999-54956/45.
 XX

PT Screening an isolated protein for Nematode-extracted Anticoagulant
 PT Protein domains
 XX
 PS Disclosure: Columns 135-138; 197pp; English.
 XX
 CC The present sequence represents a nematode-extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay; with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two-fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.

XX
 SQ Sequence 84 AA;

Query Match 93.8%; Score 30; DP 20; Length 84;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 I I I I I
 DB 56 GYRN 60

RESULT 16
 AAY30432
 ID AAY30432 standard; Protein; 84 AA.
 AC AAY30432;
 XX
 DT 15-NOV-1999 (first entry)
 DE Mature nematode extracted anticoagulant protein AcaNAPe2.
 DF
 EE Nematode extracted anticoagulant protein. NAP, anticoagulant;
 FW Serine protease inhibitor; NAP domain; factor VIIa/TF.
 KW
 XX Ancylostoma caninum.
 OS
 SS US5955294-A.
 PN
 XX
 PD 21-SEP-1999.
 XX
 PF 19-APR-1996; 960S-0634641.
 XX
 PR 19-APR-1996; 960S-0634641.
 PR 18-OCT-1994; 940S-0426110.
 PR 05-JUN-1995; 950S-0461965.
 PR 05-JUN-1995; 950S-0465360.
 PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 PR 17-OCT-1995; 95W0-US13231.
 XX
 PA (CORV-) CORVAS INT INC.
 XX
 XX Berqum PW, Gansmaus YGJ, Jaspers LS, Laroche YR;
 PI Lauwereys MJ, Meessens JHL, Moyle M, Staussens PEH;
 VIasuk GP;
 XX
 DR WPI: 1999-54956/45.
 XX

PT Screening an isolated protein for Nematode-extracted Anticoagulant

PI Protein domains
 XX Discrepancy: columns 142-144 197pp: English.
 XX
 CC The present sequence represents a nematode extracted anticoagulant protein (RAP). The protein has activity as an anticoagulant and/or serine protease inhibitor. The protein contains at least one NAB domain which has selective inhibitory activity for factor VIIa/TF. The specification describes a method for screening an isolated protein at least one domain for factor VIIa/TF selective inhibitory activity. The method comprises determining the time to clotting effected by a concentration of the isolated protein in an *ex vivo* prothrombin time (PT) assay and an *ex vivo* activated partial thromboplastin time (APTT) assay; calculating prolongation of clotting effected by the isolated protein in each of the PT and APTT assay, with respect to a baseline clotting value for each assay, where prolongation of clotting is calculated as fold elevation of clotting time relative to a baseline clotting value, where a doubling of clotting time is deemed a two-fold elevation; and calculating a PI to APTT prolongation ratio, where a ratio at least one is indicative of factor VIIa/TF inhibitory activity. The method is useful for determining if a protein has factor VIIa/TF inhibitory activity.

XX
 SQ Sequence 84 AA;
 Query Match 93.8%; Score 30; DB 20; Length 84;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
 I I I I I
 I b 55 GFYRN 59

RESULT 17
 AAR15417
 ID AAR15417 standard; Protein: 84 AA;
 AC AAR15417;

XX 19 DEC-2000 (first entry)
 XX
 XX A. caninum nematode-extracted anticoagulant protein AcanAPE2 (mature).

XX Nematode-extracted anticoagulant protein: AcanAPE2; blood clotting;
 KW canine hookworm; thrombosis; vaccine;
 XX
 XX Ancylostoma caninum.

OS
 XX US6087487-A
 XX
 XX 11-JUL-2000.

XX
 XX 12-FEB-1999; 990S-0249451.
 XX
 XX 17-OCT-1995; 950S-0814241.
 XX 17-APR-1997; 970S-0809455.
 XX 18-OCT-1994; 940S-0326110.
 XX 05-JUN-1995; 950S-0461965.
 XX 05-JUN-1995; 950S-0465480.
 XX 05-JUN-1995; 950S-0486497.
 XX 05-JUN-1995; 950S-0486495.

XX (CORV-) CORVAS INT INC.
 XX
 XX Lammertys MJ, Stanssens PER, Jaspers LS, Gaussemans YGJ, Moyle M;
 P1 Borum LW, Messens JHJ, Lapoche YK, Vlasak GP;
 XX WPL: 2000-541459/48
 XX N PSL00; AAR14475.

XX New cDNA molecule encoding a protein having factor Xa inhibitory
 P1 activity for preventing and treating blood clotting disorders,

PI comprises nematode-extracted anticoagulant protein domains
 XX
 XX Example A: Fig 16; 197pp: English.
 XX
 CC The present sequence is the Ancylostoma caninum nematode-extracted anticoagulant protein AcanAPE2. Proteins of this kind have been shown to be effective at preventing blood clotting without causing excessive bleeding. The protein can be used in blood collection tubes to aid the isolation of plasma from the blood, to prevent thrombosis which may be linked to the rupture of an atherosclerotic plaque, acute myocardial infarction, angina, thrombolytic therapy, percutaneous transluminal coronary angioplasty, disseminated intravascular coagulopathy, infection, cancer and septic shock, and to produce antibodies. In the latter instance, the antibodies can be raised in order to detect infection by nematodes (the coding sequence can also be used for this) or as diagnostic tests. The protein can also be used as a vaccine against nematode parasites.

XX
 SQ Sequence 84 AA;
 Query Match 93.8%; Score 30; DB 21; Length 84;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
 I I I I I
 I b 55 GFYRN 59

RESULT 18
 AAM91998
 ID AAM91998 standard; Protein: 86 AA;
 XX
 XX AAM91998;

XX 05-NOV-2001 (first entry)
 XX
 XX Human digestive system antigen SEQ ID NO: 1447.

XX Human digestive system antigen, gene therapy, cancer, appendicitis;
 KW ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;
 XX digestive system disorder; Meckel's diverticulum.

XX Homo sapiens.
 XX
 XX W0200155414-A2.

XX 02-AUG-2001.
 XX
 XX 17-JAN-2001; 2001W0 US01424.

XX 31-JAN-2000; 2000US-0179065.
 XX 04-FEB-2000; 2000US-0180628.
 XX 24-FEB-2000; 2000US-0184664.
 XX 02-MAR-2000; 2000US-0186350.
 XX 16-MAR-2000; 2000US-0189874.
 XX 17-MAR-2000; 2000US-0190676.
 XX 18-APR-2000; 2000US 0198123.
 XX 19-MAY-2000; 2000US-0205515.
 XX 07-JUN-2000; 2000US-0209467.
 XX 28-JUN-2000; 2000US-0214886.
 XX 30-JUN-2000; 2000US 0215145.
 XX 07-JUL-2000; 2000US-0216647.
 XX 11-JUL-2000; 2000US 0216880.
 XX 11-JUL-2000; 2000US-0217487.
 XX 14-JUL-2000; 2000US-0217496.
 XX 26-JUL-2000; 2000US-0218290.
 XX 26-JUL-2000; 2000US-0220964.
 XX 26-JUL-2000; 2000US-0220964.
 XX 14-AUG-2000; 2000US-0224518.
 XX 14-AUG-2000; 2000US-0224519.
 XX 14-AUG-2000; 2000US 0225214.
 XX 14-AUG-2000; 2000US-0225214.

RESULT 19

AA91701 ID AAY30421 standard: Protein: 89 AA.

XX AC AAY30421;
XX DT 15-NOV-1999 (first entry)
XX DE Mature nematode-extracted anticoagulant protein AcenAP4d1.
XX KW Nematode-extracted anticoagulant protein, NAP, anticoagulant,
XX KW serine protease inhibitor; NAP domain; factor VIIa/TF.
XX OS Ancylostoma ceylanicum.

XX PN US5955294 A.

XX PD 21-SEP-1999.

XX PF 19-APR-1996; 9605-0534641.

XX PR 19-APR-1996; 9605-0634641.

XX PR 18-OCT-1994; 9405-0325113.

XX PR 05-JUN-1995; 9505-0461965.

XX PR 05-JUN-1995; 9505-0465380.

XX PR 05-JUN-1995; 9505-0486397.

XX PR 05-JUN-1995; 9505-0486399.

XX PR 17-OCT-1995; 9505-0513231.

XX PA (CORV-) CORVAS INT INC.

XX PI Berquim PW, Ganssmans YGJ, Jespers LS, Laroche YR,

XX PI Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;

XX PI Vlasak GP;

XX WP1: 1999-539569/45.

XX PT Screening an isolated protein for Nematode-extracted Anticoagulant

XX PI Protein domains

XX PS Disclosure; Columns 144-146; 197pp; English.

XX CC The present sequence represents a nematode-extracted anticoagulant
XX CC protein (NAP). The protein has activity as an anticoagulant and/or serine
XX CC protease inhibitor. The protein contains at least one NAP domain which
XX CC has selective inhibitory activity for factor VIIa/TF. The specification
XX CC describes a method for screening an isolated protein at least one domain
XX CC for factor VIIa/TF selective inhibitory activity. The method comprises
XX CC determining the time to clotting effected by a concentration of the
XX CC isolated protein in an ex vivo fibrinogen time (PT) assay and an ex vivo
XX CC activated partial thromboplastin time (APTT) assay; calculating
XX CC prolongation of clotting effected by the isolated protein in each of
XX CC the PT and APTT assay, with respect to a baseline clotting value for
XX CC each assay; where prolongation of clotting is calculated as fold
XX CC elevation of clotting time relative to a baseline clotting value, where
XX CC a doubling of clotting time is deemed a two-fold elevation; and
XX CC calculating a PI to APTT prolongation ratio, where a ratio at least
XX CC one is indicative of factor VIIa/TF inhibitory activity. The method is
XX CC useful for determining if a protein has factor VIIa/TF inhibitory
XX CC activity.

XX SQ Sequence 89 AA;

Query Match 93.8%; Score 40; DB 20; Length 89;

Best Local Similarity 100.0%; Prod. No. 50;

Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

07 4 GYEN 7

10 61 GYEN 65

RESULT 20

AA91701 ID AAR91701 standard: Protein: 91 AA.

XX AC AAR91701;

XX DT 17-NOV-1996 (first entry)

XX DE AcenAPe2.

XX KW AcenAP, HcenAP, NamAP; AcenAP; AcenAP; anticoagulant;
XX KW nematode-extracted anticoagulant protein; serine protease;
XX KW nematode; thrombosis; parasitic worm.
XX OS Ancylostoma caninum.

XX PN W09612021-A2.

XX PD 25-APR-1996.

XX PF 17-OCT-1995; 9505-0513231.

XX PR 05-JUN-1995; 9505-0486399.

XX PR 18-OCT-1994; 9405-0325113.

XX PR 05-JUN-1995; 9505-0461965.

XX PR 05-JUN-1995; 9505-0465380.

XX PR 05-JUN-1995; 9505-0486397.

XX PA (CORV-) CORVAS INT INC.

XX PI Berquim PW, Ganssmans YGJ, Jespers LS, Laroche YR;

XX PI Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH;

XX PI Vlasak GP;

XX WP1: 1999-539569/45.

XX DR N-PSDB: AAT12947.

XX PT Proteins with anticoagulant and/or serine protease inhibitory

XX PI activity - isolated from nematodes and useful to inhibit blood

XX PI coagulation

XX PS Claim 89 - 96; Fig 9; 24pp; English.

XX CC Proteins with anticoagulant and/or serine protease inhibitory
XX CC activity, isolated from nematodes, are useful to inhibit blood
XX CC coagulation. The proteins can be added to blood collection tubes
XX CC defining the collection of mammalian plasma. They are also useful
XX CC to prevent or inhibit thrombosis, and may be given alone or in
XX CC combination with other therapeutic or in vivo diagnostic agents.
XX CC The proteins can serve as immunogens to raise antibodies for use in
XX CC the diagnosis and identification of NAP concn. levels in biological
XX CC fluids, e.g. to detect mammalian infection with a parasitic worm.
XX CC They can also be used as immunogens in prophylactic and therapeutic
XX CC vaccines against parasitic worm infection. The proteins may
XX CC double the clotting time of human plasma in prothrombin time assays
XX CC when present at 10-50 nMol, and double the clotting time of human
XX CC plasma in activated partial thrombin time assays when present
XX CC at 10-100 nMol.

XX CC The anticoagulant proteins are prot. derived from

XX CC Ancylostoma caninum, A. ceylanicum, A. duodenale, Necator

XX CC americanus or Heligmosomoides polygyrus.

XX CC The proteins prot. have 2 NAP domains and specifically inhibit

XX CC the catalytic activity of the factor VIIa/TF complex in the

XX CC presence of factor Xu or a catalytically inactive factor Xu derivative.

XX CC do not specifically inhibit the activation of factor VIII in the

XX CC absence of TF and do not specifically inhibit prothrombinase.

XX SQ Sequence 91 AA;

Query Match 93.8%; Score 40; DB 17; Length 91;

Best Local Similarity 100.0%; Prod. No. 51;

Matches 5; Conservation 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIIII
Db 62 GYRN 66

RESULT 21

AA30394
ID AAY30394 standard; Protein: 91 AA.

XX AC AAY30394;

XX DT 15-NOV-1999 (first entry)

XX DE Nematode extracted anticoagulant protein AcNAP2.

XX EW Nematode extracted anticoagulant protein; MAP, and anticoagulant;

XX KW serine protease inhibitor; NAP domain; factor VIIa/TF

XX OS Ancylostoma caninum.

XX PN US5455294-A.

XX PD 21-SEP-1999.

XX PF 19-APR-1996; 96US-0634641.

XX PR 19-APR-1996; 96US-0634641.

XX PR 18-OCT-1994; 94US-0326110.

XX PR 05-JUN-1995; 95US-0461965.

XX PR 05-JUN-1995; 95US-0465380.

XX PR 05-JUN-1995; 95US-0465380.

XX PR 05-JUN-1995; 95US-0465380.

XX PR 17-OCT-1995; 95WO-US13231.

XX PA (CORV-) CORVAS INT INC.

XX FI Berquin FW, Ganssmaus VGJ, Jespers LS, Lathue YK;

XX PI Lathue YK, Ganssmaus VGJ, Jespers LS, Lathue YK;

XX PI Vlasuk GP;

XX DR WPI: 1996-549569/45

XX DR N-PSDB: AA299999

XX PT Screening an isolated protein for Nematode-extracted Anticoagulant

XX PT Protein domains

XX PS Example 13; Fig 9; 197pp; English.

XX CC The present sequence represents a nematode extracted anticoagulant
XX CC protein (NAP). The protein has activity as an anticoagulant and/or serine
XX CC protease inhibitor. The protein contains at least one NAP domain which
XX CC has selective inhibitory activity for factor VIIa/TF. The specification
XX CC describes a method for screening an isolated protein at least one domain
XX CC for factor VIIa/TF selective inhibitory activity. The method comprises
XX CC determining the time to clotting effected by a concentration of the
XX CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
XX CC activated partial thromboplastin time (APTT) assay; calculating
XX CC prolongation of clotting effected by the isolated protein in each of
XX CC the PT and APTT assay, with respect to a baseline clotting value for
XX CC each assay, where prolongation of clotting is calculated as fold
XX CC elevation of clotting time relative to a baseline clotting value, where
XX CC a doubling of clotting time is deemed a two-fold elevation; and
XX CC calculating a PT to APTT prolongation ratio, where a ratio at least
XX CC one is indicative of factor VIIa/TF inhibitory activity. The method is
XX CC useful for determining if a protein has factor VIIa/TF inhibitory
XX CC activity.

XX SQ Sequence 91 AA;

Query Match 91.88; Score 30; DB 20; Length 91;
Best Local Similarity 100.00; Pred No. 1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
IIIII
Db 62 GYRN 66

RESULT 22

AA30454
ID AAY30454 standard; Protein: 91 AA.

XX AC AAY30454;

XX DT 15-NOV-1999 (first entry)

XX DE Nematode extracted anticoagulant protein AcNAP2.

XX EW Nematode extracted anticoagulant protein; MAP, and anticoagulant;

XX KW serine protease inhibitor; NAP domain; factor VIIa/TF.

XX OS Ancylostoma caninum.

XX PN US5455294-A.

XX PD 21-SEP-1999.

XX PF 19-APR-1996; 96US-0634641.

XX PR 19-APR-1996; 96US-0634641.

XX PR 18-OCT-1994; 94US-0326110.

XX PR 05-JUN-1995; 95US-0461965.

XX PR 05-JUN-1995; 95US-0465380.

XX PR 05-JUN-1995; 95US-0465380.

XX PR 17-OCT-1995; 95WO-US13231.

XX PA (CORV-) CORVAS INT INC.

XX FI Berquin FW, Ganssmaus VGJ, Jespers LS, Lathue YK;

XX PI Lathue YK, Ganssmaus VGJ, Jespers LS, Lathue YK;

XX PI Vlasuk GP;

XX DR WPI: 1996-549569/45.

XX PT Screening an isolated protein for Nematode-extracted Anticoagulant

XX PT Protein domains

XX PS Disclosure; Columns 175-176; 197pp; English.

XX CC The present sequence represents a nematode extracted anticoagulant
XX CC protein (NAP). The protein has activity as an anticoagulant and/or serine
XX CC protease inhibitor. The protein contains at least one NAP domain which
XX CC has selective inhibitory activity for factor VIIa/TF. The specification
XX CC describes a method for screening an isolated protein at least one domain
XX CC for factor VIIa/TF selective inhibitory activity. The method comprises
XX CC determining the time to clotting effected by a concentration of the
XX CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
XX CC activated partial thromboplastin time (APTT) assay; calculating
XX CC prolongation of clotting effected by the isolated protein in each of
XX CC the PT and APTT assay, with respect to a baseline clotting value for
XX CC each assay, where prolongation of clotting is calculated as fold
XX CC elevation of clotting time relative to a baseline clotting value, where
XX CC a doubling of clotting time is deemed a two-fold elevation; and
XX CC calculating a PT to APTT prolongation ratio, where a ratio at least
XX CC one is indicative of factor VIIa/TF inhibitory activity. The method is
XX CC useful for determining if a protein has factor VIIa/TF inhibitory
XX CC activity.

XX SQ Sequence 91 AA;

Query Match 91.88; Score 30; DB 20; Length 91;
Best Local Similarity 100.00; Pred No. 51;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

Db 6.2 GYRN 66
|||||

RESULT 24

AA015346
ID AAB15346 standard; Protein: 91 AA.

XX
AC AAB15346;

XX 19-DEC-2000 (first entry)

XX A. caninum nematode-extracted anticoagulant protein AcanAPc2.

XX Nematode-extracted anticoagulant protein: AcanAPc2; blood clotting

XX enzyme: blood clotting; thrombosis; parasitic worm.

XX Ancylostoma caninum.

XX US6087487-A.

XX 11 JUL-2000.

XX 12 FEB 1999; 950S-0249451.

XX 17-OCT-1995; 950S-0513241.

XX 17 APR-1997; 970S-0809455.

XX 18-OCT-1994; 940S-0426110.

XX 05-JUN-1995; 950S-0461965.

XX 05-JUN-1995; 950S-0465380.

XX 05-JUN-1995; 950S-0486397.

XX 05-JUN-1995; 950S-0486397.

XX (CORV-) CORVAS INT. INC.

XX Lauwereys MJ, Stanssens YGJ, Jaspers LS, Gausemans YGJ, Moyle M;

XX Berdum PW, Messous JHL, Laroche YB, Vlasuk GP.

XX WP1; 2000-541459/48.

XX N PSD8; AA074474.

XX New CLARA molecule encoding a protein having factor Xa inhibitory

XX activity for preventing and treating blood clotting disorders.

XX comprises nematode-extracted anticoagulant protein domains

XX Disclosure; Fig 11; 197pp; English.

XX The present sequence is the Ancylostoma caninum nematode-extracted

XX anticoagulant protein AcanAPc2. Proteins of this kind have been shown to

XX be effective at preventing blood clotting without causing excessive

XX bleeding. The protein can be used in blood collection tubes to aid the

XX isolation of plasma from the blood, to prevent thrombosis which may be

XX linked to the rupture of an atherosclerotic plaque, acute myocardial

XX infarction, angina, thrombolytic therapy, percutaneous transluminal

XX coronary angioplasty, disseminated intravascular coagulopathy, infection,

XX cancer and septic shock, and to produce antibodies. In the latter

XX instance, the antibodies can be raised in order to detect infection by

XX nematodes (the coding sequence can also be used for this) or as

XX diagnostic tests. The protein can also be used as a vaccine against

XX nematode parasites.

XX Sequence 91 AA;

Query Match

Best Local Similarity 92.89; Score 50; DB 21; Length 91;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 3 GYRN 7

Db 6.2 GYRN 66

RESULT 24

AA091709
ID AAR91709 standard; Protein: 97 AA.

XX
AC AAR91709;

XX 17-NOV-1996 (first entry)

XX AcanAP31.

XX AcanAP; HpaNAP; NamNAP; AcanAP; AcanAP; anticoagulant;

XX nematode; thrombosis; parasitic worm.

XX Ancylostoma caninum.

XX W-9512021-A2.

XX 25-APR-1996.

XX 17-OCT-1995; 950S-0513241.

XX 05-JUN-1995; 950S-0486397.

XX 18-OCT-1994; 940S-0426110.

XX 05-JUN-1995; 950S-0461965.

XX 05-JUN-1995; 950S-0465380.

XX 05-JUN-1995; 950S-0486397.

XX (CORV-) CORVAS INT. INC.

XX Berdum PW, Gausemans YGJ, Jaspers LS, Laroche YB;

XX Lauwereys MJ, Messous JHL, Moyle M, Stanssens YGJ;

XX Vlasuk GP;

XX WP1; 1999-222307/22.

XX N PSD8; AA112955.

XX Proteins with anticoagulant and/or serine protease inhibitory

XX activity - isolated from nematodes and useful to inhibit blood

XX coagulation

XX Claim 221; Fig 13D; 243pp; English.

XX Proteins with anticoagulant and/or serine protease inhibitory

XX activity, isolated from nematodes, are useful to inhibit blood

XX coagulation. The proteins can be added to blood collection tubes

XX to prevent or inhibit thrombosis, and may be given alone or in

XX combination with other therapeutic or diagnostic agents.

XX The proteins can serve as immunogens to raise antibodies for use in

XX the diagnosis and identification of NAP antigen levels in biological

XX fluids, e.g., to detect mammalian infection with a parasitic worm.

XX They can also be used as immunogens in prophylactic and therapeutic

XX vaccines against parasitic worm infection. The proteins may

XX double the clotting time of human plasma in prothrombin time assays

XX when present at 10-50 nMol, and double the clotting time of human

XX plasma in activated partial thromboplastin time assays when present

XX at 10-100 nMol.

XX The anticoagulant proteins are pref. derived from

XX Ancylostoma caninum, A. ceylanicum, A. de Bairei, Revator

XX americanus or Helicovermosis polygyrus.

XX The proteins pref. have 2 NAP domains and specifically inhibit

XX the catalytic activity of the factor VIIa/TF complex in the

XX presence of factor Xa or a catalytically inactive factor Xa derivative.

XX do not specifically inhibit the activation of factor VIIIa in the

XX absence of TF and do not specifically inhibit prothrombinase.

XX Sequence 97 AA;

Query Match

Best Local Similarity 93.88; Score 50; DB 17; Length 97;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 3 GYRN 7

XX Nematode extracted anticoagulant protein: NADP anticoagulant;
 KW serine protease inhibitor: NAP domain, factor VIIa/TF.
 XX Ancylostoma duodenale.
 OS
 XX US5955294-A.
 PN 21-SEP-1999.
 XX 19-APR-1996; 96DS-0634541.
 XX 19-APR-1996; 96DS-0634541.
 PR 18-OCT-1994; 94DS-0326110.
 PR 05-JUN-1995; 95DS-0461965.
 PR 05-JUN-1995; 95DS-0463380.
 PR 05-JUN-1995; 95DS-0486397.
 PR 05-JUN-1995; 95DS-0486399.
 PR 17-OCT-1995; 95WO-0513231.
 XX (CORV-) CORVAS INT INC.
 XX Berquim PW, Gausmanns YGJ, Jespers LS, Laroche YR;
 PI Lauwerens MJ, Messens JHL, Moyle M, Stanssens PEH;
 PI Vlasuk GP;
 XX WPI: 1999-539569/45.
 XX Screening an isolated protein for Nematode-extracted Anticoagulant
 PT Protein domains
 XX Disclosure: Column 111-112; 197pp; English.
 XX The present sequence represents a nematode-extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and a serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an assay platelet-rich plasma (PRP) assay and a factor
 CC activated partial thromboplastin time (APTT) assay, calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay, with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a twofold elevation, and
 CC calculating a PR to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX
 XX Sequence 102 AA:
 Query Match 93.8%; Score 30; DB 20; Length 102;
 Best local similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 3 GFYRN 7
 Db 74 GFYRN 78
 RESULT 28
 AAB15295
 ID AAB15295 standard; Protein: 102 AA.
 XX AAB15295.
 AC AAB15295.
 XX 19-DEC-2000 (first entry)
 DT
 XX A. duodenale nematode-extracted anticoagulant protein: AduNAP7.
 DE
 XX

KW Nematode extracted anticoagulant protein: AduNAP7. Blood clotting;
 KW serine protease inhibitor: thrombin-like molecule.
 XX Ancylostoma duodenale.
 OS
 XX US56087487-A.
 PN 11-JUL-2000.
 XX 12-FEB-1999; 96DS-0249451.
 XX 17-OCT-1996; 96WO-0513231.
 PR 17-APR-1997; 97DS-0909455.
 PR 18-OCT-1994; 94DS-0326110.
 PR 05-JUN-1995; 95DS-0461965.
 PR 05-JUN-1995; 95DS-0465480.
 PR 05-JUN-1995; 95DS-0486397.
 PR 05-JUN-1995; 95DS-0486399.
 XX (CORV-) CORVAS INT INC.
 XX Lauwerens MJ, Stanssens PEH, Jespers LS, Gausmanns YGJ, Moyle M;
 PI Berquim PW, Messens JHL, Laroche YR, Vlasuk GP;
 XX WPI: 2000-531359/48.
 XX N-PSDB: AAA73368.
 XX Raw cDNA molecule encoding a protein having factor Xa inhibitory
 CC activity; for use in a method for treating fibrinolytic disorders,
 CC comprises nematode extracted anticoagulant protein domains
 CC Disclosure: Fig 11; 197pp; English.
 XX The present sequence is the Ancylostoma duodenale nematode-extracted
 CC anticoagulant protein AduNAP7. It consists of a protein which has been shown to
 CC be effective at preventing blood clotting without causing excessive
 CC bleeding. The protein can be used in blood collection tubes to aid the
 CC isolation of plasma from the blood, to prevent thrombosis which may be
 CC linked to the nature of an atherosclerotic plaque, acute myocardial
 CC infarction, stroke, thrombolytic therapy, pericarditis, transmural
 CC coronary angioplasty, disseminated intravascular coagulation, and other
 CC cancer and septic shock, and to produce antibodies. In the latter
 CC instance, the antibodies can be raised in order to detect infection of
 CC nematodes (the coding sequence can also be used for this) or as
 CC diagnostic tests. The protein can also be used as a vaccine against
 CC nematode parasites.
 XX
 XX Sequence 102 AA:
 Query Match 92.9%; Score 20; DB 20; Length 102;
 Best local similarity 100.0%; Pred. No. 57;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 GFYRN 7
 Db 74 GFYRN 78
 RESULT 29
 AAY50398
 ID AAY50398 standard; Protein: 108 AA.
 XX AAY50398.
 AC AAY50398.
 XX 15-NOV-1999 (first entry)
 DT
 XX Nematode extracted anticoagulant protein: AduNAP4.
 DE

XX KW Nematode extracted anticoagulant protein; NAP; anticoagulant;
 XX KW serine protease inhibitor; NAP domain; factor VIIa/TF.
 XX CS Ancylostoma ceylanicum.
 XX PN US5955294-A.
 XX PD 21-SEP-1999.
 XX PF 19-APR-1996; 950S-0634641.
 XX PR 19-APR-1996; 950S-0634641.
 XX PR 18-OCT-1994; 940S-0326110.
 XX PR 05-JUN-1995; 950S-0465380.
 XX PR 05-JUN-1995; 950S-0465380.
 XX PR 05-JUN-1995; 950S-0486397.
 XX PR 17-OCT-1995; 950S-0486399.
 XX PR 17-OCT-1995; 950S-0486399.
 XX PA (CORV-) CORVAS INT INC.
 XX PI Berquim PW, Ganssmans YGL, Jaspers LS, Laroche YR,
 XX PI Lauwereys MJ, Messens JHL, Moyle M, Stanssens PER,
 XX PI Vlasak GP.
 XX DR WPI: 1999-539569/45
 XX PS Screening an isolated protein for Nematode extracted Anticoagulant
 XX PI Protein domains
 XX PS Disclosure; Column 109-110; 197pp; English.
 XX CC The present sequence represents a nematode-extracted anticoagulant
 XX CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 XX CC protease inhibitor. The protein contains at least one NAP domain which
 XX CC has selective inhibitory activity for factor VIIa/TF. The specification
 XX CC describes a method for screening an isolated protein at least one domain
 XX CC for factor VIIa/TF selective inhibitory activity. The method comprises
 XX CC determining the time to clotting effected by a concentration of the
 XX CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 XX CC activated partial thromboplastin time (APTT) assay.
 XX CC prolongation of clotting effected by the isolated protein in each of
 XX CC the PT and APTT assay with respect to a baseline clotting value for
 XX CC each assay, where prolongation of clotting is calculated as fold
 XX CC elevation of clotting time relative to a baseline clotting value, where
 XX CC a doubling of clotting time is deemed a two fold elevation, and
 XX CC calculating a PI to APTT prolongation ratio, where a ratio at least
 XX CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 XX CC useful for determining if a protein has factor VIIa/TF inhibitory
 XX CC activity.
 XX SQ Sequence 108 AA;
 Query Match 93.8%; Score 40; DB 20; Length 108;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 3 GPERN 7
 DB 80 GPERN 84
 RESULT 40
 ID AAB15292
 XX AAB15292 standard; protein; 108 AA.
 AC AAB15292;
 XX 19-DEC-2000 (first entry)
 XX A. ceylanicum nematode extracted anticoagulant protein AncyNAP4.
 XX DE

XX KW Nematode extracted anticoagulant protein; AncyNAP4; blood clotting;
 XX KW canine hookworm; thrombosts; vaccine.
 XX CS Ancylostoma ceylanicum.
 XX PN US6087487-A.
 XX PD 11-JUL-2000.
 XX PF 12-FEB-1999; 960S-0249451.
 XX PR 17-OCT-1995; 950S-0514241.
 XX PR 17-APR-1997; 970S-0809455.
 XX PR 18-OCT-1994; 940S-0326110.
 XX PR 05-JUN-1995; 950S-0465380.
 XX PR 05-JUN-1995; 950S-0465380.
 XX PR 05-JUN-1995; 950S-0486397.
 XX PR 05-JUN-1995; 950S-0486399.
 XX PA (CORV-) CORVAS INT INC.
 XX PI Lauwereys MJ, Stanssens PER, Jaspers LS, Ganssmans YGL, Moyle M,
 XX PI Berquim PW, Messens JHL, Laroche YR, Vlasak GP.
 XX DR WPI: 2000-531359/48.
 XX PS N-PSDB: AAA73364.
 XX CC New cDNA molecule encoding a protein having factor Xa inhibitory
 XX CC activity for preventing and treating blood clotting disorders,
 XX CC comprises nematode-extracted anticoagulant protein domains.
 XX PS Disclosure; Column 101-102; 197pp; English.
 XX CC The present sequence is the Ancylostoma ceylanicum nematode extracted
 XX CC anticoagulant protein AncyNAP4. Proteins of this kind have been shown to
 XX CC effectively prevent blood clotting with at least one factor Xa
 XX CC inhibition site. The protein can be used in blood collection tubes to aid the
 XX CC isolation of plasma from the blood to prevent thrombosis which may be
 XX CC linked to the rupture of an atherosclerotic plaque, acute myocardial
 XX CC infarction, angina, thrombolytic therapy, percutaneous transluminal
 XX CC coronary angioplasty, disseminated intravascular coagulation, infection,
 XX CC cancer and septic shock, and to produce antibodies. In the latter
 XX CC instance, the antibodies can be raised in order to detect infection by
 XX CC nematodes (the coding sequence can also be used for this) or as
 XX CC diagnostic tests. The protein can also be used as a vaccine against
 XX CC nematode parasites.
 XX SQ Sequence 108 AA;
 Query Match 93.8%; Score 40; DB 21; Length 108;
 Best Local Similarity 100.0%; Pred. No. 61;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 3 GPERN 7
 DB 80 GPERN 84
 RESULT 41
 ID AAY70540
 XX AAY70540 standard; peptide; 124 AA.
 AC AAY70540;
 XX 04-JUL-2000 (first entry)
 XX Maize plastid targeting transit peptide (b).
 XX DE

XX Maize: plastid targeting sequence, transit peptide.
KW Plastid ribosomal protein C19; subcellular localisation.
XX Zea mays.
XX Foy Location/Qualifiers
FT Misc-difference 4
FT /label= Unknown
FT /note= "Encoded by CNG"
FT Misc-difference 51
FT /label= Unknown
FT /note= "Encoded by AAR"
FT Misc-difference 55
FT /label= Unknown
FT /note= "Encoded by CNG"
FT Misc-difference 109
FT /label= Unknown
FT /note= "Encoded by GAR"
FT Misc-difference 122
FT /label= Unknown
FT /note= "Encoded by TN"
XX W0200012732-A2.
FN 09-MAR-2000.
XX 25-AUG-1999: 95W0-US18465
XX 28-AUG-1998: 98US-0098225
XX (PION-) PIONEER HI-BRED INT INC.
XX Benson RJ.
XX WPT: 2000-256647/22
XX N-PSDB: AA251833.
XX New oryzae targeting peptide 3rd and amino acid sequences are
XX useful in genetic engineering for modulating the subcellular
XX localization of heterologous proteins in plants
XX Claim 16: Page 44: 50pp: English.
XX The present sequence is a maize transit peptide which has been found to
XX the plastid ribosomal protein C19
XX this sequence can be used in genetic engineering for modulating
XX the subcellular localization of heterologous proteins in plants. In
XX particular, the transit peptide finds use in the localization of
XX proteins to plastids and compartments thereof.
XX Sequence 124 AA:
Query Match 93.9%; Score 30; DE 21; Length 124;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 6;
QY 3 GFYRN 7
DB 76 GFYRN 80
RESULT 32
ID ABB03987 standard: Protein; 138 AA.
XX ABB03987;
XX 08-JAN-2002 (first entry)
XX Human musculoskeletal system related polypeptide SEQ ID NO 1934.
XX Cytostatin, immunosuppressive, non-cyclic, non-peptidic, antitumor, anti-infla.

KW anti-allergic; hepatotropic; antidiabetic; anti-inflammatory; antitumor;
KW cytostatic; anti-infective; antitubercular; antiparasitic;
KW cardant; gene therapy; cancer; immune disorder; cardiovascular disorder;
KW neurological disorder; infection; human; secreted protein;
KW musculoskeletal system.
XX B566 sapiens.
XX W0200155367-A1.
XX 02-AUG-2001.
XX 17 JAN 2001. 2001W0-0501348.
XX 31-JAN-2000: 2000US-0176065.
XX 14 FEB 2000: 2000US-0187628.
XX 24-FEB-2000: 2000US-0184664.
XX 02-MAR-2000: 2000US-0186350.
XX 16 MAR 2000: 2000US-0189874.
XX 17-MAR-2000: 2000US-0190076.
XX 19 APR 2000: 2000US-0199122.
XX 19-MAY-2000: 2000US-0205515.
XX 07-JUN-2000: 2000US-0209467.
XX 28 JUN 2000: 2000US-0214886.
XX 30 JUN 2000: 2000US-0215135.
XX 07-JUL-2000: 2000US-0216447.
XX 07-JUL-2000: 2000US-0216880.
XX 11-JUL-2000: 2000US-0217487.
XX 11-JUL-2000: 2000US-0217496.
XX 14-JUL-2000: 2000US-0218290.
XX 26 JUL 2000: 2000US-0220963.
XX 24-JUL-2000: 2000US-0220964.
XX 14 AUG 2000: 2000US-0224518.
XX 14-AUG-2000: 2000US-0224519.
XX 14-AUG-2000: 2000US-0225213.
XX 14 AUG 2000: 2000US-0225214.
XX 14-AUG 2000: 2000US-0225266.
XX 14-AUG-2000: 2000US-0225267.
XX 14-AUG-2000: 2000US-0225368.
XX 14-AUG-2000: 2000US-0225470.
XX 14-AUG-2000: 2000US-0225447.
XX 14-AUG-2000: 2000US-0225757.
XX 14-AUG-2000: 2000US-0225758.
XX 14-AUG-2000: 2000US-0225759.
XX 14-AUG-2000: 2000US-0226379.
XX 22-AUG-2000: 2000US-0226681.
XX 22-AUG-2000: 2000US-0226868.
XX 22 AUG 2000: 2000US-0227192.
XX 23 AUG 2000: 2000US-0227009.
XX 30-AUG-2000: 2000US-0228924.
XX 01 SEP 2000: 2000US-0229387.
XX 01 SEP 2000: 2000US-0229443.
XX 01-SEP-2000: 2000US-0229444.
XX 01-SEP-2000: 2000US-0229445.
XX 05-SEP-2000: 2000US-0229509.
XX 05-SEP-2000: 2000US-0229513.
XX 06-SEP-2000: 2000US-0230437.
XX 06-SEP-2000: 2000US-0230438.
XX 08-SEP-2000: 2000US-0231242.
XX 08-SEP-2000: 2000US-0231243.
XX 08-SEP-2000: 2000US-0231244.
XX 08-SEP-2000: 2000US-0231413.
XX 08-SEP-2000: 2000US-0231414.
XX 08-SEP-2000: 2000US-0232080.
XX 08-SEP-2000: 2000US-0232081.
XX 12-SEP-2000: 2000US-0231968.
XX 14-SEP-2000: 2000US-0232377.
XX 14-SEP-2000: 2000US-0232398.
XX 14-SEP-2000: 2000US-0232399.
XX 14-SEP-2000: 2000US-0232400.
XX 14-SEP-2000: 2000US-0232401.
XX 14-SEP-2000: 2000US-0233063.
XX 14-SEP-2000: 2000US-0233064.

PR 05-JUN-1995; 96US-0461965.
 PR 05-JUN-1995; 96US-0465380.
 PR 05-JUN-1995; 96US-0486397.
 PR 05-JUN-1995; 96US-0486399.
 PR 17-OCT-1995; 96WO-US13231.
 XX
 XX (CORV-) CORVAS INT INC.
 XX
 XX Berquim PW, Gansseman YGJ, Jespers LS, Laroche YR;
 PI Lauwerijs MT, Messens JHL, Meyle M, Staessens PER;
 PI Vlasuk GP;
 XX
 XX WPI: 1999-539569/45.

XX Screening an isolated protein for Nematode-extracted Anticoagulant
 PI Protein domains

XX Disclosure, Fig 20; 197pp; English.

XX The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa. The specific domain
 CC describes a method for screening an isolated protein, at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay; with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.

XX Sequence 161 AA:

Query Match 93.8%; Score 40; DP 20; Length 161.
 Best Local Similarity 100.0%; Pct. Id. 91;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 II III
 Db 55 GYRN 59

RESULT 34

AAAY30436
 ID AAY30436 standard; Protein: 162 AA

XX AAY30436;

XX 15-NOV-1999 (first entry)

DE Mature nematode extracted anticoagulant protein AcanAP45.

XX Nematode extracted anticoagulant protein, NAP, anticoagulant
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.

XX Ancylostoma caninum.

XX US5955294-A.

XX 21-SEP-1999.

XX 19-APR-1996; 96US-0634641.

XX 19-APR-1996; 96US-0634641.

XX 18-OCT-1994; 94US-0326110.

XX 05-JUN-1995; 95US-0461965.

PR 05-JUN-1995; 96US-0465380.
 PR 05-JUN-1995; 96US-0486397.
 PR 05-JUN-1995; 96US-0486399.
 PR 17-OCT-1995; 96WO-US13231.
 XX
 XX (CORV-) CORVAS INT INC.
 XX
 XX Berquim PW, Gansseman YGJ, Jespers LS, Laroche YR;
 PI Lauwerijs MT, Messens JHL, Meyle M, Staessens PER;
 PI Vlasuk GP;
 XX
 XX WPI: 1999-539569/45.

XX Screening an isolated protein for Nematode-extracted Anticoagulant
 PI Protein domains

XX Disclosure, Fig 18; 197pp; English.

XX The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa. The specific domain
 CC describes a method for screening an isolated protein, at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay; with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.

XX Sequence 162 AA:

Query Match 93.8%; Score 40; DP 20; Length 162;
 Best Local Similarity 100.0%; Pct. Id. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 II III
 Db 56 GYRN 60

RESULT 35

AAAY30437
 ID AAY30437 standard; Protein: 162 AA.

XX AAY30437;

XX 15-NOV-1999 (first entry)

DE Mature nematode extracted anticoagulant protein AcanAP47.

XX Nematode extracted anticoagulant protein, NAP, anticoagulant;
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.

XX Ancylostoma caninum.

XX US5955294-A.

XX 21-SEP-1999.

XX 19-APR-1996; 96US-0634641.

XX 19-APR-1996; 96US-0634641.

XX 18-OCT-1994; 94US-0326110.

XX 05-JUN-1995; 95US-0461965.

XX 05-JUN-1995; 95US-0465380.

PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 PR 17-OCT-1995; 950S-0513241.
 XX
 XX (CORV-) CORVAS INT INC.
 XX
 XX Bertram PW, Ganssmans YSL, Jaspers LS, Laroche YP,
 P1 Lauwereys MJ, Messens JHL, Moyle M, Stanssens PEH,
 P1 Vlasuk GP;
 XX
 XX WP1: 1999-549564/45.
 XX
 XX Screening an isolated protein for nematode extracted anticoagulant
 P1 Protein domains
 P1
 P1
 PS Disclosure: Fig 19; 197pp; English.
 XX
 XX The present sequence represents a nematode extracted anticoagulant
 CC protein (NAP). The protein has activity as an anticoagulant and/or as a
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and in ex vivo
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay, with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC elevation of clotting time relative to a baseline clotting value, where
 CC a doubling of clotting time is deemed a two-fold elevation; and
 CC calculating a PT to APTT prolongation ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity. The method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX
 XX Sequence 162 AA:
 SQ
 Query Match 93.8%; Score 30; BB 23; Length 162;
 Best Local Similarity 100.0%; Prod. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 27 4 GYRN 7
 DB 56 GYRN 60
 |||||
 RESULT 46
 AAB15321
 ID AAB15321 standard; Protein: 162 AA.
 XX
 XX AAB15321:
 XX
 XX 19-DEC-2000 (first entry)
 XX
 XX A. caninum nematode-extracted anticoagulant protein AcanAP45.
 XX
 XX Nematode-extracted anticoagulant protein: AcanAP45; blood clotting;
 XX canine hookworm; thrombosis; varicose.
 XX
 XX Ancylostoma caninum.
 XX
 XX US6087447-A.
 XX
 XX 11-JUL-2000.
 XX
 XX 12-FEB-1999; 950S-0249451.
 XX
 XX 17-OCT-1995; 950S-0513241.
 XX
 XX 17-APR-1997; 950S-0829455.
 XX
 XX 18-OCT-1994; 940S-0326110.
 XX
 XX 05-JUN-1995; 950S-0461965.
 XX
 XX 05-JUN-1995; 950S-0465380.
 XX
 XX 05-JUN-1995; 950S-0486397.
 XX
 XX 05-JUN-1995; 950S-0486399.
 XX
 XX (CORV-) CORVAS INT INC.

PR 05-JUN-1995; 950S-0486397.
 PR 05-JUN-1995; 950S-0486399.
 XX
 XX (CORV-) CORVAS INT INC.
 XX
 XX Lauwereys MJ, Stanssens PEH, Jaspers LS, Ganssmans YSL, Moyle M,
 P1 Bertram PW, Messens JHL, Laroche YP, Vlasuk GP;
 XX
 XX WP1: 2000-531459/48.
 XX
 XX N-PSDB: AAA7480.
 XX
 XX New cDNA molecule encoding a protein having factor Xa inhibitory
 P1 activity for preventing and treating blood clotting disorders,
 P1 comprises nematode-extracted anticoagulant protein domains
 P1
 PS Disclosure: Fig 18; 197pp; English.
 XX
 XX The present sequence is the Ancylostoma caninum nematode extracted
 CC anticoagulant protein AcanAP45. This protein has been shown to
 CC be effective at preventing blood clotting without causing excessive
 CC blood loss. The protein can be used in blood substitute mixtures to allow the
 CC isolation of plasma from the blood, to prevent thrombosis which may be
 CC linked to the surgery of an atherosclerotic plaque, and/or myocardial
 CC infarction, and/or thrombotic therapy, percutaneous transluminal
 CC coronary angioplasty, disseminated intravascular coagulation, infection,
 CC cancer and septic shock, and to produce antibodies. In the latter
 CC instance, the antibodies can be raised in order to detect infection by
 CC nematodes (the coding sequence can also be used for this) or as
 CC diagnostic tests. The protein can also be used as a vaccine against
 CC nematode parasites.
 XX
 XX Sequence 162 AA:
 SQ
 Query Match 93.8%; Score 30; BB 21; Length 162;
 Best Local Similarity 100.0%; Prod. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 GYRN 7
 DB 56 GYRN 60
 |||||
 RESULT 47
 AAB15322
 ID AAB15322 standard; Protein: 162 AA.
 XX
 XX AAB15322:
 XX
 XX 19-DEC-2000 (first entry)
 XX
 XX A. caninum nematode-extracted anticoagulant protein AcanAP47.
 XX
 XX Nematode-extracted anticoagulant protein: AcanAP47; blood clotting;
 XX canine hookworm; thrombosis; varicose.
 XX
 XX Ancylostoma caninum.
 XX
 XX US6087447-A.
 XX
 XX 11-JUL-2000.
 XX
 XX 12-FEB-1999; 950S-0249451.
 XX
 XX 17-OCT-1995; 950S-0513241.
 XX
 XX 17-APR-1997; 950S-0829455.
 XX
 XX 18-OCT-1994; 940S-0326110.
 XX
 XX 05-JUN-1995; 950S-0461965.
 XX
 XX 05-JUN-1995; 950S-0465380.
 XX
 XX 05-JUN-1995; 950S-0486397.
 XX
 XX 05-JUN-1995; 950S-0486399.
 XX
 XX (CORV-) CORVAS INT INC.

PI Lauwereys MJ, Stanssens PER, Jespers LS, Ganssens YGJ, Moyle M;
 PI Berquim PW, Messens JHL, Laroche YR, Vlasuk GP.
 XX WPI: 2000-531459/48.
 DR N-PSDB: AAA73481.
 XX
 PT New cDNA molecule encoding a protein having factor Xa inhibitory
 PT activity for preventing and treating blood clotting disorders.
 PI comprises nematode-extracted anticoagulant protein domains.
 XX
 PS Disclosure, Fig 19, 197pp; English.
 XX
 CC The present sequence is the Ancylostoma caninum nematode-extracted
 CC anticoagulant protein AcanAP47. Proteins of this kind have been shown to
 CC be effective at preventing blood clotting without causing excessive
 CC bleeding. The protein can be used in blood collection tubes to aid the
 CC isolation of plasma from the blood, to prevent thrombosis which may be
 CC linked to the rupture of an atherosclerotic plaque, acute myocardial
 CC infarction, angina, thrombolytic therapy, percutaneous transluminal
 CC coronary angioplasty, disseminated intravascular coagulation, infection,
 CC cancer and septic shock, and to produce antibodies. In the latter
 CC instance, the antibodies can be raised in order to detect infection by
 CC nematodes (the coding sequence can also be used for this) or as
 CC diagnostic tests. The protein can also be used as a vaccine against
 CC nematode parasites.
 XX
 SO Sequence 162 AA;

Query Match 93.88; Score 30; DR 21; Length 162;
 Best Local Similarity 100.0%; Prod. No. 92;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 ID 56 GYRN 60

RESULT 38
 AAY30435
 ID AAY30435 standard; Protein: 171 AA.
 XX
 AC AAY30435;
 XX
 DT 15-NOV-1999 (first entry)
 XX
 DE Mature nematode extracted anticoagulant protein AcanAP4
 XX
 KW Nematode extracted anticoagulant protein; NAP: anticoagulant;
 KW serine protease inhibitor; NAP domain; factor VIIa/TF.
 XX

OS Ancylostoma ceylanicum.
 XX
 FN 06955204 A.
 XX
 PD 21-SEP-1999
 XX
 PF 14-APR-1996; 9505-0634541.
 XX
 PR 14-APR-1996; 9505-0634541.
 PR 18-OCT-1994; 9405-0326110.
 PR 05-JUN-1995; 9505-0461965.
 PR 05-JUN-1995; 9505-0465380.
 PR 05-JUN-1995; 9505-0486399.
 PR 05-JUN-1995; 9505-0486399.
 PR 17-OCT-1995; 9505-0513231.
 XX
 PA (CORV-) CORVAS INT INC.

XX
 XX Berquim PW, Ganssens YGJ, Jespers LS, Laroche YR;
 PI Lauwereys MJ, Messens JHL, Moyle M, Stanssens PER;
 XX Vlasuk GP.
 DR WPI: 1999-539569/45.

XX Screening an isolated protein for Nematode-extracted Anticoagulant
 PI Protein domains
 XX
 PS Disclosure, Fig 17, 197pp; English.
 XX
 CC The present sequence represents a nematode-extracted anticoagulant
 CC protein (NAP); the protein has activity as an anticoagulant and/or serine
 CC protease inhibitor. The protein contains at least one NAP domain which
 CC has selective inhibitory activity for factor VIIa/TF. The specification
 CC describes a method for screening an isolated protein at least one domain
 CC for factor VIIa/TF selective inhibitory activity. The method comprises
 CC determining the time to clotting effected by a concentration of the
 CC isolated protein in an ex vivo prothrombin time (PT) assay and an ex vivo
 CC activated partial thromboplastin time (APTT) assay; calculating
 CC prolongation of clotting effected by the isolated protein in each of
 CC the PT and APTT assay, with respect to a baseline clotting value for
 CC each assay, where prolongation of clotting is calculated as fold
 CC variation of clotting time relative to a baseline clotting value, where
 CC a clotting of clotting time is based on a fold variation, and
 CC calculating a PI to anti-prothrombin ratio, where a ratio at least
 CC one is indicative of factor VIIa/TF inhibitory activity; the method is
 CC useful for determining if a protein has factor VIIa/TF inhibitory
 CC activity.
 XX
 SO Sequence 171 AA;

Query Match 93.88; Score 30; DR 20; Length 171;
 Best Local Similarity 100.0%; Prod. No. 97;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 ID 140 GYRN 144

RESULT 39
 AAR91713
 ID AAR91713 standard; Protein: 180 AA.
 XX
 AC AAR91713;
 XX
 DT 17-NOV-1996 (first entry)
 XX
 DE AduNAP7.
 XX
 KW AcanAP: HponAP; NamNAP; AcanNAP; AduNAP; anticoagulant;
 KW nematode extracted anticoagulant protein, serine protease;
 KW nematode, thrombosis; parasitic worm.
 XX

OS Ancylostoma duodenale.
 XX
 FN Localizing/Qualifications
 XX
 PD 1-102
 XX
 PD 2-label AduNAP7d1
 XX
 PD 103-180
 XX
 PD 7-label AduNAP7d2

W-9512021-A2.
 XX
 PD 25-APR-1996.
 XX
 PF 17-OCT-1995; 9505-0513231.
 XX
 PR 05-JUN-1995; 9505-0486399.
 PR 18-OCT-1994; 9405-0426110.
 PR 05-JUN-1995; 9505-0461965.
 PR 05-JUN-1995; 9505-0465380.
 PR 05-JUN-1995; 9505-0486399.
 XX
 PA (CORV-) CORVAS INT INC.

XX
 PI Berquim PW, Ganssens YGJ, Jespers LS, Laroche YR;

```

P1 Lauwereys MJ, Messens JBL, Moyle M, Strausens PER;
P1 Vlasuk GP;
XX
XX WPI: 1996-222097/222;
DR N-PSDB; AAT12959;
XX
XX Proteins with anticoagulant and/or serine protease inhibitory
P1 activity isolated from nematodes and useful to inhibit blood
P1 coagulation
XX
XX claim 221; Fig 2E; 24pp; English;
PS
XX
XX Proteins with anticoagulant and/or serine protease inhibitory
CC activity, isolated from nematodes, are useful to inhibit blood
CC coagulation. The proteins can be added to blood collection tubes
CC defining the collection of mammalian plasma. They are also useful
CC to prevent or inhibit thrombosis, and may be given alone or in
CC combination with other therapeutic or in vivo diagnostic agents.
CC The proteins can serve as immunogens to raise antibodies for use in
CC the diagnosis and identification of NAP concn levels in biological
CC fluids, e.g. to detect mammalian infection with a parasitic worm.
CC They can also be used as immunogens in prophylactic and therapeutic
CC vaccines against parasitic worm infection. The proteins may
CC double the clotting time of human plasma in prothrombin time assays
CC when present at 10-50 nMol, and double the clotting time of human
CC plasma in activated partial thrombin time assays when present
CC at 10-100 nMol.
CC The anticoagulant proteins are pref. derived from
CC Ancylostoma caninum, A. ceylanicum, A. duodenale, Necator
CC americanus or Heligmosomoides polygyrus.
CC The catalytic pref. have 2 NAP domains and specifically inhibit
CC the catalytic activity of the factor VIIa/TF complex in the
CC presence of factor Xa or a catalytically inactive factor Xa derivative.
CC do not specifically inhibit the activation of factor VIIa in the
CC absence of TF and do not specifically inhibit prothrombinase.
XX
XX Sequence 180 AA;
SQ
Query Match 97.8%; Score 36; DB 17; Length 180;
Best Local Similarity 100.0%; Prod. No. 1002;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GYRN 7
DB 74 GYRN 78
1111
RESULT 40
AAY0488
ID AAY0488 standard; Protein: 180 AA.
XX
XX AAY0488;
XX
XX 15-NOV-1999 (first entry)
XX
XX Nematode extracted anticoagulant protein AduNAP7.
DE
XX
XX Nematode extracted anticoagulant protein, NAP, anticoagulant,
KW serine protease inhibitor, NAP domain, factor VIIa/TF.
XX
XX Ancylostoma duodenale.
XX
XX OS5955294 A.
XX
XX 21-SEP-1999.
XX
XX 19-AUG-1996; 950S-0646641.
XX
XX 19-AUG-1996; 950S-0646641.
PR 18-OCT-1994; 940S-0326110.
PR 05-JUN-1995; 950S-0461965.
PR 05-JUN-1995; 950S-0465480.
PR 05-JUN-1995; 950S-0486497.
P1 Lauwereys MJ, Messens JBL, Moyle M, Strausens PER;
P1 Vlasuk GP;
XX
XX WPI: 1996-222097/222;
DR N-PSDB; AAT12959;
XX
XX Proteins with anticoagulant and/or serine protease inhibitory
P1 activity isolated from nematodes and useful to inhibit blood
P1 coagulation
XX
XX claim 221; Fig 2E; 24pp; English;
PS
XX
XX Proteins with anticoagulant and/or serine protease inhibitory
CC activity, isolated from nematodes, are useful to inhibit blood
CC coagulation. The proteins can be added to blood collection tubes
CC defining the collection of mammalian plasma. They are also useful
CC to prevent or inhibit thrombosis, and may be given alone or in
CC combination with other therapeutic or in vivo diagnostic agents.
CC The proteins can serve as immunogens to raise antibodies for use in
CC the diagnosis and identification of NAP concn levels in biological
CC fluids, e.g. to detect mammalian infection with a parasitic worm.
CC They can also be used as immunogens in prophylactic and therapeutic
CC vaccines against parasitic worm infection. The proteins may
CC double the clotting time of human plasma in prothrombin time assays
CC when present at 10-50 nMol, and double the clotting time of human
CC plasma in activated partial thrombin time assays when present
CC at 10-100 nMol.
CC The anticoagulant proteins are pref. derived from
CC Ancylostoma caninum, A. ceylanicum, A. duodenale, Necator
CC americanus or Heligmosomoides polygyrus.
CC The catalytic pref. have 2 NAP domains and specifically inhibit
CC the catalytic activity of the factor VIIa/TF complex in the
CC presence of factor Xa or a catalytically inactive factor Xa derivative.
CC do not specifically inhibit the activation of factor VIIa in the
CC absence of TF and do not specifically inhibit prothrombinase.
XX
XX Sequence 180 AA;
SQ
Query Match 97.8%; Score 36; DB 17; Length 180;
Best Local Similarity 100.0%; Prod. No. 1002;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GYRN 7
DB 74 GYRN 78
1111
RESULT 41
AAR91711
ID AAR91711 standard; Protein: 181 AA.
XX
XX AAR91711;
XX
XX 17-NOV-1996 (first entry)
XX
XX AcanAP45.
DE
XX
XX AcanAP, HsCANAP, NamNAP, AcanNAP, AduNAP; anticoagulant;
KW nematode extracted anticoagulant protein; serine protease;
KW nematode; thrombosis; parasitic worm.
XX
XX Ancylostoma caninum.
XX
XX W09612021-A2.
XX
XX 25-APR-1996.
XX
XX 17-OCT-1995; 95W0-DS14241.
XX
XX 05-JUN-1995; 950S-0486497.
PR 18-OCT-1994; 940S-0326110.
PR 05-JUN-1995; 950S-0461965.
PR 05-JUN-1995; 950S-0465480.

```


05-JUN-1995; 95US-0486397.

(CORV-) CORVAS INT INC.

Berquim PW, Ganssens YGJ, Jespers LS, Laroche YR;
Lauwereys MJ, Messens JH, Moyle M, Stanssens PEH;
Vlasuk GP;

WPI: 1996 222907/22.
N-PSDB: AAT12957.

Proteins with anticoagulant and/or serine protease inhibitory
activity isolated from nematodes and useful to inhibit blood
coagulation

Claim 221; Fig 13F; 243pp; English.

Proteins with anticoagulant and/or serine protease inhibitory
activity, isolated from nematodes, are useful to inhibit blood
coagulation. The proteins can be added to blood collection tubes
defining the collection of mammalian plasma. They are also useful
to prevent or inhibit thrombosis, and may be given alone or in
combination with other therapeutic or in vivo diagnostic agents.
The proteins can serve as immunogens to raise antibodies for use in
the diagnosis and identification of NAP conen. levels in biological
fluids, e.g. to detect mammalian infection with a parasitic worm.
They can also be used as immunogens in prophylactic and therapeutic
vaccines against parasitic worm infection. The proteins may
double the clotting time of human plasma in prothrombin time assays
when present at 10-50 nmol, and double the clotting time of human
plasma in activated partial thrombin time assays when present
at 10-100 nmol

The anticoagulant proteins are pref. derived from
Ancylostoma caninum, A. ceylanicum, A. dendriticum, Necator
americanus or Helicoverma polygyrus.
The proteins pref. have 2 NAP domains and specifically inhibit
the catalytic activity of the factor VIIa/TF complex in the
presence of factor Xa or a catalytically inactive factor Xa deriv.
do not specifically inhibit the activation of factor VIIa in the
absence of TF and do not specifically inhibit prothrombinase.

Sequence 181 AA.

Query Match 93.8%; Score 30; DB 17; Length 181;
Best Local Similarity 100.0%; Pred. No. 10-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
IIIIII
Db 75 GFYRN 79

RESULT 42

AAR91712

Db AAR91712 standard; Protein: 181 AA.

XX AAR91712;

XX 17-NOV-1996 (first entry)

DE AcanAP47.

XX AcanAP: IpoNAP, NamNAP, AcanNAP, AcanNAP; anticoagulant;
KW nematode-extracted anticoagulant protein; serine protease;
KW nematode; thrombosis; parasitic worm.

XX Ancylostoma caninum.

XX W09612021-A2.

XX 25-APR-1996.

XX 17-OCT-1995; 95WO-US13231.

XX 05-JUN-1995; 95US-0486399.

XX 18-OCT-1994; 94US-0426110.

XX 05-JUN-1995; 95US-0461965.

XX 05-JUN-1995; 95US-0465380.

XX 05-JUN-1995; 95US-0486397.

XX (CORV-) CORVAS INT INC.

Berquim PW, Ganssens YGJ, Jespers LS, Laroche YR;
Lauwereys MJ, Messens JH, Moyle M, Stanssens PEH;
Vlasuk GP;

WPI: 1996 222907/22.
N-PSDB: AAT12958.

Proteins with anticoagulant and/or serine protease inhibitory
activity isolated from nematodes and useful to inhibit blood
coagulation

Claim 221; Fig 13F; 243pp; English.

Proteins with anticoagulant and/or serine protease inhibitory
activity, isolated from nematodes, are useful to inhibit blood
coagulation. The proteins can be added to blood collection tubes
defining the collection of mammalian plasma. They are also useful
to prevent or inhibit thrombosis, and may be given alone or in
combination with other therapeutic or in vivo diagnostic agents.
The proteins can serve as immunogens to raise antibodies for use in
the diagnosis and identification of NAP conen. levels in biological
fluids, e.g. to detect mammalian infection with a parasitic worm.
They can also be used as immunogens in prophylactic and therapeutic
vaccines against parasitic worm infection. The proteins may
double the clotting time of human plasma in prothrombin time assays
when present at 10-50 nmol, and double the clotting time of human
plasma in activated partial thrombin time assays when present
at 10-100 nmol

The anticoagulant proteins are pref. derived from
Ancylostoma caninum, A. ceylanicum, A. dendriticum, Necator
americanus or Helicoverma polygyrus.

The proteins pref. have 2 NAP domains and specifically inhibit
the catalytic activity of the factor VIIa/TF complex in the
presence of factor Xa or a catalytically inactive factor Xa deriv.
do not specifically inhibit the activation of factor VIIa in the
absence of TF and do not specifically inhibit prothrombinase.

Sequence 181 AA.

Query Match 93.8%; Score 30; DB 17; Length 181;
Best Local Similarity 100.0%; Pred. No. 10-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
IIIIII
Db 75 GFYRN 79

RESULT 43

AAV30409

Db AAV30409 standard; Protein: 181 AA.

XX AAV30409;

XX 15-NOV-1999 (first entry)

XX Nematode extracted anticoagulant protein AcanAP44.

XX Nematode extracted anticoagulant protein; NAP; anticoagulant;
KW serine protease inhibitor; NAP domain; factor VIIa/TF.

XX Ancylostoma caninum.

XX US955244-A.


```

XX
PD 27-SEP-2001.
XX
XX PF 23-MAR-2001; 2501W-US0231.
XX
XX PF 23-MAR-2000; 2000US 151637P.
XX
XX PF 11-JUL-2000; 2000HS-0614150.
XX
XX PA (PEKE ) PE CORP NY.
XX
XX Venter JC, Adams M, Li PWD, Myers EW;
XX
XX WPI; 2001-656860/75.
XX
XX N-PSOH; ABL13829.
XX
PT New isolated nucleic acid detection reagent for detecting 1000 or more
PT genes from Drosophila and for elucidating cell signalling and cell-cell
PT interactions -
XX
XX PS Disclosure; SEQ ID NO 35970; 21pp - Sequence Listing; English.
XX
XX CC The invention relates to an isolated nucleic acid detection reagent
XX capable of detecting 1000 or more genes from Drosophila. The invention is
XX useful in developmental biology and in elucidating cell signalling and
XX cell-cell interactions in higher eukaryotes for the development of
XX insecticides, therapeutics and pharmaceutical drugs. The invention
XX discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
XX sequences (ABL01840-ABL16175) and the encoded proteins
XX (ABR57737-ABR72072).
XX The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pat_sequences.
XX
XX SO Sequence 184 AA:

Query Match 33.9%; Score 30; E-Value 184;
Best local Similarity 100.0%; Pred. No. 10-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
Db 31 GFYRN 35

Search completed: April 30, 2003, 14:34:08
Job time : 61.4545 secs

```



Copyright (c) 1993 - 2002 Computer Aid.
 Core version 5.1.4-5-4579

OM protein - protein search, using sw model

Run on: April 30, 2002 13:31.03 ; Search time 19.4545 seconds

336.465 Million coll. updates/sec
(without alignments)

Title: US-09-498-556C-79

Perfect score:

Sequence: 1 XXGFYRN 7

Scoring table:

Gapop 10.0 , Gapext 0.5

searched: 2004-2006, 2007-2008, 2009-2010, 2011-2012

Total number of hits satisfying the 500 hit rule.

Minimum DB seq length: 0

Maximum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match on

Maximum Match 100%

Listing first 1000 summaries

Database :

PIR 73:*

1: pir1: *

```
1: pir1: *
2: pir2: *
```

1000

pir4:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query			IP	Description
	Score	Match	Length bp		
1	30	93.8	77	2	885694
2	30	93.8	134	2	976180
3	30	92.8	172	2	887783
4	30	92.8	172	2	873466
5	30	93.8	172	2	761252
6	30	93.8	223	2	823702
7	30	93.8	223	2	837738
8	30	92.8	227	2	881299
9	30	93.8	361	2	A50166
10	30	93.8	362	2	C92572
11	30	93.8	408	2	T95524
12	30	93.8	435	2	746716
13	30	93.8	465	2	A96562
14	30	93.8	481	2	S50082
15	30	93.8	533	1	YMS05
16	30	93.8	747	2	T12774
17	30	93.8	824	2	S49937
18	30	93.8	824	2	S70630
19	30	93.8	940	2	U41345
20	30	93.8	1031	2	C87645
21	30	93.8	1564	2	S55517
22	27	94.4	36	1	B03251
23	27	84.4	60	1	T76787
24	27	84.4	199	2	T59488
25	27	84.4	201	2	A86635
26	27	84.4	234	2	A47993
27	27	81.4	258	2	T22052
28	27	81.4	275	2	A59413
29	27	84.4	292	2	U54431

103	24	81.2	10.4	2	A1673	H ₂ O ₂ exchanging A	176	25	78.1	229	2	A54274	sulfur recombined 3
104	26	81.2	10.4	2	JN9994	H ₂ O ₂ exchanging A	177	25	78.1	342	2	B89974	hypothetical prote
105	26	81.2	10.4	2	A32992	H ₂ O ₂ exchanging A	178	25	78.1	345	2	C82728	phage for chlamydia
106	26	81.2	10.4	2	S2406	H ₂ O ₂ exchanging A	179	25	78.1	348	2	C71174	hypothetical prote
107	26	81.2	10.4	2	115621	hypothetical prote	180	25	78.1	352	2	C80924	bradykinin B1 rece
108	26	81.2	10.4	2	A56236	probable RNA helic	181	25	78.1	355	2	C81195	probably oxidoredu
109	26	81.2	10.4	2	A56158	eye development fr	182	25	78.1	355	2	A10408	hypothetical prote
110	26	78.1	7.0	2	E70790	hypothetical prote	183	25	78.1	357	2	S54663	hypothetical prote
111	26	78.1	7.1	2	I51744	MHC class II alpha	184	25	78.1	357	2	G91295	hypothetical prote
112	26	78.1	7.1	2	I51750	MHC class II alpha	185	25	78.1	357	2	B86137	hypothetical prote
113	25	78.1	7.2	2	AH3473	lactoyglutathione	186	25	78.1	363	2	G81445	hypothetical prote
114	25	78.1	7.9	2	S33755	fibulin-1c - mouse	187	25	78.1	370	2	H74423	oxygen-independent
115	26	78.1	9.0	2	E12849	maturation (p15a2)	188	25	78.1	381	2	A01113	hypothetical prote
116	25	78.1	9.1	2	S72575	B1456_22_163 prote	189	25	78.1	381	2	AH1474	hypothetical prote
117	25	78.1	9.6	2	A25374	phospholipase	190	25	78.1	385	2	T23375	probable secreted
118	25	78.1	10.0	2	E78209	ribosomal protein	191	25	78.1	397	1	K18870	phosphorylase, kin
119	25	78.1	10.0	2	E23309	hypothetical prote	192	25	78.1	397	1	K18870	probable phenome
120	25	78.1	12.3	2	E98946	conserved hypotet	193	25	78.1	398	2	C76680	hypothetical prote
121	26	78.1	12.4	2	A22329	hypothetical prote	194	25	78.1	400	2	T44383	hypothetical prote
122	25	78.1	12.7	2	E27727	hypothetical prote	195	25	78.1	401	2	T34661	probable RNA polym
123	25	78.1	13.8	2	E95060	acetyltransferase,	196	25	78.1	405	2	T45117	probable secreted
124	25	78.1	13.8	2	E97901	conserved hypotet	197	25	78.1	409	2	T45118	probable secreted
125	25	78.1	14.3	2	C83467	conserved hypotet	198	25	78.1	414	1	H78360	atolysin A (B ₁ C)
126	25	78.1	14.5	2	H85529	acetyltransferase,	199	25	78.1	414	2	S41638	atolysin B (B ₁ C)
127	25	78.1	15.0	2	C64233	conserved hypotet	200	25	78.1	414	2	S41639	atolysin C (B ₁ C)
128	25	78.1	16.4	2	C85336	peptidylprolyl iso	201	25	78.1	425	2	C39467	3-deoxy-D-amino ac
129	25	78.1	16.4	2	C95702	peptidylprolyl ci	202	25	78.1	425	2	C39467	3-deoxy-D-amino ac
130	25	78.1	16.4	2	E95552	peptidylprolyl ci	203	25	78.1	425	2	E95552	hypothetical prote
131	25	78.1	16.4	2	A95656	peptidylprolyl ci	204	25	78.1	425	2	E95639	probable glutamate
132	25	78.1	16.5	2	A95661	conserved hypotet	205	25	78.1	427	2	B81978	thioamide 1,3 omal
133	25	78.1	16.8	2	H83643	peptide deform	206	25	78.1	427	2	A91334	phosphoribosylam
134	25	78.1	16.9	2	E54047	peptidylprolyl iso	207	25	78.1	441	2	A14341	hypothetical prote
135	25	78.1	19.0	1	C85874	peptidylprolyl iso	208	25	78.1	445	2	AH1598	weakly methyltrans
136	25	78.1	19.0	1	C85874	peptidylprolyl iso	209	25	78.1	445	2	AH1549	hypothetical prote
137	25	78.1	19.6	2	C66061	peptidylprolyl iso	210	25	78.1	452	2	T29116	hypothetical prote
138	25	78.1	19.6	2	E94155	peptidylprolyl iso	211	25	78.1	470	2	B44339	hypothetical prote
139	25	78.1	19.6	2	E51280	peptidylprolyl iso	212	25	78.1	477	2	C84833	4-phosphoribitol
140	25	78.1	20.3	1	H70109	conserved hypotet	213	25	78.1	478	2	J18890	4-phosphoribitol
141	25	78.1	20.3	1	S15111	hemorrhagic factor	214	25	78.1	491	1	I1H2A2	alpha 2-antiplasmi
142	25	78.1	20.9	2	E93034	conserved hypotet	215	25	78.1	494	2	F84199	probable carboxydr
143	25	78.1	20.9	2	E94482	hypothetical prote	216	25	78.1	503	2	J15721	3,5-dibromo-4-50 mo
144	25	78.1	21.0	2	A91438	hypothetical prote	217	25	78.1	505	2	E55246	4-alpha-albumin
145	25	78.1	21.4	2	B66630	acyl carrier prote	218	25	78.1	505	2	B98111	4-alpha-albumin
146	25	78.1	21.5	2	E84819	transcription regu	219	25	78.1	506	2	C99226	hypothetical prote
147	25	78.1	22.7	2	H65014	conserved hypotet	220	25	78.1	510	2	S68116	4-aminobutyrate tr
148	25	78.1	22.7	2	E12908	hypothetical prote	221	25	78.1	515	2	C84192	hypothetical prote
149	25	78.1	22.7	2	A67998	conserved hypotet	222	25	78.1	522	2	A34103	11-azacyclotriaz-4-yl
150	25	78.1	23.6	2	E53741	MHC class II alpha	223	25	78.1	524	2	E96784	hypothetical prote
151	25	78.1	23.9	2	A89967	serine proteinase	224	25	78.1	526	2	108541	hypothetical prote
152	25	78.1	23.9	2	B89666	serine proteinase	225	25	78.1	527	2	C95760	hypothetical prote
153	25	78.1	24.1	2	A75418	phosphotransfer re	226	25	78.1	527	2	B90858	hypothetical prote
154	25	78.1	24.5	2	C72578	probable flagellin	227	25	78.1	534	2	119414	hypothetical prote
155	25	78.1	24.5	2	C95798	hypothetical prote	228	25	78.1	538	2	B93329	phage 25 protein
156	25	78.1	24.6	2	C25667	hypothetical prote	229	25	78.1	540	2	149874	hypothetical prote
157	25	78.1	24.6	2	C95627	hypothetical prote	230	25	78.1	547	2	A33803	albumin 1.4 alpha m
158	25	78.1	24.6	2	C72352	probable endonuc	231	25	78.1	551	2	S05567	albumin 1.4 alpha m
159	25	78.1	24.7	2	A95273	probable Atac fami	232	25	78.1	552	2	154388	127R 1 human
160	25	78.1	24.8	2	E71946	probable transcrip	233	25	78.1	553	2	C84149	adipocyte amino ac
161	25	78.1	24.8	2	E46447	response regulator	234	25	78.1	565	2	C70674	probable 2,3 dihyd
162	25	78.1	24.8	2	E19410	hypothetical prote	235	25	78.1	573	2	118523	arginin regulated pr
163	25	78.1	24.8	2	E51717	palmitoyl-protein	236	25	78.1	573	2	118523	arginin regulated pr
164	25	78.1	24.8	2	A54717	palmitoyl-protein	237	25	78.1	576	2	A81302	arginin regulated pr
165	25	78.1	24.8	2	E58997	palmitoyl-protein	238	25	78.1	577	1	SYB081	arginine TRNA synth
166	25	78.1	24.8	2	E30001	hypothetical prote	239	25	78.1	577	2	B93952	arginine TRNA synth
167	25	78.1	24.8	2	E43416	hypothetical prote	240	25	78.1	577	2	F85900	arginine TRNA synth
168	25	78.1	24.8	2	E90917	hypothetical prote	241	25	78.1	577	2	A13744	arginine TRNA synth
169	25	78.1	24.8	2	C85766	hypothetical prote	242	25	78.1	591	2	B54655	methionine precursor
170	25	78.1	24.8	2	A05693	probable expect	243	25	78.1	585	2	B94941	ApC transporter (A
171	25	78.1	24.8	2	E92292	structural protein	244	25	78.1	585	2	C45992	arginin regulated pr
172	25	78.1	24.8	2	E92292	conserved hypotet	245	25	78.1	585	2	B96349	phage family prote
173	25	78.1	24.8	2	E14451	hypothetical prote	246	25	78.1	589	2	A02932	GDEF family prote
174	25	78.1	24.8	2	E97971	phosphoribosylam	247	25	78.1	594	2	145583	arginin regulated pr
175	25	78.1	24.8	2	B94560	probable peroxidase	248	25	78.1	598	2	145583	acid shock protein
176	25	78.1	24.8	2	B94560	probable peroxidase	249	25	78.1	599	2	C29712	acid shock protein

249	25	79.1	606	2	A51665	actin 1 precursor	322	75	26	1	360111	actin 1 precursor
250	25	79.1	608	2	E90373	hypothetical protein	323	75	26	1	E90373	hypothetical protein
251	25	78.1	616	2	E84424	probable auxin efflux	324	75	26	2	E84424	probable auxin efflux
252	25	78.1	625	2	G73420	oligopeptide ABC transporter	325	75	26	2	S82867	hypothetical protein
253	25	79.1	621	2	G64874	probable membrane	326	75	26	4	E77146	hypothetical protein
254	25	78.1	633	2	E72284	oligopeptide ABC transporter	327	75	26	4	A87515	hypothetical protein
255	25	79.1	648	2	E75749	hypothetical protein	328	75	26	3	E67384	hypothetical protein
256	25	78.1	665	2	G71261	probable membrane	329	75	26	3	E46264	hypothetical protein
257	25	78.1	670	2	E36790	hypothetical protein	330	75	26	3	E61150	hypothetical protein
258	25	78.1	679	2	E64182	DNA ligase (NAD ⁺)	331	75	26	2	E68827	probable transmembrane
259	25	78.1	682	2	E73612	hypothetical protein	332	75	26	2	E26111	hypothetical protein
260	25	78.1	686	2	E73612	hypothetical protein	333	75	26	2	E73612	hypothetical protein
261	25	78.1	692	2	A70932	probable membrane	334	75	26	2	E62927	hypothetical protein
262	25	78.1	710	2	E64979	hypothetical protein	335	75	26	2	E66941	hypothetical protein
263	25	78.1	733	2	E64058	outer membrane protein	336	75	26	2	E83114	50S ribosomal protein
264	25	78.1	725	2	E51148	outer membrane protein	337	75	26	2	E97515	RADH dehydrogenase
265	25	78.1	725	2	E70539	hypothetical protein	338	75	26	2	E70539	hypothetical protein
266	25	78.1	735	2	A00711	probable membrane	339	75	26	2	E13212	hypothetical protein
267	25	78.1	736	2	E73406	probable membrane	340	75	26	1	E47264	hypothetical protein
268	25	78.1	737	2	E47264	hypothetical protein	341	75	26	1	E47264	hypothetical protein
269	25	78.1	737	2	E47264	hypothetical protein	342	75	26	1	E47264	hypothetical protein
270	25	78.1	720	2	E70539	hypothetical protein	343	75	26	2	E70539	hypothetical protein
271	25	78.1	802	2	E70539	outer membrane protein	344	75	26	2	E70539	outer membrane protein
272	25	78.1	803	2	E70539	outer membrane protein	345	75	26	2	E70539	outer membrane protein
273	25	78.1	905	2	E70539	probable transmembrane	346	75	26	2	E70539	probable transmembrane
274	25	78.1	917	2	E85649	probable transmembrane	347	75	26	2	E85649	probable transmembrane
275	25	78.1	960	2	E70539	probable sensor protein	348	75	26	2	E70539	probable sensor protein
276	25	78.1	982	2	E70539	glutamate aminopeptidase	349	75	26	2	E70539	glutamate aminopeptidase
277	25	78.1	982	2	E70539	glutamate aminopeptidase	350	75	26	2	E70539	glutamate aminopeptidase
278	25	78.1	884	2	E70539	hypothetical protein	351	75	26	2	E70539	hypothetical protein
279	25	78.1	905	2	E70539	conserved hypothetical	352	75	26	2	E70539	conserved hypothetical
280	25	78.1	920	2	E70539	hypothetical protein	353	75	26	2	E70539	hypothetical protein
281	25	78.1	937	2	E70539	aminopeptidase (NAD ⁺)	354	75	26	2	E70539	aminopeptidase (NAD ⁺)
282	25	78.1	955	2	E70539	CS2 filling synthase	355	75	26	2	E70539	CS2 filling synthase
283	25	78.1	955	2	E70539	alpha-amylase (EC 3.2.1.1)	356	75	26	2	E70539	alpha-amylase (EC 3.2.1.1)
284	25	78.1	965	2	E70539	membrane alpha-amylase	357	75	26	2	E70539	membrane alpha-amylase
285	25	78.1	965	2	E70539	membrane alpha-amylase	358	75	26	2	E70539	membrane alpha-amylase
286	25	78.1	995	2	E70539	carboxyl peptidase	359	75	26	2	E70539	carboxyl peptidase
287	25	78.1	995	2	E70539	carboxyl peptidase	360	75	26	2	E70539	carboxyl peptidase
288	25	78.1	1000	2	E70539	DNA directed RNA polymerase	361	75	26	2	E70539	DNA directed RNA polymerase
289	25	78.1	1000	2	E70539	DNA directed RNA polymerase	362	75	26	2	E70539	DNA directed RNA polymerase
290	25	78.1	1055	2	E70539	DNA directed RNA polymerase	363	75	26	2	E70539	DNA directed RNA polymerase
291	25	78.1	1055	2	E70539	DNA directed RNA polymerase	364	75	26	2	E70539	DNA directed RNA polymerase
292	25	78.1	1083	2	E70539	DNA polymerase III	365	75	26	2	E70539	DNA polymerase III
293	25	78.1	1121	2	E70539	hypothetical protein	366	75	26	2	E70539	hypothetical protein
294	25	78.1	1182	2	E70539	hypothetical protein	367	75	26	2	E70539	hypothetical protein
295	25	78.1	1335	2	E70539	lysine 321 chain	368	75	26	2	E70539	lysine 321 chain
296	25	78.1	1335	2	E70539	lysine 321 chain	369	75	26	2	E70539	lysine 321 chain
297	25	78.1	1394	2	E70539	nitrate reductase	370	75	26	2	E70539	nitrate reductase
298	25	78.1	1394	2	E70539	hypothetical protein	371	75	26	2	E70539	hypothetical protein
299	25	78.1	1394	2	E70539	hypothetical protein	372	75	26	2	E70539	hypothetical protein
300	25	78.1	1394	2	E70539	hypothetical protein	373	75	26	2	E70539	hypothetical protein
301	25	78.1	1394	2	E70539	hypothetical protein	374	75	26	2	E70539	hypothetical protein
302	25	78.1	1394	2	E70539	hypothetical protein	375	75	26	2	E70539	hypothetical protein
303	25	78.1	1394	2	E70539	hypothetical protein	376	75	26	2	E70539	hypothetical protein
304	25	78.1	1394	2	E70539	hypothetical protein	377	75	26	2	E70539	hypothetical protein
305	25	78.1	1394	2	E70539	hypothetical protein	378	75	26	2	E70539	hypothetical protein
306	25	78.1	1394	2	E70539	hypothetical protein	379	75	26	2	E70539	hypothetical protein
307	25	78.1	1394	2	E70539	hypothetical protein	380	75	26	2	E70539	hypothetical protein
308	25	78.1	1394	2	E70539	hypothetical protein	381	75	26	2	E70539	hypothetical protein
309	25	78.1	1394	2	E70539	hypothetical protein	382	75	26	2	E70539	hypothetical protein
310	25	78.1	1394	2	E70539	hypothetical protein	383	75	26	2	E70539	hypothetical protein
311	25	78.1	1394	2	E70539	hypothetical protein	384	75	26	2	E70539	hypothetical protein
312	25	78.1	1394	2	E70539	hypothetical protein	385	75	26	2	E70539	hypothetical protein
313	25	78.1	1394	2	E70539	hypothetical protein	386	75	26	2	E70539	hypothetical protein
314	25	78.1	1394	2	E70539	hypothetical protein	387	75	26	2	E70539	hypothetical protein
315	25	78.1	1394	2	E70539	hypothetical protein	388	75	26	2	E70539	hypothetical protein
316	25	78.1	1394	2	E70539	hypothetical protein	389	75	26	2	E70539	hypothetical protein
317	25	78.1	1394	2	E70539	hypothetical protein	390	75	26	2	E70539	hypothetical protein
318	25	78.1	1394	2	E70539	hypothetical protein	391	75	26	2	E70539	hypothetical protein
319	25	78.1	1394	2	E70539	hypothetical protein	392	75	26	2	E70539	hypothetical protein
320	25	78.1	1394	2	E70539	hypothetical protein	393	75	26	2	E70539	hypothetical protein
321	25	78.1	1394	2	E70539	hypothetical protein	394	75	26	2	E70539	hypothetical protein

495	24	75.0	165	2	H90319	hypothetical prote	469	24	75.0	214	2	324794	hypothetical prote
496	24	75.0	165	2	H90466	3-isopropylmalate	469	24	75.0	215	2	326075	hypothetical prote
497	24	75.0	165	2	H97417	uncharacterized co	470	24	75.0	216	2	169400	conserved hypothet
498	24	75.0	165	2	H97546	probable ring-clea	471	24	75.0	216	2	115417	hypothetical prote
499	24	75.0	165	2	H97394	hypothetical prote	472	24	75.0	216	2	179520	hypothetical conse
400	24	75.0	167	2	H94904	atrial protein p	473	24	75.0	216	2	115174	hypothetical prote
401	24	75.0	167	2	H56544	fimbrial protein f	474	24	75.0	217	1	A65026	uracil phosphoribo
402	24	75.0	167	2	H00952	probable fimbrial	475	24	75.0	217	2	H91948	uracil phosphoribo
403	24	75.0	167	2	H91289	fimbrial morpholog	476	24	75.0	217	2	H85894	uracil phosphoribo
404	24	75.0	167	2	A86138	fimbrial morpholog	477	24	75.0	217	2	H96188	protein 125820.5 l
405	24	75.0	167	2	H87725	probable fimbrial	478	24	75.0	217	2	C70779	hypothetical prote
406	24	75.0	168	2	H94459	3-isopropylmalate	479	24	75.0	218	2	B93862	chitinase III (
407	24	75.0	170	2	H69210	3-isopropylmalate	480	24	75.0	218	2	T44287	translation initia
408	24	75.0	170	2	H64458	3-isopropylmalate	481	24	75.0	219	2	I40525	endonuclease III (
409	24	75.0	171	2	H96562	amino group acetyl	482	24	75.0	219	2	H89924	endonuclease-like
410	24	75.0	171	2	H72951	SSU ribosomal prot	483	24	75.0	219	2	AF1411	probable endonucle
411	24	75.0	172	2	H99535	SSU ribosomal prot	484	24	75.0	219	2	AF1684	probable endonucle
412	24	75.0	172	2	H97621	hypothetical prote	485	24	75.0	220	2	H5015	hypothetical 24.8K
413	24	75.0	172	2	H99946	conserved hypothet	486	24	75.0	220	2	H70316	c4.1 nuclease III
414	24	75.0	173	2	H97430	transcription requ	487	24	75.0	220	2	H70659	probable lipoprote
415	24	75.0	174	2	H49454	cathapsin B-like p	488	24	75.0	221	2	H94288	hypothetical prote
416	24	75.0	174	2	H94189	N-methyltransferas	489	24	75.0	221	2	H72418	hypothetical prote
417	24	75.0	175	2	H74196	hypothetical prote	490	24	75.0	223	2	H59125	HWA 3.6 subunit BHA
418	24	75.0	176	2	H8615	transcription requ	491	24	75.0	223	2	S16652	hypothetical prote
419	24	75.0	177	2	H75041	hypothetical prote	492	24	75.0	224	2	H99988	probable tail asso
420	24	75.0	178	2	H55720	hypothetical prote	493	24	75.0	224	2	H85742	probable tail comp
421	24	75.0	179	2	H46839	c7a protein - vari	494	24	75.0	224	2	H95842	probable tail comp
422	24	75.0	179	2	A72154	B3c protein - vari	495	24	75.0	225	2	H91049	hypothetical prote
423	24	75.0	180	2	H45375	hypothetical prote	496	24	75.0	225	2	H61101	hypothetical prote
424	24	75.0	180	2	A99421	hypothetical 15.0K	497	24	75.0	225	2	A57271	protein c4.1 type
425	24	75.0	181	2	H88508	protein H4A12.1 l	498	24	75.0	226	2	H90464	insulin-like grow
426	24	75.0	181	2	H90442	N-methyl-D-asparta	499	24	75.0	226	2	T30199	carboxypeptidase (p
427	24	75.0	185	2	H49432	hypothetical prote	500	24	75.0	227	2	H23899	probable tail asso
428	24	75.0	185	2	H49486	transcription requ	501	24	75.0	227	2	G81118	hypothetical prote
429	24	75.0	186	2	A66984	transcription requ	502	24	75.0	229	2	H86944	conserved hypothet
430	24	75.0	185	2	H94988	transcription requ	503	24	75.0	231	2	AF0336	aspartate tautomate
431	24	75.0	185	2	H94988	conserved hypothet	504	24	75.0	231	2	A10722	hypothetical prote
432	24	75.0	185	2	H94988	hypothetical prote	505	24	75.0	233	2	H82073	hypothetical prote
433	24	75.0	186	2	AF0348	conserved hypothet	506	24	75.0	234	2	G46098	phospho 3'-phos. Pup
434	24	75.0	187	2	H74872	hsc70 protein hem	507	24	75.0	236	1	H2831	lectin - common sa
435	24	75.0	188	2	H31552	penicillin binding	508	24	75.0	236	2	AF4104	endonuclease III l
436	24	75.0	189	2	H96964	probable tail asso	509	24	75.0	236	2	H94319	URA repair protein
437	24	75.0	189	2	AF03197	hypothetical prote	510	24	75.0	236	2	H74574	hypothetical prote
438	24	75.0	192	2	H97601	hypothetical prote	511	24	75.0	236	2	H86575	hypothetical prote
439	24	75.0	195	2	H95297	probable allantoic	512	24	75.0	237	2	H82002	probable cell divi
440	24	75.0	196	2	H64968	acetyl CoA acetyl	513	24	75.0	237	2	H81240	septum site determ
441	24	75.0	197	2	H94389	unknown protein f	514	24	75.0	237	2	114778	hypothetical prote
442	24	75.0	200	2	H20522	hypothetical prote	515	24	75.0	237	2	H89990	hypothetical prote
443	24	75.0	200	2	H74059	hypothetical prote	516	24	75.0	238	2	I48605	insulin-like grow
444	24	75.0	201	2	A34710	beta-lactamase sub	517	24	75.0	238	2	S62809	type I restriction
445	24	75.0	202	2	A44357	tumor-specific tra	518	24	75.0	239	2	H71543	probable lipoprote
446	24	75.0	202	2	A71995	hypothetical prote	519	24	75.0	240	2	A39742	insulin-like grow
447	24	75.0	202	2	H99929	ribosomal protein	520	24	75.0	242	2	H75143	hypothetical prote
448	24	75.0	203	2	A54204	ribosomal protein	521	24	75.0	243	2	T49646	translation initia
449	24	75.0	203	2	H20529	ribosomal protein	522	24	75.0	243	2	H44129	kinase protein bar
450	24	75.0	203	2	H20529	transplantation an	523	24	75.0	245	2	H90823	probable tail asso
451	24	75.0	205	2	A92024	conserved hypothet	524	24	75.0	245	2	H96092	probable tail asso
452	24	75.0	205	2	H64346	hypothetical prote	525	24	75.0	245	2	S48395	9997 protein yes
453	24	75.0	207	2	H82941	uracil phosphoribo	526	24	75.0	246	1	H99994	polyhedrin - Arct
454	24	75.0	207	2	H94110	hypothetical prote	527	24	75.0	246	1	H44705	arct2 protein Be
455	24	75.0	207	2	H20590	hypothetical prote	528	24	75.0	246	2	S27441	chitinase (p5.2)
456	24	75.0	207	2	H46985	hypothetical prote	529	24	75.0	246	2	H71917	uracil phosphoribo
457	24	75.0	207	2	AF17925	multibacterium gran	530	24	75.0	246	2	A80793	probably export
458	24	75.0	208	1	H41111	uracil phosphoribo	531	24	75.0	247	2	S27412	chitinase (p5.2)
459	24	75.0	208	2	H00918	uracil phosphoribo	532	24	75.0	247	2	H96977	probable tail asso
460	24	75.0	209	2	H94461	endonuclease III (533	24	75.0	247	2	H90997	probable tail asso
461	24	75.0	209	2	H95148	endonuclease III l	534	24	75.0	247	2	A11754	hypothetical prote
462	24	75.0	209	2	H98016	DNA (apurinic or a	535	24	75.0	248	2	A12175	hypothetical prote
463	24	75.0	209	2	H20980	hypothetical prote	536	24	75.0	249	2	S12609	polyacrylimin asso
464	24	75.0	209	2	H96289	conserved hypothet	537	24	75.0	249	2	S93557	restriction modifi
465	24	75.0	211	2	H95758	probable tail asso	538	24	75.0	249	2	H71342	probable B1.1 asso
466	24	75.0	211	2	H97723	hypothetical prote	539	24	75.0	250	2	S51508	chitinase (p5.2)
467	24	75.0	214	2	H70425	endonuclease III -	540	24	75.0	251	2	A64395	hypothetical prote

541	24	75.0	551	0	550313	hypothetical prote	614	24	75.0	614	0	55732	hypothetical prote
542	24	75.0	552	0	550364	ribosomal protein	615	24	75.0	615	0	559679	transcription requ
543	24	75.0	553	0	551589	chitinase (EC 3.2.	616	24	75.0	616	0	564459	probable retrovira
544	24	75.0	554	0	553743	chitinase (EC 3.2.	617	24	75.0	617	0	565221	chitinase (EC 3.2.
545	24	75.0	555	0	553847	ribosomal protein	618	24	75.0	618	0	570126	phosphate Ape tran
546	24	75.0	556	0	556199	endonuclease III 4	619	24	75.0	619	0	580679	probable mitochond
547	24	75.0	557	0	597880	conserved hypotet	620	24	75.0	620	0	582418	ADP ribosyl cyclas
548	24	75.0	558	0	598163	high affinity Eron	621	24	75.0	621	0	587627	lacitase transpo
549	24	75.0	559	0	598499	endoglycosyl kinase	622	24	75.0	622	0	591692	beta protein - bar
550	24	75.0	560	0	635019	proteoglycan 3,	623	24	75.0	623	0	593876	protein p118 homer
551	24	75.0	561	0	693481	conserved hypotet	624	24	75.0	624	0	598152	hypothetical prote
552	24	75.0	562	0	695999	chemotactic methyl	625	24	75.0	625	0	599938	chitinase (EC 3.2.
553	24	75.0	563	0	695167	hypothetical prote	626	24	75.0	626	0	601196	hypothetical prote
554	24	75.0	564	0	701236	EMA-directed RNA p	627	24	75.0	627	0	605695	conserved hypotet
555	24	75.0	565	0	708182	endonuclease III 1	628	24	75.0	628	0	608212	conserved hypotet
556	24	75.0	566	0	732290	hypothetical prote	629	24	75.0	629	0	612316	thioredoxin reduct
557	24	75.0	567	0	738046	hypothetical prote	630	24	75.0	630	0	612938	thioredoxin reduct
558	24	75.0	568	0	739489	hypothetical prote	631	24	75.0	631	0	615622	thioredoxin reduct
559	24	75.0	569	0	759184	chitinase (EC 3.2.	632	24	75.0	632	0	615929	chitinase (EC 3.2.
560	24	75.0	570	0	826625	chitinase (EC 3.2.	633	24	75.0	633	0	616909	probable dihydropi
561	24	75.0	571	0	875907	hypothetical prote	634	24	75.0	634	0	623364	hypothetical prote
562	24	75.0	572	0	884302	hypothetical prote	635	24	75.0	635	0	625534	hypothetical prote
563	24	75.0	573	0	884908	hypothetical prote	636	24	75.0	636	0	625543	conserved hypotet
564	24	75.0	574	0	882187	hypothetical prote	637	24	75.0	637	0	625611	thioredoxin disulf
565	24	75.0	575	0	885935	spc7 RNA methylas	638	24	75.0	638	0	626186	thioredoxin disulf
566	24	75.0	576	0	887997	restriction enzyme	639	24	75.0	639	0	628231	thioredoxin reduct
567	24	75.0	577	0	920290	hypothetical prote	640	24	75.0	640	0	633917	chitinase (EC 3.2.
568	24	75.0	578	0	984314	hypothetical prote	641	24	75.0	641	0	635316	chitinase (EC 3.2.
569	24	75.0	579	0	984314	hypothetical prote	642	24	75.0	642	0	635316	chitinase (EC 3.2.
570	24	75.0	580	0	984314	hypothetical prote	643	24	75.0	643	0	635316	chitinase (EC 3.2.
571	24	75.0	581	0	984314	hypothetical prote	644	24	75.0	644	0	635316	chitinase (EC 3.2.
572	24	75.0	582	0	984314	hypothetical prote	645	24	75.0	645	0	635316	chitinase (EC 3.2.
573	24	75.0	583	0	984314	hypothetical prote	646	24	75.0	646	0	635316	chitinase (EC 3.2.
574	24	75.0	584	0	984314	hypothetical prote	647	24	75.0	647	0	635316	chitinase (EC 3.2.
575	24	75.0	585	0	984314	hypothetical prote	648	24	75.0	648	0	635316	chitinase (EC 3.2.
576	24	75.0	586	0	984314	hypothetical prote	649	24	75.0	649	0	635316	chitinase (EC 3.2.
577	24	75.0	587	0	984314	hypothetical prote	650	24	75.0	650	0	635316	chitinase (EC 3.2.
578	24	75.0	588	0	984314	hypothetical prote	651	24	75.0	651	0	635316	chitinase (EC 3.2.
579	24	75.0	589	0	984314	hypothetical prote	652	24	75.0	652	0	635316	chitinase (EC 3.2.
580	24	75.0	590	0	984314	hypothetical prote	653	24	75.0	653	0	635316	chitinase (EC 3.2.
581	24	75.0	591	0	984314	hypothetical prote	654	24	75.0	654	0	635316	chitinase (EC 3.2.
582	24	75.0	592	0	984314	hypothetical prote	655	24	75.0	655	0	635316	chitinase (EC 3.2.
583	24	75.0	593	0	984314	hypothetical prote	656	24	75.0	656	0	635316	chitinase (EC 3.2.
584	24	75.0	594	0	984314	hypothetical prote	657	24	75.0	657	0	635316	chitinase (EC 3.2.
585	24	75.0	595	0	984314	hypothetical prote	658	24	75.0	658	0	635316	chitinase (EC 3.2.
586	24	75.0	596	0	984314	hypothetical prote	659	24	75.0	659	0	635316	chitinase (EC 3.2.
587	24	75.0	597	0	984314	hypothetical prote	660	24	75.0	660	0	635316	chitinase (EC 3.2.
588	24	75.0	598	0	984314	hypothetical prote	661	24	75.0	661	0	635316	chitinase (EC 3.2.
589	24	75.0	599	0	984314	hypothetical prote	662	24	75.0	662	0	635316	chitinase (EC 3.2.
590	24	75.0	600	0	984314	hypothetical prote	663	24	75.0	663	0	635316	chitinase (EC 3.2.
591	24	75.0	601	0	984314	hypothetical prote	664	24	75.0	664	0	635316	chitinase (EC 3.2.
592	24	75.0	602	0	984314	hypothetical prote	665	24	75.0	665	0	635316	chitinase (EC 3.2.
593	24	75.0	603	0	984314	hypothetical prote	666	24	75.0	666	0	635316	chitinase (EC 3.2.
594	24	75.0	604	0	984314	hypothetical prote	667	24	75.0	667	0	635316	chitinase (EC 3.2.
595	24	75.0	605	0	984314	hypothetical prote	668	24	75.0	668	0	635316	chitinase (EC 3.2.
596	24	75.0	606	0	984314	hypothetical prote	669	24	75.0	669	0	635316	chitinase (EC 3.2.
597	24	75.0	607	0	984314	hypothetical prote	670	24	75.0	670	0	635316	chitinase (EC 3.2.
598	24	75.0	608	0	984314	hypothetical prote	671	24	75.0	671	0	635316	chitinase (EC 3.2.
599	24	75.0	609	0	984314	hypothetical prote	672	24	75.0	672	0	635316	chitinase (EC 3.2.
600	24	75.0	610	0	984314	hypothetical prote	673	24	75.0	673	0	635316	chitinase (EC 3.2.
601	24	75.0	611	0	984314	hypothetical prote	674	24	75.0	674	0	635316	chitinase (EC 3.2.
602	24	75.0	612	0	984314	hypothetical prote	675	24	75.0	675	0	635316	chitinase (EC 3.2.
603	24	75.0	613	0	984314	hypothetical prote	676	24	75.0	676	0	635316	chitinase (EC 3.2.
604	24	75.0	614	0	984314	hypothetical prote	677	24	75.0	677	0	635316	chitinase (EC 3.2.
605	24	75.0	615	0	984314	hypothetical prote	678	24	75.0	678	0	635316	chitinase (EC 3.2.
606	24	75.0	616	0	984314	hypothetical prote	679	24	75.0	679	0	635316	chitinase (EC 3.2.
607	24	75.0	617	0	984314	hypothetical prote	680	24	75.0	680	0	635316	chitinase (EC 3.2.
608	24	75.0	618	0	984314	hypothetical prote	681	24	75.0	681	0	635316	chitinase (EC 3.2.
609	24	75.0	619	0	984314	hypothetical prote	682	24	75.0	682	0	635316	chitinase (EC 3.2.
610	24	75.0	620	0	984314	hypothetical prote	683	24	75.0	683	0	635316	chitinase (EC 3.2.
611	24	75.0	621	0	984314	hypothetical prote	684	24	75.0	684	0	635316	chitinase (EC 3.2.
612	24	75.0	622	0	984314	hypothetical prote	685	24	75.0	685	0	635316	chitinase (EC 3.2.
613	24	75.0	623	0	984314	hypothetical prote	686	24	75.0	686	0	635316	chitinase (EC 3.2.

687	24	75.0	641	2	AB2777	conserved hypothetical	769	24	75.0	762	2	136079	hypothetical prote
688	24	75.0	641	2	S76480	hypothetical prote	761	24	75.0	363	2	824661	hypothetical prote
689	24	75.0	642	2	T16561	C protein-coupled	762	24	75.0	363	2	E4616	hypothetical prote
690	24	75.0	643	2	D91748	glutaryl tRNA red	763	24	75.0	363	2	A21696	hypothetical prote
691	24	75.0	644	2	G95211	anthranilate phosph	764	24	75.0	362	2	747240	amino acid transpo
692	24	75.0	644	2	A08076	anthranilate phosph	765	24	75.0	364	2	H69831	acetyl CoA transac
693	24	75.0	644	2	I25427	hypothetical prote	766	24	75.0	364	2	355529	p46 bet a2 mitoch
694	24	75.0	644	2	S20962	cellinase (EC 3.2.2)	767	24	75.0	364	2	384367	hypothetical prote
695	24	75.0	644	2	G54961	hypothetical prote	768	24	75.0	365	2	D89980	conserved hypobhel
696	24	75.0	644	2	E90967	probable reductase	769	24	75.0	366	1	I25259	phosphoprotein pho
697	24	75.0	644	2	D85816	probable reductase	770	24	75.0	366	1	AB3445	conserved hypobhel
698	24	75.0	644	2	AF0912	conserved hypobhel	771	24	75.0	366	2	JF0368	doublet in hemol
699	24	75.0	645	1	S36194	anthranilate phosph	772	24	75.0	367	2	J76139	age-related in hem
700	24	75.0	646	2	I48171	PC gamma (H4C) pro	773	24	75.0	367	2	808683	stress activated p
701	24	75.0	646	2	I23849	hypothetical prote	774	24	75.0	367	2	J17252	actin, activated
702	24	75.0	646	2	S22591	probable membrane	775	24	75.0	367	2	356592	fastidium channel
703	24	75.0	647	1	W08P42	ribonucleoside dip	776	24	75.0	367	2	A53141	alpha 42 protein
704	24	75.0	647	1	W08P42	ribonucleoside dip	777	24	75.0	367	2	345312	hypothetical prote
705	24	75.0	647	2	F69890	dolichol phosphate	778	24	75.0	367	2	096726	probable membrane
706	24	75.0	647	2	C84059	conserved hypobhel	779	24	75.0	370	1	064650	probable membrane
707	24	75.0	649	2	T34423	hypothetical prote	780	24	75.0	370	1	H71937	stomach 1 phosphat
708	24	75.0	642	2	D85898	hypothetical prote	781	24	75.0	373	2	A24003	protein kinase homol
709	24	75.0	642	2	H21259	protein tp33 pro	782	24	75.0	372	2	I34273	WAP kinase (p72.7)
710	24	75.0	642	2	A70162	hypothetical prote	783	24	75.0	372	2	382524	hypothetical prote
711	24	75.0	643	1	H01V1A	hemagglutinin HA1	784	24	75.0	372	2	A85249	probable mitochond
712	24	75.0	643	2	J62378	hemagglutinin in	785	24	75.0	372	2	I48416	acetylserine amin
713	24	75.0	643	2	J62373	hemagglutinin in	786	24	75.0	373	2	I27463	hypothetical prote
714	24	75.0	643	2	J62372	hemagglutinin in	787	24	75.0	373	2	I05462	phosphoprotein pho
715	24	75.0	643	2	G56513	weakly ATP synthas	788	24	75.0	373	1	I27314	pyroglutathione q
716	24	75.0	643	2	A01419	hemagglutinin - in	789	24	75.0	372	2	A43244	zinc metalloprotei
717	24	75.0	644	2	J21543	hemagglutinin - in	790	24	75.0	372	2	759644	probable alpha 1-2
718	24	75.0	644	2	P00319	hemagglutinin - in	791	24	75.0	378	2	311713	hypothetical prote
719	24	75.0	644	2	P00321	hemagglutinin - in	792	24	75.0	378	2	671244	calcium utilization
720	24	75.0	644	2	E84377	protein export (im	793	24	75.0	379	2	59604W	phosphoserine amin
721	24	75.0	644	2	T19639	hypothetical prote	794	24	75.0	380	2	582233	hypothetical prote
722	24	75.0	645	2	C86195	hypothetical prote	795	24	75.0	380	2	I29181	acid protei - E1e
723	24	75.0	645	2	A91266	hypothetical prote	796	24	75.0	380	2	S20157	hypothetical prote
724	24	75.0	646	2	S21255	acetylserine amin	797	24	75.0	382	2	D23397	hypothetical prote
725	24	75.0	646	2	P00660	probable reductase	798	24	75.0	382	2	375945	probable dihydrog
726	24	75.0	646	2	P00660	probable reductase	799	24	75.0	382	2	095903	probable nucleoti
727	24	75.0	646	2	H22237	Cyma protein pro	800	24	75.0	384	2	096689	probable fructokin
728	24	75.0	646	2	I31179	hypothetical prote	801	24	75.0	384	2	I27587	probable histidin
729	24	75.0	648	2	C37693	thioredoxin reduct	802	24	75.0	384	2	I36312	amino acid transp
730	24	75.0	648	2	H71487	probable glutamyl	803	24	75.0	384	2	I32252	amino acid transp
731	24	75.0	649	2	A40141	mitochondrial solu	804	24	75.0	384	2	I95201	hypothetical prote
732	24	75.0	649	2	383321	recombinant ion pr	805	24	75.0	385	2	S05114	cytochrome oxid
733	24	75.0	651	2	D87991	hypothetical prote	806	24	75.0	387	2	740339	hypothetical prote
734	24	75.0	652	2	AB2249	N-acetyl glutamate	807	24	75.0	389	2	572740	conserved hypobhel
735	24	75.0	653	2	S16789	hemagglutinin in	808	24	75.0	389	2	582140	conserved hypobhel
736	24	75.0	653	2	S16789	probable mitochond	809	24	75.0	389	2	763271	conserved hypobhel
737	24	75.0	654	2	C93673	oribitol dehydrog	810	24	75.0	391	2	372662	hypothetical prote
738	24	75.0	654	2	A95788	hemagglutinin - in	811	24	75.0	394	2	AB2211	S-adenosylmet hion
739	24	75.0	655	2	354785	peroxidase (EC 1.1	812	24	75.0	395	2	H69147	13S ribonucleos
740	24	75.0	655	2	I21129	hypothetical prote	813	24	75.0	395	2	I11248	chloroform synth
741	24	75.0	655	2	T10482	recombinant prote	814	24	75.0	396	2	A09107	putative nucleos
742	24	75.0	656	2	S01766	protein kinase A1N	815	24	75.0	397	2	A96681	hypothetical prote
743	24	75.0	656	2	A54230	class I histocompa	816	24	75.0	400	2	AB2280	hypothetical prote
744	24	75.0	656	2	C95134	integrase/recombin	817	24	75.0	401	1	V03890	sodium glutamate S
745	24	75.0	656	2	H96779	integrase recombin	818	24	75.0	401	2	A98195	glutamate transpo
746	24	75.0	656	2	EB3192	hypothetical prote	819	24	75.0	401	2	B86042	glutamate transpo
747	24	75.0	656	2	F08002	integrase/recombin	820	24	75.0	401	2	AB0969	glutamate permeas
748	24	75.0	657	2	A01972	conserved hypobhel	821	24	75.0	402	2	I23701	hypothetical prote
749	24	75.0	657	2	T22247	hypothetical prote	822	24	75.0	402	2	345541	probable membrane
750	24	75.0	658	2	S69886	hemagglutinin pro	823	24	75.0	403	2	R-2774	probable proteas
751	24	75.0	661	1	XN8P42	phosphoserine tran	824	24	75.0	403	2	H83783	hypothetical prote
752	24	75.0	661	2	H95260	conserved hypobhel	825	24	75.0	404	2	A46480	PC gamma (H4C) pro
753	24	75.0	661	2	G82530	hypothetical prote	826	24	75.0	404	2	A60397	sodium glutamate S
754	24	75.0	662	1	I33512	phosphoserine tran	827	24	75.0	404	2	B84593	hypothetical prote
755	24	75.0	662	1	I64836	phosphoserine tran	828	24	75.0	404	2	582183	conserved hypobhel
756	24	75.0	662	2	S21439	phosphoserine tran	829	24	75.0	407	2	I12086	reverse transcript
757	24	75.0	662	2	I92752	3-phosphoserine am	830	24	75.0	407	2	A46672	alpha 42 protein
758	24	75.0	662	2	I35751	3-phosphoserine am	831	24	75.0	407	2	A00706	alpha 42 protein
759	24	75.0	662	2	A09613	phosphoserine amin	832	24	75.0	408	2	I19463	hypothetical prote

833	24	75.0	409	2	T25155	hypothetical prote	906	24	75.0	450	2	T34426	hypothetical prote
834	24	75.0	410	1	22BFD	gene 11 protein	907	24	75.0	450	2	B60722	conserved hypothet
835	24	75.0	410	1	22BFD	gene 11 protein	908	24	75.0	461	2	120163	hypothetical prote
836	24	75.0	410	1	22BFD	gene 11 protein	909	24	75.0	461	2	G86498	hypothetical prote
837	24	75.0	410	2	T16132	hypothetical prote	910	24	75.0	461	2	T30972	hypothetical prote
838	24	75.0	410	2	T16132	hypothetical prote	911	24	75.0	461	2	G72121	hypothetical prote
839	24	75.0	410	2	A10506	early protein EPO	912	24	75.0	462	2	S27638	naphthalene 1,2 di
840	24	75.0	412	2	S63539	hypothetical prote	913	24	75.0	462	2	E85438	hypothetical prote
841	24	75.0	413	2	P97416	peptate lyase limp	914	24	75.0	462	2	E85438	hypothetical prote
842	24	75.0	413	2	C84994	oxo-acyl thiolase	915	24	75.0	462	2	T40205	hypothetical prote
843	24	75.0	413	2	T22108	hypothetical prote	916	24	75.0	463	2	A26552	type 1 site-specif
844	24	75.0	415	2	F36886	hypothetical prote	917	24	75.0	463	2	J35376	hypothetical prote
845	24	75.0	416	2	F47116	trifluoroxin synth	918	24	75.0	464	2	F72512	hypothetical prote
846	24	75.0	417	2	F70660	hypothetical prote	919	24	75.0	465	2	F72512	hypothetical prote
847	24	75.0	420	2	A83418	hypothetical prote	920	24	75.0	465	2	F72512	hypothetical prote
848	24	75.0	421	1	22BFD	gene 11 protein	921	24	75.0	465	2	F72512	hypothetical prote
849	24	75.0	421	2	B67973	hypothetical prote	922	24	75.0	465	2	F72512	hypothetical prote
850	24	75.0	425	2	E79323	PRM methyltransfer	923	24	75.0	465	2	F72512	hypothetical prote
851	24	75.0	425	2	A10471	3-oxoacyl transfer	924	24	75.0	465	2	F72512	hypothetical prote
852	24	75.0	426	2	C64949	stereomutational f	925	24	75.0	465	2	F72512	hypothetical prote
853	24	75.0	427	2	E83984	isocitrate lyase B	926	24	75.0	465	2	F72512	hypothetical prote
854	24	75.0	427	2	H87285	phosphoribosylamin	927	24	75.0	465	2	F72512	hypothetical prote
855	24	75.0	428	2	P70928	probable isocitrat	928	24	75.0	465	2	F72512	hypothetical prote
856	24	75.0	428	2	A94759	seryl tRNA synthet	929	24	75.0	465	2	F72512	hypothetical prote
857	24	75.0	429	2	G71018	hypothetical prote	930	24	75.0	465	2	F72512	hypothetical prote
858	24	75.0	429	2	G71018	hypothetical prote	931	24	75.0	465	2	F72512	hypothetical prote
859	24	75.0	430	2	AH0394	probable amino aci	932	24	75.0	465	2	F72512	hypothetical prote
860	24	75.0	430	2	H81039	valine-glycyl am	933	24	75.0	465	2	F72512	hypothetical prote
861	24	75.0	431	2	P81982	probable valine-g	934	24	75.0	465	2	F72512	hypothetical prote
862	24	75.0	431	2	G73433	2-oxoglutarate-ly	935	24	75.0	465	2	F72512	hypothetical prote
863	24	75.0	433	2	T06407	monohydroxyacoba	936	24	75.0	465	2	F72512	hypothetical prote
864	24	75.0	434	1	MEMSB	phosphogluconate b	937	24	75.0	465	2	F72512	hypothetical prote
865	24	75.0	434	2	A21011	isocitrate lyase	938	24	75.0	465	2	F72512	hypothetical prote
866	24	75.0	434	2	S03072	phosphogluconate b	939	24	75.0	465	2	F72512	hypothetical prote
867	24	75.0	434	2	S03072	phosphogluconate b	940	24	75.0	465	2	F72512	hypothetical prote
868	24	75.0	435	2	P96636	hypothetical prote	941	24	75.0	465	2	F72512	hypothetical prote
869	24	75.0	436	2	T00810	hypothetical prote	942	24	75.0	465	2	F72512	hypothetical prote
870	24	75.0	436	2	D70693	probable wpp lip	943	24	75.0	465	2	F72512	hypothetical prote
871	24	75.0	437	2	P84277	probable lipase	944	24	75.0	465	2	F72512	hypothetical prote
872	24	75.0	437	2	H82288	isocitrate lyase V	945	24	75.0	465	2	F72512	hypothetical prote
873	24	75.0	439	2	A03731	hypothetical prote	946	24	75.0	465	2	F72512	hypothetical prote
874	24	75.0	440	2	A03731	hypothetical prote	947	24	75.0	465	2	F72512	hypothetical prote
875	24	75.0	440	2	AH1736	nitrilolactate	948	24	75.0	465	2	F72512	hypothetical prote
876	24	75.0	442	2	H84496	DNA polymerase III	949	24	75.0	465	2	F72512	hypothetical prote
877	24	75.0	442	2	G72127	DNA polymerase III	950	24	75.0	465	2	F72512	hypothetical prote
878	24	75.0	442	2	C75067	hypothetical prote	951	24	75.0	465	2	F72512	hypothetical prote
879	24	75.0	443	2	P63067	conserved hypothet	952	24	75.0	465	2	F72512	hypothetical prote
880	24	75.0	447	2	OC5352	2-nitroethanol de	953	24	75.0	465	2	F72512	hypothetical prote
881	24	75.0	447	2	AE2418	hypothetical prote	954	24	75.0	465	2	F72512	hypothetical prote
882	24	75.0	447	2	T03435	probable mitochond	955	24	75.0	465	2	F72512	hypothetical prote
883	24	75.0	447	2	S82729	outer membrane pro	956	24	75.0	465	2	F72512	hypothetical prote
884	24	75.0	449	2	D89646	protein 2K45.8 II	957	24	75.0	465	2	F72512	hypothetical prote
885	24	75.0	449	2	C55217	polyketide aromati	958	24	75.0	465	2	F72512	hypothetical prote
886	24	75.0	449	2	J05097	polyketide aromati	959	24	75.0	465	2	F72512	hypothetical prote
887	24	75.0	449	2	J05097	naphthalene dioxy	960	24	75.0	465	2	F72512	hypothetical prote
888	24	75.0	451	2	J05097	naphthalene 1,2 di	961	24	75.0	465	2	F72512	hypothetical prote
889	24	75.0	452	2	F72309	glutathione disulf	962	24	75.0	465	2	F72512	hypothetical prote
890	24	75.0	453	2	A95212	hypothetical prote	963	24	75.0	465	2	F72512	hypothetical prote
891	24	75.0	453	2	H89077	anthranilate synth	964	24	75.0	465	2	F72512	hypothetical prote
892	24	75.0	454	2	H70118	hypothetical prote	965	24	75.0	465	2	F72512	hypothetical prote
893	24	75.0	454	2	E75291	UDP-N-methylmena	966	24	75.0	465	2	F72512	hypothetical prote
894	24	75.0	456	2	A81194	probable cell wall	967	24	75.0	465	2	F72512	hypothetical prote
895	24	75.0	456	2	E71537	seryl tRNA synthet	968	24	75.0	465	2	F72512	hypothetical prote
896	24	75.0	456	2	F81622	probable replicati	969	24	75.0	465	2	F72512	hypothetical prote
897	24	75.0	456	2	F81622	probable replicati	970	24	75.0	465	2	F72512	hypothetical prote
898	24	75.0	456	2	F81622	probable replicati	971	24	75.0	465	2	F72512	hypothetical prote
899	24	75.0	456	2	F81622	probable replicati	972	24	75.0	465	2	F72512	hypothetical prote
900	24	75.0	456	2	F81622	probable replicati	973	24	75.0	465	2	F72512	hypothetical prote
901	24	75.0	458	2	F81622	probable replicati	974	24	75.0	465	2	F72512	hypothetical prote
902	24	75.0	458	2	F81622	probable replicati	975	24	75.0	465	2	F72512	hypothetical prote
903	24	75.0	459	2	T21134	naphthalene dioxy	976	24	75.0	465	2	F72512	hypothetical prote
904	24	75.0	459	2	H85529	replication initia	977	24	75.0	465	2	F72512	hypothetical prote
905	24	75.0	460	2	H85529	chromosomal repli	978	24	75.0	465	2	F72512	hypothetical prote
906	24	75.0	460	2	C95964	SAR dependent meth	979	24	75.0	465	2	F72512	hypothetical prote

979 24 75.0 535 2 089 931
 980 24 75.0 506 2 069 963
 981 24 75.0 506 2 F88954
 982 24 75.0 508 2 D81225
 983 24 75.0 509 2 S45413
 984 24 75.0 509 2 G83432
 985 24 75.0 510 2 H83195
 986 24 75.0 511 1 S54720
 987 24 75.0 512 2 T44982
 988 24 75.0 512 2 G74505
 989 24 75.0 513 2 E72495
 990 24 75.0 514 2 B86355
 991 24 75.0 516 2 A69527
 992 24 75.0 516 2 E84019
 993 24 75.0 516 2 T44982
 994 24 75.0 520 2 H75110
 995 24 75.0 520 2 P90494
 996 24 75.0 521 2 T27192
 997 24 75.0 525 2 T30445
 998 24 75.0 525 2 T17443
 999 24 75.0 525 2 A52332
 1000 24 75.0 525 2 P46039

ALIGNMENTS

RESULT 1
 B85684
 unknown protein encoded by prophage CP-933C [imported] - Escherichia coli (strain O157:H7)
 C:Species: Escherichia coli
 C:Date: 16-Feb-2001 #sequence_revision 15 Feb-2001 #text_change 14 Sep-2001
 C:Accession: B85684
 E:Berni, N.T.; Plunkett, III, G.; Borland, V.; Mau, P.; Glasner, J.D.; Rose, D.J.; Mayhew
 Miller, L.; Grobeck, F.; Davis, N.W.; Im, A.; Pimlunta, E.; Potamousis, K.; Apostola,
 Nature 409, 529-533, 2001
 A:Title: Genomic sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; M01D:21074935; PMID:11206551
 A:Accession: B85684
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-77 -STOs
 A:Cross-references: CB:AE005374; EMBL:AF2514756; F01B:AA055934.1; GSPDB:GM03145; U03P:218
 A:Protein:411 source: strain O157:H7, Escherichia, F8943
 C:Genetics:
 A:Gene: Z1846

Query Match 93.8% Score 40; Db 2; Length 77;
 Best Local Similarity 100.0%; Pred. No. 9; Mismatches 0; Indels 0; Gaps 0;
 Matches 5; Conservative 0

QY 4 GYRN 7
 DB 15 GYRN 19

RESULT 2
 S76180
 hypothetical protein - Synecocystis sp. (strain pvc 6803)
 C:Species: Synecocystis sp.
 C:Date: 25-Apr-1997 #sequence_revision 25 Apr 1997 #text_change 08 Oct 1999
 C:Accession: S76180
 E:Kaneko, T.; Sato, S.; Katami, P.; Tanaka, A.; Asanuma, E.; Nakamura, Y.; Miyajima, N.;
 O. K.; Okumura, S.; Shimpo, S.; Takouchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
 DNA Res. 4, 109-146, 1996
 A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synecocystis
 sp.
 A:Reference number: S74322; M01D:97061291; PMID:8905241
 A:Accession: S76180
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-134 -KAN

A:Cross-references: EMBL:AF093144; GB:AA061339; K01:dl65477; F01B:AA018459.1; F01:dl101
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996

Query Match 93.8% Score 40; Db 2; Length 144;
 Best Local Similarity 100.0%; Pred. No. 17;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 DB 27 GYRN 41

RESULT 3
 B87703
 conserved hypothetical protein Y3460 [imported] - Caulobacter crescentus
 C:Species: Caulobacter crescentus
 C:Date: 20-Apr-2001 #sequence_revision 23 Apr 2001 #text_change 20 Apr 2001
 C:Accession: B87703
 E:Norman, W.C.; Goldblum, L.V.; Paulson, L.L.; Nelson, K.E.; Elson, J.; Beidell, R.;
 B. Laub, H.T.; Booy, R.L.; Rodman, R.J.; Link, A.S.; DeRubeis, R.M.; Hall, D.B.; Ko
 n. S.; Emolteva, M.; White, C.; Sallberg, S.; Shapiro, J.; Venter, J.C.; Fraser, J.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4197-4141, 2001
 A:Title: Complete genome sequence of Caulobacter crescentus.
 A:Reference number: A87249; M01D:2117698; PMID:11259647
 A:Accession: B87703
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-172 -STOs
 A:Cross-references: GB:AE005573; NID:q1425419; F01B:AA025622.1; GSPDB:GM00148
 C:Genetics:
 A:Gene: CC3660

Query Match 93.8% Score 40; Db 2; Length 172;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 DB 73 GYRN 77

RESULT 4
 S74396
 hypothetical protein, P. phlegelii, catalase 143
 N:Alternate names: hypothetical protein K05_01175
 C:Species: Mycoplasma pneumoniae
 A:Variety: ATCC 29442
 C:Date: 27-Feb-1997 #sequence_revision 25 Apr 1997 #text_change 07 Jan 1999
 C:Accession: S74396
 E:Himmelfrich, E.; Hilbert, B.; Plapp, B.; Pohl, E.; Li, R.; Hermann, R.
 Nucleic Acids Res. 24, 4420-4449, 1996
 A:Title: Complete sequence analysis of the genome of the bacterium Mycoplasma pneumoniae
 A:Reference number: S74327; M01D:97105885; PMID:8948634
 A:Accession: S74396
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-175 -HIM

A:Cross-references: EMBL:AF000018; GB:000089; NID:q1674827; F01B:AA095618.1; F01:dl17
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1996
 C:Genetics:
 A:Gene: bpt
 A:Gene code: 3883
 C:Superfamily: hypoxanthine phosphoribosyl transferase

Query Match 93.8% Score 40; Db 2; Length 175;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
 DB 159 GYRN 164

C;Keywords: aminotransferase

Query Match 94.8%; Score 40; DB 2; Length 361;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

|||||

DB 283 GYRN 287

RESULT 10

CR2572

phosphoserine aminotransferase XF2426 [imported] - Xylella fastidiosa (strain 9a5c)

C;Species: Xylella fastidiosa

C;Date: 14 Aug 2000 #sequence_revision 29 Aug 2000 #text_change 02 Sep 2000

C;Accession: CR2572

C;Anonymous: The Xylella fastidiosa Consortium of the Organizational for Non-ribid- Sequen

Nature 406, 151-157, 2000

A;Title: The genome sequence of the plant pathogen Xylella fastidiosa.

A;Reference number: AB2515; MIMB:20065717; PMID:1091047

A;Note: for a complete list of authors see reference number: A59328 below

A;Accession: CR2572

A;Status: preliminary

A;Molecule type: DNA

A;Residues: 1-362 <SIM>

A;Cross-references: GB:AE004043; GR:AE003849; NID:q107486; PIDN:AAF85125.1; GSPDR:GN001

R;Simpson, A.J.G.; Reinaub, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; A

Brites, M.R.S.; Bueno, M.R.F.; Camargo, A.A.; Camargo, E.E.A.; Carraro, D.M.; Carrer, H

submitted to GenBank, June 2000

A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.R.; Franca, S.C.; Franco, M.C.; Froh

J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramao, E.E.; Laig

chado, M.A.; Madeira, A.M.B.N.; Madeira, R.M.P.; Marico, C.L.; Marques, M.V.; Martins, F

A;Authors: Martins, F.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miranda, E.C.; Miyaki, C.Y.;

Rodrigues, V.; Rosa, A.J.; de Rosa, J.R.; V.F.; de Sa, R.G.; Santelli, R.V.; Sawasak

A;Authors: da Silva, A.C.P.; da Silva, P.P.; da Silva, A.M.; Silva, J.R.; W.A.; da Silveir

M.; Tsubaki, M.H.; Vilella, H.; Van Elteren, M.A.; Vojtisek, A.; Vojtisek, A.; V

A;Reference number: A59428

A;Contents: annotation

C;Genetics:

A;Gene: XF2426

C;Superfamily: phosphoserine aminotransferase

Query Match 94.8%; Score 30; DB 2; Length 362;

Best Local Similarity 100.0%; Pred. No. 46;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

|||||

DB 284 GYRN 298

RESULT 11

125524

hypothetical protein C06A5.9 - Caenorhabditis elegans

C;Species: Caenorhabditis elegans

C;Date: 15 Oct 1999 #sequence_revision 15 Oct 1999 #text_change 15 Oct 1999

C;Accession: 125524

R;Davidson, S.; Wohldmann, P.

submitted to the EMBL Data Library, April 1997

A;Description: The sequence of C. elegans cosmid C06A5.

A;Reference number: Z25044

A;Accession: 125524

A;Status: preliminary; translated from CR25MP.TT2

A;Molecule type: DNA

A;Residues: 1-408 <DAY>

A;Cross-references: EMBL:1997193; PIDN:AAF52442.1; GSPDR:GN00019; GSP:C06A5.9

A;Experimental source: strain B12d1 N2; clone C06A5

C;Genetics:

A;Gene: GSP-C06A5.9

A;Map position: 1

A;Features: 47, 125, 201, 251, 252, 253, 254, 255, 256, 257, 258, 259, 260, 261, 262, 263, 264, 265, 266, 267, 268, 269, 270, 271, 272, 273, 274, 275, 276, 277, 278, 279, 280, 281, 282, 283, 284, 285, 286, 287, 288, 289, 290, 291, 292, 293, 294, 295, 296, 297, 298, 299, 300, 301, 302, 303, 304, 305, 306, 307, 308, 309, 310, 311, 312, 313, 314, 315, 316, 317, 318, 319, 320, 321, 322, 323, 324, 325, 326, 327, 328, 329, 330, 331, 332, 333, 334, 335, 336, 337, 338, 339, 340, 341, 342, 343, 344, 345, 346, 347, 348, 349, 350, 351, 352, 353, 354, 355, 356, 357, 358, 359, 360, 361, 362, 363, 364, 365, 366, 367, 368, 369, 370, 371, 372, 373, 374, 375, 376, 377, 378, 379, 380, 381, 382, 383, 384, 385, 386, 387, 388, 389, 390, 391, 392, 393, 394, 395, 396, 397, 398, 399, 400, 401, 402, 403, 404, 405, 406, 407, 408, 409, 410, 411, 412, 413, 414, 415, 416, 417, 418, 419, 420, 421, 422, 423, 424, 425, 426, 427, 428, 429, 430, 431, 432, 433, 434, 435, 436, 437, 438, 439, 440, 441, 442, 443, 444, 445, 446, 447, 448, 449, 450, 451, 452, 453, 454, 455, 456, 457, 458, 459, 460, 461, 462, 463, 464, 465, 466, 467, 468, 469, 470, 471, 472, 473, 474, 475, 476, 477, 478, 479, 480, 481, 482, 483, 484, 485, 486, 487, 488, 489, 490, 491, 492, 493, 494, 495, 496, 497, 498, 499, 500, 501, 502, 503, 504, 505, 506, 507, 508, 509, 510, 511, 512, 513, 514, 515, 516, 517, 518, 519, 520, 521, 522, 523, 524, 525, 526, 527, 528, 529, 530, 531, 532, 533, 534, 535, 536, 537, 538, 539, 540, 541, 542, 543, 544, 545, 546, 547, 548, 549, 550, 551, 552, 553, 554, 555, 556, 557, 558, 559, 560, 561, 562, 563, 564, 565, 566, 567, 568, 569, 570, 571, 572, 573, 574, 575, 576, 577, 578, 579, 580, 581, 582, 583, 584, 585, 586, 587, 588, 589, 590, 591, 592, 593, 594, 595, 596, 597, 598, 599, 600, 601, 602, 603, 604, 605, 606, 607, 608, 609, 610, 611, 612, 613, 614, 615, 616, 617, 618, 619, 620, 621, 622, 623, 624, 625, 626, 627, 628, 629, 630, 631, 632, 633, 634, 635, 636, 637, 638, 639, 640, 641, 642, 643, 644, 645, 646, 647, 648, 649, 650, 651, 652, 653, 654, 655, 656, 657, 658, 659, 660, 661, 662, 663, 664, 665, 666, 667, 668, 669, 670, 671, 672, 673, 674, 675, 676, 677, 678, 679, 680, 681, 682, 683, 684, 685, 686, 687, 688, 689, 690, 691, 692, 693, 694, 695, 696, 697, 698, 699, 700, 701, 702, 703, 704, 705, 706, 707, 708, 709, 710, 711, 712, 713, 714, 715, 716, 717, 718, 719, 720, 721, 722, 723, 724, 725, 726, 727, 728, 729, 730, 731, 732, 733, 734, 735, 736, 737, 738, 739, 740, 741, 742, 743, 744, 745, 746, 747, 748, 749, 750, 751, 752, 753, 754, 755, 756, 757, 758, 759, 760, 761, 762, 763, 764, 765, 766, 767, 768, 769, 770, 771, 772, 773, 774, 775, 776, 777, 778, 779, 780, 781, 782, 783, 784, 785, 786, 787, 788, 789, 790, 791, 792, 793, 794, 795, 796, 797, 798, 799, 800, 801, 802, 803, 804, 805, 806, 807, 808, 809, 810, 811, 812, 813, 814, 815, 816, 817, 818, 819, 820, 821, 822, 823, 824, 825, 826, 827, 828, 829, 830, 831, 832, 833, 834, 835, 836, 837, 838, 839, 840, 841, 842, 843, 844, 845, 846, 847, 848, 849, 850, 851, 852, 853, 854, 855, 856, 857, 858, 859, 860, 861, 862, 863, 864, 865, 866, 867, 868, 869, 870, 871, 872, 873, 874, 875, 876, 877, 878, 879, 880, 881, 882, 883, 884, 885, 886, 887, 888, 889, 890, 891, 892, 893, 894, 895, 896, 897, 898, 899, 900, 901, 902, 903, 904, 905, 906, 907, 908, 909, 910, 911, 912, 913, 914, 915, 916, 917, 918, 919, 920, 921, 922, 923, 924, 925, 926, 927, 928, 929, 930, 931, 932, 933, 934, 935, 936, 937, 938, 939, 940, 941, 942, 943, 944, 945, 946, 947, 948, 949, 950, 951, 952, 953, 954, 955, 956, 957, 958, 959, 960, 961, 962, 963, 964, 965, 966, 967, 968, 969, 970, 971, 972, 973, 974, 975, 976, 977, 978, 979, 980, 981, 982, 983, 984, 985, 986, 987, 988, 989, 990, 991, 992, 993, 994, 995, 996, 997, 998, 999, 1000, 1001, 1002, 1003, 1004, 1005, 1006, 1007, 1008, 1009, 1010, 1011, 1012, 1013, 1014, 1015, 1016, 1017, 1018, 1019, 1020, 1021, 1022, 1023, 1024, 1025, 1026, 1027, 1028, 1029, 1030, 1031, 1032, 1033, 1034, 1035, 1036, 1037, 1038, 1039, 1040, 1041, 1042, 1043, 1044, 1045, 1046, 1047, 1048, 1049, 1050, 1051, 1052, 1053, 1054, 1055, 1056, 1057, 1058, 1059, 1060, 1061, 1062, 1063, 1064, 1065, 1066, 1067, 1068, 1069, 1070, 1071, 1072, 1073, 1074, 1075, 1076, 1077, 1078, 1079, 1080, 1081, 1082, 1083, 1084, 1085, 1086, 1087, 1088, 1089, 1090, 1091, 1092, 1093, 1094, 1095, 1096, 1097, 1098, 1099, 1100, 1101, 1102, 1103, 1104, 1105, 1106, 1107, 1108, 1109, 1110, 1111, 1112, 1113, 1114, 1115, 1116, 1117, 1118, 1119, 1120, 1121, 1122, 1123, 1124, 1125, 1126, 1127, 1128, 1129, 1130, 1131, 1132, 1133, 1134, 1135, 1136, 1137, 1138, 1139, 1140, 1141, 1142, 1143, 1144, 1145, 1146, 1147, 1148, 1149, 1150, 1151, 1152, 1153, 1154, 1155, 1156, 1157, 1158, 1159, 1160, 1161, 1162, 1163, 1164, 1165, 1166, 1167, 1168, 1169, 1170, 1171, 1172, 1173, 1174, 1175, 1176, 1177, 1178, 1179, 1180, 1181, 1182, 1183, 1184, 1185, 1186, 1187, 1188, 1189, 1190, 1191, 1192, 1193, 1194, 1195, 1196, 1197, 1198, 1199, 1200, 1201, 1202, 1203, 1204, 1205, 1206, 1207, 1208, 1209, 1210, 1211, 1212, 1213, 1214, 1215, 1216, 1217, 1218, 1219, 1220, 1221, 1222, 1223, 1224, 1225, 1226, 1227, 1228, 1229, 1230, 1231, 1232, 1233, 1234, 1235, 1236, 1237, 1238, 1239, 1240, 1241, 1242, 1243, 1244, 1245, 1246, 1247, 1248, 1249, 1250, 1251, 1252, 1253, 1254, 1255, 1256, 1257, 1258, 1259, 1260, 1261, 1262, 1263, 1264, 1265, 1266, 1267, 1268, 1269, 1270, 1271, 1272, 1273, 1274, 1275, 1276, 1277, 1278, 1279, 1280, 1281, 1282, 1283, 1284, 1285, 1286, 1287, 1288, 1289, 1290, 1291, 1292, 1293, 1294, 1295, 1296, 1297, 1298, 1299, 1300, 1301, 1302, 1303, 1304, 1305, 1306, 1307, 1308, 1309, 1310, 1311, 1312, 1313, 1314, 1315, 1316, 1317, 1318, 1319, 1320, 1321, 1322, 1323, 1324, 1325, 1326, 1327, 1328, 1329, 1330, 1331, 1332, 1333, 1334, 1335, 1336, 1337, 1338, 1339, 1340, 1341, 1342, 1343, 1344, 1345, 1346, 1347, 1348, 1349, 1350, 1351, 1352, 1353, 1354, 1355, 1356, 1357, 1358, 1359, 1360, 1361, 1362, 1363, 1364, 1365, 1366, 1367, 1368, 1369, 1370, 1371, 1372, 1373, 1374, 1375, 1376, 1377, 1378, 1379, 1380, 1381, 1382, 1383, 1384, 1385, 1386, 1387, 1388, 1389, 1390, 1391, 1392, 1393, 1394, 1395, 1396, 1397, 1398, 1399, 1400, 1401, 1402, 1403, 1404, 1405, 1406, 1407, 1408, 1409, 1410, 1411, 1412, 1413, 1414, 1415, 1416, 1417, 1418, 1419, 1420, 1421, 1422, 1423, 1424, 1425, 1426, 1427, 1428, 1429, 1430, 1431, 1432, 1433, 1434, 1435, 1436, 1437, 1438, 1439, 1440, 1441, 1442, 1443, 1444, 1445, 1446, 1447, 1448, 1449, 1450, 1451, 1452, 1453, 1454, 1455, 1456, 1457, 1458, 1459, 1460, 1461, 1462, 1463, 1464, 1465, 1466, 1467, 1468, 1469, 1470, 1471, 1472, 1473, 1474, 1475, 1476, 1477, 1478, 1479, 1480, 1481, 1482, 1483, 1484, 1485, 1486, 1487, 1488, 1489, 1490, 1491, 1492, 1493, 1494, 1495, 1496, 1497, 1498, 1499, 1500, 1501, 1502, 1503, 1504, 1505, 1506, 1507, 1508, 1509, 1510, 1511, 1512, 1513, 1514, 1515, 1516, 1517, 1518, 1519, 1520, 1521, 1522, 1523, 1524, 1525, 1526, 1527, 1528, 1529, 1530, 1531, 1532, 1533, 1534, 1535, 1536, 1537, 1538, 1539, 1540, 1541, 1542, 1543, 1544, 1545, 1546, 1547, 1548, 1549, 1550, 1551, 1552, 1553, 1554, 1555, 1556, 1557, 1558, 1559, 1560, 1561, 1562, 1563, 1564, 1565, 1566, 1567, 1568, 1569, 1570, 1571, 1572, 1573, 1574, 1575, 1576, 1577, 1578, 1579, 1580, 1581, 1582, 1583, 1584, 1585, 1586, 1587, 1588, 1589, 1590, 1591, 1592, 1593, 1594, 1595, 1596, 1597, 1598, 1599, 1600, 1601, 1602, 1603, 1604, 1605, 1606, 1607, 1608, 1609, 1610, 1611, 1612, 1613, 1614, 1615, 1616, 1617, 1618, 1619, 1620, 1621, 1622, 1623, 1624, 1625, 1626, 1627, 1628, 1629, 1630, 1631, 1632, 1633, 1634, 1635, 1636, 1637, 1638, 1639, 1640, 1641, 1642, 1643, 1644, 1645, 1646, 1647, 1648, 1649, 1650, 1651, 1652, 1653, 1654, 1655, 1656, 1657, 1658, 1659, 1660, 1661, 1662, 1663, 1664, 1665, 1666, 1667, 1668, 1669, 1670, 1671, 1672, 1673, 1674, 1675, 1676, 1677, 1678, 1679, 1680, 1681, 1682, 1683, 1684, 1685, 1686, 1687, 1688, 1689, 1690, 1691, 1692, 1693, 1694, 1695, 1696, 1697, 1698, 1699, 1700, 1701, 1702, 1703, 1704, 1705, 1706, 1707, 1708, 1709, 1710, 1711, 1712, 1713, 1714, 1715, 1716, 1717, 1718, 1719, 1720, 1721, 1722, 1723, 1724, 1725, 1726, 1727, 1728, 1729, 1730, 1731, 1732, 1733, 1734, 1735, 1736, 1737, 1738, 1739, 1740, 1741, 1742, 1743, 1744, 1745, 1746, 1747, 1748, 1749, 1750, 1751, 1752, 1753, 1754, 1755, 1756, 1757, 1758, 1759, 1760, 1761, 1762, 1763, 1764, 1765, 1766, 1767, 1768, 1769, 1770, 1771, 1772, 1773, 1774, 1775, 1776, 1777, 1778, 1779, 1780, 1781, 1782, 1783, 1784, 1785, 1786, 1787, 1788, 1789, 1790, 1791, 1792, 1793, 1794, 1795, 1796, 1797, 1798, 1799, 1800, 1801, 1802, 1803, 1804, 1805, 1806, 1807, 1808, 1809, 1810, 1811, 1812, 1813, 1814, 1815, 1816, 1817, 1818, 1819, 1820, 1821, 1822, 1823, 1824, 1825, 1826, 1827, 1828, 1829, 1830, 1831, 1832, 1833, 1834, 183

Db 458 GYFN 462

RESULT 16

116274

hypothetical protein F45D2.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20 Sep 1999 #sequence_revision 24 Nov 1999

C:Accession: 116274

C:Gene: mXic

submitted to the EMBL data library, June 1995

A:Description: the sequence of C. elegans cosmid F35D2.

A:Reference number: Z18488

A:Accession: 116274

A:Status: preliminary; translated from ORF4MP7.DIRJ

A:Molecule type: DNA

A:Residues: 1747 cons.

A:Cross-references: EMBL:U08741, MIPS:961200, F15:961204, F15:961204, F15:961204

A:Experimental source: strain Bristol N2

C:Genetics:

A:Gene: CSP:F45D2.4

A:Introns: 17, 58, 125, 176, 243, 374, 471, 541, 605, 679

C:Superfamily: Caenorhabditis elegans hypothetical protein F45D2.4

Query Match: 94.8%; Score 40; DB 2; Length 747;

Best Local Similarity: 100.0%; Pred. No. 96;

Matches: 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GYFN 7

|||||

Db 106 GYFN 110

RESULT 17

S40937

hypothetical protein Z6432.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 06 Jan 1999 #sequence_revision 06 Jan 1999 #text_change 24 Nov 1999

C:Accession: S40937

C:Gene: mXic

submitted to the EMBL data library, February 1999

A:Reference number: S40933

A:Accession: S40937

A:Molecule type: DNA

A:Residues: 1824 cons.

A:Cross-references: EMBL:U22191, MIPS:920798, F15:920798

C:Genetics:

A:Introns: 13, 24, 31, 36, 43, 50, 57, 64, 71, 78, 85, 92, 99, 106, 113, 120, 127, 134, 141, 148, 155, 162, 169, 176, 183, 190, 197, 204, 211, 218, 225, 232, 239, 246, 253, 260, 267, 274, 281, 288, 295, 302, 309, 316, 323, 330, 337, 344, 351, 358, 365, 372, 379, 386, 393, 400, 407, 414, 421, 428, 435, 442, 449, 456, 463, 470, 477, 484, 491, 498, 505, 512, 519, 526, 533, 540, 547, 554, 561, 568, 575, 582, 589, 596, 603, 610, 617, 624, 631, 638, 645, 652, 659, 666, 673, 680, 687, 694, 701, 708, 715, 722, 729, 736, 743, 750, 757, 764, 771, 778, 785, 792, 799, 806, 813, 820, 827, 834, 841, 848, 855, 862, 869, 876, 883, 890, 897, 904, 911, 918, 925, 932, 939, 946, 953, 960, 967, 974, 981, 988, 995, 1002, 1009, 1016, 1023, 1030, 1037, 1044, 1051, 1058, 1065, 1072, 1079, 1086, 1093, 1100, 1107, 1114, 1121, 1128, 1135, 1142, 1149, 1156, 1163, 1170, 1177, 1184, 1191, 1198, 1205, 1212, 1219, 1226, 1233, 1240, 1247, 1254, 1261, 1268, 1275, 1282, 1289, 1296, 1303, 1310, 1317, 1324, 1331, 1338, 1345, 1352, 1359, 1366, 1373, 1380, 1387, 1394, 1401, 1408, 1415, 1422, 1429, 1436, 1443, 1450, 1457, 1464, 1471, 1478, 1485, 1492, 1499, 1506, 1513, 1520, 1527, 1534, 1541, 1548, 1555, 1562, 1569, 1576, 1583, 1590, 1597, 1604, 1611, 1618, 1625, 1632, 1639, 1646, 1653, 1660, 1667, 1674, 1681, 1688, 1695, 1702, 1709, 1716, 1723, 1730, 1737, 1744, 1751, 1758, 1765, 1772, 1779, 1786, 1793, 1800, 1807, 1814, 1821, 1828, 1835, 1842, 1849, 1856, 1863, 1870, 1877, 1884, 1891, 1898, 1905, 1912, 1919, 1926, 1933, 1940, 1947, 1954, 1961, 1968, 1975, 1982, 1989, 1996, 2003, 2010, 2017, 2024, 2031, 2038, 2045, 2052, 2059, 2066, 2073, 2080, 2087, 2094, 2101, 2108, 2115, 2122, 2129, 2136, 2143, 2150, 2157, 2164, 2171, 2178, 2185, 2192, 2199, 2206, 2213, 2220, 2227, 2234, 2241, 2248, 2255, 2262, 2269, 2276, 2283, 2290, 2297, 2304, 2311, 2318, 2325, 2332, 2339, 2346, 2353, 2360, 2367, 2374, 2381, 2388, 2395, 2402, 2409, 2416, 2423, 2430, 2437, 2444, 2451, 2458, 2465, 2472, 2479, 2486, 2493, 2500, 2507, 2514, 2521, 2528, 2535, 2542, 2549, 2556, 2563, 2570, 2577, 2584, 2591, 2598, 2605, 2612, 2619, 2626, 2633, 2640, 2647, 2654, 2661, 2668, 2675, 2682, 2689, 2696, 2703, 2710, 2717, 2724, 2731, 2738, 2745, 2752, 2759, 2766, 2773, 2780, 2787, 2794, 2801, 2808, 2815, 2822, 2829, 2836, 2843, 2850, 2857, 2864, 2871, 2878, 2885, 2892, 2899, 2906, 2913, 2920, 2927, 2934, 2941, 2948, 2955, 2962, 2969, 2976, 2983, 2990, 2997, 3004, 3011, 3018, 3025, 3032, 3039, 3046, 3053, 3060, 3067, 3074, 3081, 3088, 3095, 3102, 3109, 3116, 3123, 3130, 3137, 3144, 3151, 3158, 3165, 3172, 3179, 3186, 3193, 3200, 3207, 3214, 3221, 3228, 3235, 3242, 3249, 3256, 3263, 3270, 3277, 3284, 3291, 3298, 3305, 3312, 3319, 3326, 3333, 3340, 3347, 3354, 3361, 3368, 3375, 3382, 3389, 3396, 3403, 3410, 3417, 3424, 3431, 3438, 3445, 3452, 3459, 3466, 3473, 3480, 3487, 3494, 3501, 3508, 3515, 3522, 3529, 3536, 3543, 3550, 3557, 3564, 3571, 3578, 3585, 3592, 3599, 3606, 3613, 3620, 3627, 3634, 3641, 3648, 3655, 3662, 3669, 3676, 3683, 3690, 3697, 3704, 3711, 3718, 3725, 3732, 3739, 3746, 3753, 3760, 3767, 3774, 3781, 3788, 3795, 3802, 3809, 3816, 3823, 3830, 3837, 3844, 3851, 3858, 3865, 3872, 3879, 3886, 3893, 3900, 3907, 3914, 3921, 3928, 3935, 3942, 3949, 3956, 3963, 3970, 3977, 3984, 3991, 3998, 4005, 4012, 4019, 4026, 4033, 4040, 4047, 4054, 4061, 4068, 4075, 4082, 4089, 4096, 4103, 4110, 4117, 4124, 4131, 4138, 4145, 4152, 4159, 4166, 4173, 4180, 4187, 4194, 4201, 4208, 4215, 4222, 4229, 4236, 4243, 4250, 4257, 4264, 4271, 4278, 4285, 4292, 4299, 4306, 4313, 4320, 4327, 4334, 4341, 4348, 4355, 4362, 4369, 4376, 4383, 4390, 4397, 4404, 4411, 4418, 4425, 4432, 4439, 4446, 4453, 4460, 4467, 4474, 4481, 4488, 4495, 4502, 4509, 4516, 4523, 4530, 4537, 4544, 4551, 4558, 4565, 4572, 4579, 4586, 4593, 4600, 4607, 4614, 4621, 4628, 4635, 4642, 4649, 4656, 4663, 4670, 4677, 4684, 4691, 4698, 4705, 4712, 4719, 4726, 4733, 4740, 4747, 4754, 4761, 4768, 4775, 4782, 4789, 4796, 4803, 4810, 4817, 4824, 4831, 4838, 4845, 4852, 4859, 4866, 4873, 4880, 4887, 4894, 4901, 4908, 4915, 4922, 4929, 4936, 4943, 4950, 4957, 4964, 4971, 4978, 4985, 4992, 4999, 5006, 5013, 5020, 5027, 5034, 5041, 5048, 5055, 5062, 5069, 5076, 5083, 5090, 5097, 5104, 5111, 5118, 5125, 5132, 5139, 5146, 5153, 5160, 5167, 5174, 5181, 5188, 5195, 5202, 5209, 5216, 5223, 5230, 5237, 5244, 5251, 5258, 5265, 5272, 5279, 5286, 5293, 5300, 5307, 5314, 5321, 5328, 5335, 5342, 5349, 5356, 5363, 5370, 5377, 5384, 5391, 5398, 5405, 5412, 5419, 5426, 5433, 5440, 5447, 5454, 5461, 5468, 5475, 5482, 5489, 5496, 5503, 5510, 5517, 5524, 5531, 5538, 5545, 5552, 5559, 5566, 5573, 5580, 5587, 5594, 5601, 5608, 5615, 5622, 5629, 5636, 5643, 5650, 5657, 5664, 5671, 5678, 5685, 5692, 5699, 5706, 5713, 5720, 5727, 5734, 5741, 5748, 5755, 5762, 5769, 5776, 5783, 5790, 5797, 5804, 5811, 5818, 5825, 5832, 5839, 5846, 5853, 5860, 5867, 5874, 5881, 5888, 5895, 5902, 5909, 5916, 5923, 5930, 5937, 5944, 5951, 5958, 5965, 5972, 5979, 5986, 5993, 6000, 6007, 6014, 6021, 6028, 6035, 6042, 6049, 6056, 6063, 6070, 6077, 6084, 6091, 6098, 6105, 6112, 6119, 6126, 6133, 6140, 6147, 6154, 6161, 6168, 6175, 6182, 6189, 6196, 6203, 6210, 6217, 6224, 6231, 6238, 6245, 6252, 6259, 6266, 6273, 6280, 6287, 6294, 6301, 6308, 6315, 6322, 6329, 6336, 6343, 6350, 6357, 6364, 6371, 6378, 6385, 6392, 6399, 6406, 6413, 6420, 6427, 6434, 6441, 6448, 6455, 6462, 6469, 6476, 6483, 6490, 6497, 6504, 6511, 6518, 6525, 6532, 6539, 6546, 6553, 6560, 6567, 6574, 6581, 6588, 6595, 6602, 6609, 6616, 6623, 6630, 6637, 6644, 6651, 6658, 6665, 6672, 6679, 6686, 6693, 6700, 6707, 6714, 6721, 6728, 6735, 6742, 6749, 6756, 6763, 6770, 6777, 6784, 6791, 6798, 6805, 6812, 6819, 6826, 6833, 6840, 6847, 6854, 6861, 6868, 6875, 6882, 6889, 6896, 6903, 6910, 6917, 6924, 6931, 6938, 6945, 6952, 6959, 6966, 6973, 6980, 6987, 6994, 7001, 7008, 7015, 7022, 7029, 7036, 7043, 7050, 7057, 7064, 7071, 7078, 7085, 7092, 7099, 7106, 7113, 7120, 7127, 7134, 7141, 7148, 7155, 7162, 7169, 7176, 7183, 7190, 7197, 7204, 7211, 7218, 7225, 7232, 7239, 7246, 7253, 7260, 7267, 7274, 7281, 7288, 7295, 7302, 7309, 7316, 7323, 7330, 7337, 7344, 7351, 7358, 7365, 7372, 7379, 7386, 7393, 7400, 7407, 7414, 7421, 7428, 7435, 7442, 7449, 7456, 7463, 7470, 7477, 7484, 7491, 7498, 7505, 7512, 7519, 7526, 7533, 7540, 7547, 7554, 7561, 7568, 7575, 7582, 7589, 7596, 7603, 7610, 7617, 7624, 7631, 7638, 7645, 7652, 7659, 7666, 7673, 7680, 7687, 7694, 7701, 7708, 7715, 7722, 7729, 7736, 7743, 7750, 7757, 7764, 7771, 7778, 7785, 7792, 7799, 7806, 7813, 7820, 7827, 7834, 7841, 7848, 7855, 7862, 7869, 7876, 7883, 7890, 7897, 7904, 7911, 7918, 7925, 7932, 7939, 7946, 7953, 7960, 7967, 7974, 7981, 7988, 7995, 8002, 8009, 8016, 8023, 8030, 8037, 8044, 8051, 8058, 8065, 8072, 8079, 8086, 8093, 8100, 8107, 8114, 8121, 8128, 8135, 8142, 8149, 8156, 8163, 8170, 8177, 8184, 8191, 8198, 8205, 8212, 8219, 8226, 8233, 8240, 8247, 8254, 8261, 8268, 8275, 8282, 8289, 8296, 8303, 8310, 8317, 8324, 8331, 8338, 8345, 8352, 8359, 8366, 8373, 8380, 8387, 8394, 8401, 8408, 8415, 8422, 8429, 8436, 8443, 8450, 8457, 8464, 8471, 8478, 8485, 8492, 8499, 8506, 8513, 8520, 8527, 8534, 8541, 8548, 8555, 8562, 8569, 8576, 8583, 8590, 8597, 8604, 8611, 8618, 8625, 8632, 8639, 8646, 8653, 8660, 8667, 8674, 8681, 8688, 8695, 8702, 8709, 8716, 8723, 8730, 8737, 8744, 8751, 8758, 8765, 8772, 8779, 8786, 8793, 8800, 8807, 8814, 8821, 8828, 8835, 8842, 8849, 8856, 8863, 8870, 8877, 8884, 8891, 8898, 8905, 8912, 8919, 8926, 8933, 8940, 8947, 8954, 8961, 8968, 8975, 8982, 8989, 8996, 9003, 9010, 9017, 9024, 9031, 9038, 9045, 9052, 9059, 9066, 9073, 9080, 9087, 9094, 9101, 9108, 9115, 9122, 9129, 9136, 9143, 9150, 9157, 9164, 9171, 9178, 9185, 9192, 9199, 9206, 9213, 9220, 9227, 9234, 9241, 9248, 9255, 9262, 9269, 9276, 9283, 9290, 9297, 9304, 9311, 9318, 9325, 9332, 9339, 9346, 9353, 9360, 9367, 9374, 9381, 9388, 9395, 9402, 9409, 9416, 9423, 9430, 9437, 9444, 9451, 9458, 9465, 9472, 9479, 9486, 9493, 9500, 9507, 9514, 9521, 9528, 9535, 9542, 9549, 9556, 9563, 9570, 9577, 9584, 9591, 9598, 9605, 9612, 9619, 9626, 9633, 9640, 9647, 9654, 9661, 9668, 9675, 9682, 9689, 9696, 9703, 9710, 9717, 9724, 9731, 9738, 9745, 9752, 9759, 9766, 9773, 9780, 9787, 9794, 9801, 9808, 9815, 9822, 9829, 9836, 9843, 9850, 9857, 9864, 9871, 9878, 9885, 9892, 9899, 9906, 9913, 9920, 9927, 9934, 9941, 9948, 9955, 9962, 9969, 9976, 9983, 9990, 9997, 10004, 10011, 10018, 10025, 10032, 10039, 10046, 10053, 10060, 10067, 10074, 10081, 10088, 10095, 10102, 10109, 10116, 10123, 10130, 10137, 10144, 10151, 10158, 10165, 10172, 10179, 10186, 10193, 10200, 10207, 10214, 10221, 10228, 10235, 10242, 10249, 10256, 10263, 10270, 10277, 10284, 10291, 10298, 10305, 10312, 10319, 10326, 10333, 10340, 10347, 10354, 10361, 10368, 10375, 10382, 10389, 10396, 10403, 10410, 10417, 10424, 10431, 10438, 10445, 10452, 10459, 10466, 10473, 10480, 10487, 10494, 10501, 10508, 10515, 10522, 10529, 10536, 10543, 10550, 10557, 10564, 10571, 10578, 10585, 10592, 10599, 10606, 10613, 10620, 10627, 10634, 10641, 10648, 10655, 10662, 10669, 10676, 10683, 10690, 10697, 10704, 10711, 10718, 10725, 10732, 10739, 10746, 10753, 10760, 10767, 10774, 10781, 10788, 10795, 10802, 10809, 10816, 10823, 10830, 10837, 10844, 10851, 10858, 10865, 10872, 10879, 10886, 10893, 10900, 10907, 10914, 10921, 10928, 10935, 10942, 10949, 10956, 10963, 10970, 10977, 10984, 10991, 10998, 11005, 11012, 11019, 11026, 11033, 11040, 11047, 11054, 11061, 11068, 11075, 11082, 11089, 11096, 11103, 11110, 11117, 11124, 11131, 11138, 11145, 11152, 11159, 11166, 11173, 11180, 11187, 11194, 11201, 11208, 11215, 11222, 11229, 11236, 11243, 11250, 11257, 11264, 11271, 11278, 11285, 11292, 11299, 11306, 11313, 11320, 11327, 11334, 11341, 11348, 11355, 11362, 11369, 11376, 11383, 11390, 11397, 11404, 11411, 11418, 11425, 11432, 11439, 11446, 11453, 11460, 11467, 11474, 11481, 11488, 11495, 11502, 11509, 11516, 11523, 11530, 11537, 11544, 11551, 11558, 11565, 11572, 11579, 11586, 11593, 11600, 11607, 11614, 11621, 11628, 11635, 11642, 11649, 11656, 11663, 11670, 11677, 11684, 11691, 11698, 11705, 11712, 11719, 11726, 11733, 11740, 11747, 11754, 11761, 11768, 11775, 11782, 11789, 11796, 11803, 11810, 11817, 11824, 11831, 11838, 11845, 11852, 11859, 11866, 11873, 11880, 11887, 11894, 11901, 11908, 11915, 11922, 11929, 11936, 11943, 11950, 11957,

A:Cross-references: GB:AF006674; M10:313424973; F10:AAV26159 1; GSTTP GM20148
 C:Genetics:
 A:Gene: GC3157

Query Match 93.8%, Score 38, DB 2: Length 1041,
 Best Local Similarity 100.0%, Pred. No. 2: 60-92,
 Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0.

QY 3 GYRN 7

DB 516 GYRN 520

RESULT 21

S55517

Probable transport protein PDR10 - yeast (Saccharomyces cerevisiae)
 N:Alternate names: Probable ABC transporter PDR10; protein YOR328W

C:Species: Saccharomyces cerevisiae

C:Date: 01-Aug-1995; accession: S55517; S67245; S71968

R:Parle, A.G., Hand, N.J., Goulding, S.F., Wolfe, K.H.

submitted to the EMBL Data Library, June 1995

A:Description: PDR10, a candidate pleiotropic drug resistance locus encoding a new ABC

A:Reference number: S55517

A:Accession: S55517

A:Molecule type: DNA

A:Residues: 1-1564 <PAF>

A:Cross references: EMBL:Z49821; M10:313424973; F10:AAV26159 1; F10:30119

R:Parle, A.G., Hand, N.J., Goulding, S.F., Wolfe, K.H.

submitted to the EMBL Data Library, June 1995

A:Description: Sequence of 29 kilobases around the PDR10 locus on the right arm of Sacch

A:Reference number: S62058

A:Accession: S62058

A:Molecule type: DNA

A:Residues: 1-1564 <PAF>

A:Cross references: EMBL:Z49821; M10:313424973; F10:AAV26159 1; F10:30119

R:Song, J.M.; Cheung, E.; Rabinowitz, J.C.

submitted to the EMBL Data Library, December 1995

A:Description: Cloning and characterization of the Saccharomyces cerevisiae FIB1 gene.

A:Reference number: S61955

A:Accession: S61957

A:Molecule type: DNA

A:Residues: 1392-1427, 1436-1564 <GOW>

A:Cross-references: EMBL:Z42227; M10:31147766; F10:AAV26159 1; F10:30119

R:Goulding, S.F.; Hand, N.J.; Parle-McDermott, A.G.; Wolfe, K.H.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S67233

A:Accession: S67235

A:Molecule type: DNA

A:Residues: 1-1564 <GOW>

A:Cross-references: EMBL:Z42227; M10:31147766; F10:AAV26159 1; F10:30119

R:Parle-McDermott, A.G.; Hand, N.J.; Goulding, S.F.; Wolfe, K.H.

Yeast 12, 994-1004, 1996

A:Title: Sequence of the FIB1 locus on the right arm of Saccharomyces cere

A:Reference number: S71966; M10:37051586; M10:37051586

A:Accession: S71968

A:Molecule type: DNA

A:Status: nucleic acid sequence not shown; translation not shown

A:Residues: 1-1564 <PAF>

A:Cross-references: EMBL:Z49821; M10:31147766; F10:AAV26159 1; F10:30119

A:Note: the nucleic acid sequence was submitted to the EMBL Data Library, June 1995

C:Genetics:

A:Gene: SGP-PDR10

A:Cross references: SGP:SGP00696; M10:37051586

A:Map position: 159

C:Keywords: ABC-binding cassette protein; ABC-binding cassette homology

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)

F10:406/Domain: ABC-binding cassette homology (ABC)
 F10:406/Domain: ABC-binding cassette homology (ABC)
 F10:406/Domain: ABC-binding cassette homology (ABC)
 F10:406/Domain: ABC-binding cassette homology (ABC)
 F10:406/Domain: ABC-binding cassette homology (ABC)
 F10:406/Domain: ABC-binding cassette homology (ABC)
 F10:406/Domain: ABC-binding cassette homology (ABC)
 F10:406/Domain: ABC-binding cassette homology (ABC)
 F10:406/Domain: ABC-binding cassette homology (ABC)
 F10:406/Domain: ABC-binding cassette homology (ABC)

Query Match 93.8%, Score 38, DB 2: Length 1041

Best Local Similarity 100.0%, Pred. No. 2: 60-92

Matches 5, Conservative 0, Mismatches 0, Indels 0, Gaps 0

QY 3 GYRN 7

DB 1111

DB 1063 GYRN 1467

RESULT 22

H70251

Agglutinin protein H70251 - Lym disease spirochaete

C:Species: Borrelia burgdorferi (Lyme disease spirochaete)

C:Date: 13-Feb-1994; accession: H70251; H70251; H70251

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; W

son, D.; Peterson, J.; Kitzberger, A.P.; Galloway, J.; Salzman, S.; Hanson, M.; V

homann, C.; Gattand, S.; Fujita, C.; Gatten, M.; Horst, K.; Roberts, K.; Hatch, B

ature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi.

A:Reference number: A70100; M10:37051586; F10:AAV26159 1; F10:30119

A:Accession: H70251

A:Status: protein; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-36 <KDE>

A:Cross references: EMBL:Z49821; M10:37051586; F10:AAV26159 1; F10:30119

A:Experimental source: strain B31

C:Genetics:

A:Genome: plasmid

Query Match 84.1%, Score 27, DB 2: Length 36

Best Local Similarity 80.0%, Pred. No. 2: 1

Matches 4, Conservative 1, Mismatches 0, Indels 0, Gaps 0

QY 3 GYRN 7

DB 1111

DB 6 GYRN 10

RESULT 23

F70187

Ribosomal protein L22 - Lyme disease spirochaete

C:Species: Borrelia burgdorferi (Lyme disease spirochaete)

C:Date: 22-Oct-1992; accession: F70187; F70187; F70187

R:Fraser, C.M.; Casjens, S.; Huang, W.M.; Sutton, G.G.; Clayton, R.; Lathigra, R.; W

son, D.; Peterson, J.; Kitzberger, A.P.; Galloway, J.; Salzman, S.; Hanson, M.; V

homann, C.; Gattand, S.; Fujita, C.; Gatten, M.; Horst, K.; Roberts, K.; Hatch, B

Nature 390, 580-586, 1997

A:Authors: Smith, H.O.; Venter, J.C.

A:Title: Genomic sequence of a Lyme disease spirochaete, Borrelia burgdorferi

A:Reference number: A70100; M10:37051586; F10:AAV26159 1; F10:30119

A:Accession: F70187

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-60 <KDE>

A:Cross references: EMBL:Z49821; M10:37051586; F10:AAV26159 1; F10:30119

A:Experimental source: strain B31

C:Function:

A:Pathway: protein biosynthesis

C:Keywords: protein biosynthesis; ribosome

F10:406/Domain: ribosome; protein biosynthesis

F10:406/Domain: ribosome; protein biosynthesis

F10:406/Domain: ribosome; protein biosynthesis

F10:406/Domain: ribosome; protein biosynthesis

F10:406/Domain: ribosome; protein biosynthesis

F10:406/Domain: ribosome; protein biosynthesis

F10:406/Domain: ribosome; protein biosynthesis

F10:406/Domain: ribosome; protein biosynthesis

F10:406/Domain: ribosome; protein biosynthesis


```

Query Match      84.4% Score 27; ID 2; Length 340;
Best Local Similarity 80.0%; Pred. No. 2.5e-02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 254 GYRN 258
11111

RESULT 44
E64376
endonuclease III - Methanococcus jannaschii
C:Species: Methanococcus jannaschii
C:Date: 14-Sep-1996 #sequence_revision 14-Sep-1996 #text_change 10-Oct-1997
C:Accession: E64376
R:Bull, C.J.; White, G.J.; Zhou, L.; Fleischmann, P.B.; Satchell, G.O.; Plake,
  T.D.; Sgadiw, P.W.; Hana, M.C.; Goffen, M.E.; Roberts, K.M.; Hurst, M.A.
  Science 274, 1058-1073, 1996
A:Title: Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii
A:Reference number: A64300; MIMD:96337044; PMID:8686087
A:Accession: E64376
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-455,801
A:Cross-references: GR:067699; CH:177117; NID:4159145; PID:41591323; TIGR:MJ0614; PID:4
  1591323
A:Map position: REV544197-544946
A:Start codon: 1165

Query Match      84.4% Score 27; ID 2; Length 353;
Best Local Similarity 80.0%; Pred. No. 2.1e-02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 86 GYRN 90
11111

RESULT 45
E64193
acetyl CoA synthetase related protein - Methanobacterium thermoautotrophicum (strain Del
  ta H)
C:Species: Methanobacterium thermoautotrophicum
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 09-Oct-1999
C:Accession: E64193
R:Smith, D.K.; Deonier-Stamm, L.A.; DeLonghery, C.; Lee, H.; Dubois, J.; Aldredge, T.;
  Gou, D.; Scudator, R.; Vigueire, R.; Wang, Y.; Wierzbowski, J.; Gibson, K.; Wilson, N.
  K.; St. Charles, G.M.; Daniels, C.J.; Mab, J.; Rice, P.; Noelling, J.; Reeve, J.N.
  J. Bacteriol. 179, 7146-7155, 1997
A:Title: Complete genome sequence of Methanobacterium thermoautotrophicum Delta H: func
  tion
A:Reference number: A64000; MIMD:98037514; PMID:9371463
A:Accession: E64193
A>Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-425,211
A:Cross-references: GR:AE000949; GR:AE000946; NID:4252178; PID:4252178
A:Experimental source: strain Delta H
C:Genetics:
A:Gene: MH701
C:Superfamily: human SA protein; acetate-CoA ligase homology
E:84-47% similarity; reactive-CoA ligase homology #status typical #ACLS

Query Match      84.4% Score 27; ID 2; Length 425;
Best Local Similarity 80.0%; Pred. No. 2.5e-02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 411 GYRN 415
11111

```

RESULT 36

E96994

uncharacterized conserved protein (CA0769 [imported]) - Clostridium acetabutylicum

C:Species: Clostridium acetabutylicum

C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001

C:Accession: E96994

R:Willing, J.; Brelvi, G.; Smolchenko, M.V.; Markovica, K.S.; Zeng, G.; Gibson, K.; L. J. Bacteriol. 183, 4824-4838, 2001

A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium

A:Reference number: A96900; MIMD:21459425; PMID:21459425

A:Accession: E96994

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-426,408

A:Cross-references: GR:AE001437; PIN:AAK78745.1; PID:15024654; GSU:6300168

A:Experimental source: Clostridium acetabutylicum A95824

C:Genetics:

A:Gene: CA0769

Query Match 84.4% Score 27; ID 2; Length 426;

Best Local Similarity 80.0%; Pred. No. 2.5e-02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

DB 329 GYRN 333

11111

RESULT 37

E95152

v-type sodium ATP synthase, chain B [imported] - Streptococcus pneumoniae (strain TIC

C:Species: Streptococcus pneumoniae

C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 24-Aug-2001

C:Accession: E95152

R:Reitelin, B.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; H

on, J.D.; Umayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radome, D.; Boltzapp

nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Title: Complete Genome Sequence of a Virulent Isolate of Streptococcus pneumoniae

A:Reference number: A95000; MIMD:21457269; PMID:11460916

A:Accession: E95152

A>Status: preliminary

A:Molecule type: DNA

A:Residues: 1-441,208

A:Cross-references: GR:AE006472; PIN:AAK76414.1; PID:1472747; GSU:6300164; TIGR

C:Genetics:

A:Gene: SPI36

C:Superfamily: B-transported ATP synthase alpha chain; B-transported ATP synthase

Query Match 84.4% Score 27; ID 2; Length 461;

Best Local Similarity 80.0%; Pred. No. 2.7e-02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

DB 418 GYRN 422

11111

RESULT 38

H85745

unknown protein encoded within prophage CP-938k [imported] - Escherichia coli (strain

C:Species: Escherichia coli

C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C:Accession: H85745

R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, K.; Glasner, J.D.; Rose, J.; May

hiller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Boudreau, E.; Beckmann, K.; Apud

Nature 409, 529-533, 2001

A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A:Reference number: A85480; MIMD:21074966; PMID:11266561

A:Accession: H85745

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-465 <HAY>
 A:Cross-references: GB:AE005174; NID:912515380; PID:AA056420.1, GSPB:GR00145, SWGP:223
 A:Experimental source: strain 0157:H7, substrain EDL933
 C:Genetics:
 A:Gene: Z2486

Query Match 84.4% Score 27; DB 2; Length 463;
 Best Local Similarity 80.0%; Pred. No. 2,7e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 3 GFYKN 7
 III:I
 Db 247 GFYKN 251

RESULT 39
 C90873
 hypothetical protein, Ecol95 (imported) - Escherichia coli (strain 0157:H7, substrain K12)
 C:Species: Escherichia coli
 C:Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 18 Jul 2001
 C:Accession: C90873
 E:Hayashi, T.; Matsuo, K.; Okajima, K.; Ishii, K.; Yokoyama, K.; Hara, S.;
 Sasawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 JNA Pos. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and
 A:Reference number: A9629; MIMD:2115621; PMID:11258796
 A:Accession: C90873
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-463 <HAY>
 A:Cross-references: GB:BA000007; PID:BA005370.1; PID:313361420, GSPB:GN00154
 A:Experimental source: strain 0157:H7, substrain K12 0509452
 C:Genetics:
 A:Gene: Ecol955

Query Match 84.4% Score 27; DB 2; Length 463;
 Best Local Similarity 80.0%; Pred. No. 2,7e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 3 GFYKN 7
 III:I
 Db 247 GFYKN 251

RESULT 40
 D64881
 yefX protein - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01 Mar 2002
 C:Accession: D64881
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co-
 A.; Rose, D.J.; Mau, R.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MIMD:97426617, PMID:9274583
 A:Accession: D64881
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-465 <HAY>
 A:Cross-references: GB:AE000900; CP:000094; NID:1797579; PID:AA074102.1, PID:51737581;
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: yefX
 C:Keywords: nucleotide binding; p-loop
 E:2532, yefX, nucleotide binding and if A (p-loop)

Query Match 84.4% Score 27; DB 2; Length 463;
 Best Local Similarity 80.0%; Pred. No. 2,7e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 3 GFYKN 7

III:I
 Db 270 GFYKN 274

RESULT 41
 D90866
 probable enzyme (imported) - Escherichia coli (strain 0157:H7, substrain K12 0509452)
 C:Species: Escherichia coli
 C:Date: 19 Jul 2001 #sequence_revision 18 Jul 2001 #text_change 19 Jul 2001
 C:Accession: D90866
 E:Hayashi, T.; Matsuo, K.; Okajima, K.; Ishii, K.; Yokoyama, K.; Hara, S.;
 Sasawara, N.; Yasunaga, T.; Kohara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
 JNA Pos. 8, 11-22, 2001
 A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and
 A:Reference number: A9629; MIMD:2115621; PMID:11258796
 A:Accession: D90866
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-465 <HAY>
 A:Cross-references: GB:PA000907; PID:BA005370.1; PID:313361465, GSPB:GN00154
 A:Experimental source: strain 0157:H7, substrain K12 0509452
 C:Genetics:
 A:Gene: Ecol955

Query Match 84.4% Score 27; DB 2; Length 463;
 Best Local Similarity 80.0%; Pred. No. 2,7e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 3 GFYKN 7
 III:I
 Db 270 GFYKN 274

RESULT 42
 E85752
 probable EC 2.1.1 enzymes yefX (imported) - Escherichia coli (strain 0157:H7, substrain
 C:Species: Escherichia coli
 C:Date: 16 Feb 2001 #sequence_revision 16 Feb 2001 #text_change 14 Sep 2001
 C:Accession: E85752
 E:Rocha, R.I.; Plucknett III, G.; Burland, V.; Mau, R.; Glasner, J.; Rose, D.; Hara, M.;
 Miller, T.; Giesbrecht, E.; Fouts, N.W.; Lam, A.; Pimlana, E.; Peterson, K.; Apple-
 Nature 409, 529-531, 2001
 A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A:Reference number: A85480; MIMD:21074945; PMID:11206551
 A:Accession: E85752
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-465 <SLD>
 A:Cross-references: GB:AE005174; NID:912515380; PID:AA056420.1, GSPB:GR00145; DWP:
 A:Experimental source: strain 0157:H7, substrain EDL933
 C:Genetics:
 A:Gene: yefX

Query Match 84.4% Score 27; DB 2; Length 463;
 Best Local Similarity 80.0%; Pred. No. 2,7e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0

QY 3 GFYKN 7
 III:I
 Db 270 GFYKN 274

RESULT 43
 AC0659
 probable ATP binding protein, SLY1476 (imported) - Salmonella enterica subsp. enterica
 C:Species: Salmonella enterica subsp. enterica serovar typhi
 A:Note: this species has also been called Salmonella typhi
 C:Date: 09 Nov 2001 #sequence_revision 09 Nov 2001 #text_change 09 Nov 2001
 C:Accession: AC0659
 E:Parkhill, J.; Badger, J.; Evans, K.; Henderson, N.; Kirk, P.; Kitchin, P.; Wain, J.; Church-
 the Typhimurium, Typhimurium, A.; Davis, J.; Davison, A.M.; Good, J.; White, N.; Farr-
 S.; Mout, S.; O'Grada, P.
 Nature 413, 848-852, 2001

107	107	25	78.1	965	1	AMEN_MOUSE	P92419 mus musculus	190	24	75.0	209	1	HF_MYCB	P43849 mycoplasma
108	108	25	78.1	965	1	AMEN_FABAT	P15541 arctophobus	181	24	75.0	209	1	Y622_SUSE	P9416 sulfobobus
109	109	25	78.1	966	1	AMEN_FELCA	P79171 felis silve	182	24	75.0	210	1	KRT1_ARCBL	P29841 archaeobadi
110	110	25	78.1	966	1	AMEN_HUMAR	P11441 homo sapien	183	24	75.0	210	1	MYE5_ADEL	P3628 canthabadi
111	111	25	78.1	985	1	AMV_FZARV	P11451 human spina	184	24	75.0	219	1	HEH1_CHEP	P29541 scapharadi
112	112	25	78.1	990	1	AMV_MANGU	P11451 manduca sex	185	24	75.0	219	1	END1_BA7SU	P6788 bacillus su
113	113	25	78.1	1009	1	BH92_HUSVA	P24907 herpesvirus	186	24	75.0	220	1	EXOB_MERBE	P9547 meristella m
114	114	25	78.1	1029	1	B757_HUMAN	P14709 hofe5_saditu	187	24	75.0	221	1	Y319_AE7YT	P5544 archaeobadi
115	115	25	78.1	1055	1	BH92_PELAC	P77917 pediculus	188	24	75.0	225	1	Y418_MELIA	P5820 melastoma
116	116	25	78.1	1182	1	R1P2_TETRC	P15594 trypanosoma	189	24	75.0	226	1	HA96_KAT	P5572 latius mof
117	117	25	78.1	1194	1	LMC2_HHAR	P15751 homo sapien	190	24	75.0	226	1	Y112_SPH7	P5243 schizosach
118	118	25	78.1	1319	1	YAP2_SPH7	P5984 scapharadi	191	24	75.0	232	1	APX2_LAR7	P19241 larva scap
119	119	25	78.1	4695	1	LMAS_HUMAN	P15240 homo sapien	192	24	75.0	236	1	AMHA_MERBE	P5544 meristella
120	120	24	75.0	26	1	STP1_RP14	P19288 bacterioph	193	24	75.0	236	1	LAB1_MNVI	P6284 escherichia
121	121	24	75.0	50	1	NR1_BROCH	P61311 procthinys	194	24	75.0	236	1	BAIB_HA1M1	P9412 bacterioph
122	122	24	75.0	51	1	HE2_MYC53	P11350 myocystis	195	24	75.0	236	1	Y418_MELIA	P5820 melastoma
123	123	24	75.0	54	1	R142_YERHE	P82419 yersinia pe	196	24	75.0	236	1	YH76_AQUAR	P6762 aquifex aco
124	124	24	75.0	59	1	R142_PSEAR	P82419 pseudomonas	197	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
125	125	24	75.0	61	1	R142_TREDA	P83295 treponema p	198	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
126	126	24	75.0	73	1	UPX8_FY7TU	P43475 escherichia	199	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
127	127	24	75.0	73	1	YH76_FY7TU	P43475 escherichia	200	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
128	128	24	75.0	77	1	YH76_FY7TU	P43475 escherichia	201	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
129	129	24	75.0	75	1	YH76_FY7TU	P43475 escherichia	202	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
130	130	24	75.0	85	1	YH76_FY7TU	P43475 escherichia	203	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
131	131	24	75.0	88	1	YH76_FY7TU	P43475 escherichia	204	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
132	132	24	75.0	89	1	YH76_FY7TU	P43475 escherichia	205	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
133	133	24	75.0	100	1	YH76_FY7TU	P43475 escherichia	206	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
134	134	24	75.0	101	1	YH76_FY7TU	P43475 escherichia	207	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
135	135	24	75.0	105	1	YH76_FY7TU	P43475 escherichia	208	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
136	136	24	75.0	107	1	YH76_FY7TU	P43475 escherichia	209	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
137	137	24	75.0	109	1	YH76_FY7TU	P43475 escherichia	210	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
138	138	24	75.0	119	1	YH76_FY7TU	P43475 escherichia	211	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
139	139	24	75.0	121	1	YH76_FY7TU	P43475 escherichia	212	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
140	140	24	75.0	122	1	YH76_FY7TU	P43475 escherichia	213	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
141	141	24	75.0	125	1	YH76_FY7TU	P43475 escherichia	214	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
142	142	24	75.0	131	1	YH76_FY7TU	P43475 escherichia	215	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
143	143	24	75.0	132	1	YH76_FY7TU	P43475 escherichia	216	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
144	144	24	75.0	137	1	YH76_FY7TU	P43475 escherichia	217	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
145	145	24	75.0	138	1	YH76_FY7TU	P43475 escherichia	218	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
146	146	24	75.0	139	1	YH76_FY7TU	P43475 escherichia	219	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
147	147	24	75.0	142	1	YH76_FY7TU	P43475 escherichia	220	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
148	148	24	75.0	142	1	YH76_FY7TU	P43475 escherichia	221	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
149	149	24	75.0	156	1	YH76_FY7TU	P43475 escherichia	222	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
150	150	24	75.0	158	1	YH76_FY7TU	P43475 escherichia	223	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
151	151	24	75.0	160	1	YH76_FY7TU	P43475 escherichia	224	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
152	152	24	75.0	161	1	YH76_FY7TU	P43475 escherichia	225	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
153	153	24	75.0	162	1	YH76_FY7TU	P43475 escherichia	226	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
154	154	24	75.0	162	1	YH76_FY7TU	P43475 escherichia	227	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
155	155	24	75.0	162	1	YH76_FY7TU	P43475 escherichia	228	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
156	156	24	75.0	167	1	YH76_FY7TU	P43475 escherichia	229	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
157	157	24	75.0	167	1	YH76_FY7TU	P43475 escherichia	230	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
158	158	24	75.0	168	1	YH76_FY7TU	P43475 escherichia	231	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
159	159	24	75.0	170	1	YH76_FY7TU	P43475 escherichia	232	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
160	160	24	75.0	170	1	YH76_FY7TU	P43475 escherichia	233	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
161	161	24	75.0	172	1	YH76_FY7TU	P43475 escherichia	234	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
162	162	24	75.0	174	1	YH76_FY7TU	P43475 escherichia	235	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
163	163	24	75.0	177	1	YH76_FY7TU	P43475 escherichia	236	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
164	164	24	75.0	185	1	YH76_FY7TU	P43475 escherichia	237	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
165	165	24	75.0	187	1	YH76_FY7TU	P43475 escherichia	238	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
166	166	24	75.0	189	1	YH76_FY7TU	P43475 escherichia	239	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
167	167	24	75.0	190	1	YH76_FY7TU	P43475 escherichia	240	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
168	168	24	75.0	190	1	YH76_FY7TU	P43475 escherichia	241	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
169	169	24	75.0	194	1	YH76_FY7TU	P43475 escherichia	242	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
170	170	24	75.0	196	1	YH76_FY7TU	P43475 escherichia	243	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
171	171	24	75.0	201	1	YH76_FY7TU	P43475 escherichia	244	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
172	172	24	75.0	202	1	YH76_FY7TU	P43475 escherichia	245	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
173	173	24	75.0	202	1	YH76_FY7TU	P43475 escherichia	246	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
174	174	24	75.0	202	1	YH76_FY7TU	P43475 escherichia	247	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
175	175	24	75.0	207	1	YH76_FY7TU	P43475 escherichia	248	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
176	176	24	75.0	207	1	YH76_FY7TU	P43475 escherichia	249	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
177	177	24	75.0	207	1	YH76_FY7TU	P43475 escherichia	250	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
178	178	24	75.0	208	1	YH76_FY7TU	P43475 escherichia	251	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco
179	179	24	75.0	208	1	YH76_FY7TU	P43475 escherichia	252	24	75.0	237	1	YH76_AQUAR	P6762 aquifex aco

252	24	75.0	320	1	FLA1_TREHY	P24520	carpenteria	126	21	75.0	407	1	EXP_SALTY	P24479	salmonella
253	24	75.0	320	1	TRAB_ECOLI	P04620	escherichia	127	24	75.0	410	1	EXP_TREHY	P24129	psuedomonas
254	24	75.0	320	1	YIH7_YEAST	P40508	saccharomye	128	24	75.0	410	1	YAG2_BIFID	P06559	bacterioph
255	24	75.0	322	1	CHIC_LYCIS	P05078	lysozyme	129	24	75.0	412	1	YAG7_SCHIF	P04871	escherichia
256	24	75.0	322	1	CHIC_LYCIS	P16261	ratius nery	130	24	75.0	413	1	EXP_P241	P05720	bacterioph
257	24	75.0	322	1	YEBL_ECOLI	P76482	escherichia	131	24	75.0	416	1	EXP_RH117	P42726	ribitolium
258	24	75.0	324	1	CHIL2_TOBAC	P24091	nicotiana	132	24	75.0	416	1	TR24_M238	P01113	mus musculus
259	24	75.0	324	1	CHIL2_TOBAC	P05315	solanum tub	133	24	75.0	417	1	EXP_ERRE	P02992	dracophila
260	24	75.0	326	1	CHIL2_TOBAC	P06252	nicotiana	134	24	75.0	421	1	EXP_STRIP	P04177	strophomen
261	24	75.0	326	1	CHIL2_TOBAC	P01982	bos taurus	135	24	75.0	421	1	EXP_H1EE	P04660	bacterioph
262	24	75.0	320	1	EXP_MYCPN	P75435	mycoplasma	136	24	75.0	423	1	TR19_HUMAN	P04668	bacterioph
263	24	75.0	320	1	Y274_HUMAN	P04961	homo sapien	137	24	75.0	423	1	EXP_RAC30	P11772	bacillus su
264	24	75.0	321	1	Y274_HUMAN	P04961	homo sapien	138	24	75.0	423	1	ACPA_BACCH	P11940	bacillus su
265	24	75.0	321	1	Y274_HUMAN	P04961	homo sapien	139	24	75.0	423	1	EXP_GABER	P04412	caulibacter
266	24	75.0	321	1	Y274_HUMAN	P04961	homo sapien	140	24	75.0	427	1	ACPA_MF210	P04752	cyobacteri
267	24	75.0	322	1	EXP_SALTY	P16260	homo sapien	141	24	75.0	428	1	EXP_MF210	P04752	cyobacteri
268	24	75.0	322	1	EXP_SALTY	P16260	homo sapien	142	24	75.0	428	1	EXP_MF210	P04752	cyobacteri
269	24	75.0	323	1	HEM1_CHLMO	P04112	chlamydia m	143	24	75.0	431	1	EXP_A2CHAE	P11949	homo sapien
270	24	75.0	324	1	HEM1_CHLMO	P04112	chlamydia m	144	24	75.0	431	1	EXP_A2CHAE	P11949	homo sapien
271	24	75.0	324	1	YELV_ECOLI	P04959	nicotiana	145	24	75.0	433	1	EXP_RH117	P04177	strophomen
272	24	75.0	324	1	YELV_ECOLI	P04959	nicotiana	146	24	75.0	433	1	EXP_RH117	P04177	strophomen
273	24	75.0	324	1	YELV_ECOLI	P04959	nicotiana	147	24	75.0	433	1	EXP_RH117	P04177	strophomen
274	24	75.0	324	1	YELV_ECOLI	P04959	nicotiana	148	24	75.0	433	1	EXP_RH117	P04177	strophomen
275	24	75.0	324	1	YELV_ECOLI	P04959	nicotiana	149	24	75.0	433	1	EXP_RH117	P04177	strophomen
276	24	75.0	325	1	EXP_SALTY	P16260	homo sapien	150	24	75.0	433	1	EXP_RH117	P04177	strophomen
277	24	75.0	326	1	EXP_SALTY	P16260	homo sapien	151	24	75.0	433	1	EXP_RH117	P04177	strophomen
278	24	75.0	326	1	EXP_SALTY	P16260	homo sapien	152	24	75.0	433	1	EXP_RH117	P04177	strophomen
279	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	153	24	75.0	433	1	EXP_RH117	P04177	strophomen
280	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	154	24	75.0	433	1	EXP_RH117	P04177	strophomen
281	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	155	24	75.0	433	1	EXP_RH117	P04177	strophomen
282	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	156	24	75.0	433	1	EXP_RH117	P04177	strophomen
283	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	157	24	75.0	433	1	EXP_RH117	P04177	strophomen
284	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	158	24	75.0	433	1	EXP_RH117	P04177	strophomen
285	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	159	24	75.0	433	1	EXP_RH117	P04177	strophomen
286	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	160	24	75.0	433	1	EXP_RH117	P04177	strophomen
287	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	161	24	75.0	433	1	EXP_RH117	P04177	strophomen
288	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	162	24	75.0	433	1	EXP_RH117	P04177	strophomen
289	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	163	24	75.0	433	1	EXP_RH117	P04177	strophomen
290	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	164	24	75.0	433	1	EXP_RH117	P04177	strophomen
291	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	165	24	75.0	433	1	EXP_RH117	P04177	strophomen
292	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	166	24	75.0	433	1	EXP_RH117	P04177	strophomen
293	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	167	24	75.0	433	1	EXP_RH117	P04177	strophomen
294	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	168	24	75.0	433	1	EXP_RH117	P04177	strophomen
295	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	169	24	75.0	433	1	EXP_RH117	P04177	strophomen
296	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	170	24	75.0	433	1	EXP_RH117	P04177	strophomen
297	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	171	24	75.0	433	1	EXP_RH117	P04177	strophomen
298	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	172	24	75.0	433	1	EXP_RH117	P04177	strophomen
299	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	173	24	75.0	433	1	EXP_RH117	P04177	strophomen
300	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	174	24	75.0	433	1	EXP_RH117	P04177	strophomen
301	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	175	24	75.0	433	1	EXP_RH117	P04177	strophomen
302	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	176	24	75.0	433	1	EXP_RH117	P04177	strophomen
303	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	177	24	75.0	433	1	EXP_RH117	P04177	strophomen
304	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	178	24	75.0	433	1	EXP_RH117	P04177	strophomen
305	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	179	24	75.0	433	1	EXP_RH117	P04177	strophomen
306	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	180	24	75.0	433	1	EXP_RH117	P04177	strophomen
307	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	181	24	75.0	433	1	EXP_RH117	P04177	strophomen
308	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	182	24	75.0	433	1	EXP_RH117	P04177	strophomen
309	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	183	24	75.0	433	1	EXP_RH117	P04177	strophomen
310	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	184	24	75.0	433	1	EXP_RH117	P04177	strophomen
311	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	185	24	75.0	433	1	EXP_RH117	P04177	strophomen
312	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	186	24	75.0	433	1	EXP_RH117	P04177	strophomen
313	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	187	24	75.0	433	1	EXP_RH117	P04177	strophomen
314	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	188	24	75.0	433	1	EXP_RH117	P04177	strophomen
315	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	189	24	75.0	433	1	EXP_RH117	P04177	strophomen
316	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	190	24	75.0	433	1	EXP_RH117	P04177	strophomen
317	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	191	24	75.0	433	1	EXP_RH117	P04177	strophomen
318	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	192	24	75.0	433	1	EXP_RH117	P04177	strophomen
319	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	193	24	75.0	433	1	EXP_RH117	P04177	strophomen
320	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	194	24	75.0	433	1	EXP_RH117	P04177	strophomen
321	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	195	24	75.0	433	1	EXP_RH117	P04177	strophomen
322	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	196	24	75.0	433	1	EXP_RH117	P04177	strophomen
323	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	197	24	75.0	433	1	EXP_RH117	P04177	strophomen
324	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	198	24	75.0	433	1	EXP_RH117	P04177	strophomen
325	24	75.0	327	1	EXP_SALTY	P16260	homo sapien	199	24	75.0	433	1	EXP_RH117	P04177	strophomen

399	24	75.0	5.4	1	EPAL_MOUSE	Q60759 mus musculus	472	24	75.0	6.75	1	RYAN_MOUSE	Q62374 acrid hameci
400	24	75.0	5.48	1	REL_MELCA	P01125 melospiza g	473	24	75.0	7.06	1	2225_HUMAN	Q06K10 homo sapien
401	24	75.0	5.48	1	2155_HUMAN	Q12991 homo sapien	474	24	75.0	7.07	1	2225_HUMAN	Q06K10 homo sapien
402	24	75.0	5.49	1	1086_MOUSE	P04071 bacillus su	475	24	75.0	7.10	1	0501_HUMAN	P26027 the monom
403	24	75.0	5.50	1	SYM_CHILM	Q9P107 chlamydia m	476	24	75.0	7.10	1	0501_HUMAN	Q06K10 homo sapien
404	24	75.0	5.50	1	SYM_CHILM	Q64045 chlamydia t	477	24	75.0	7.11	1	0501_HUMAN	Q06K10 homo sapien
405	24	75.0	5.51	1	1086_MOUSE	Q53427 xenopus lae	478	24	75.0	7.11	1	0501_HUMAN	Q06K10 homo sapien
406	24	75.0	5.51	1	1086_MOUSE	P56180 homo sapien	479	24	75.0	7.11	1	0501_HUMAN	Q06K10 homo sapien
407	24	75.0	5.51	1	0501_HUMAN	Q9P107 bacillus su	480	24	75.0	7.12	1	0501_HUMAN	Q06K10 homo sapien
408	24	75.0	5.52	1	0501_HUMAN	Q9P107 bacillus su	481	24	75.0	7.13	1	0501_HUMAN	Q06K10 homo sapien
409	24	75.0	5.52	1	0501_HUMAN	Q57424 gallus gall	482	24	75.0	7.15	1	0501_HUMAN	Q06K10 homo sapien
410	24	75.0	5.52	1	0501_HUMAN	Q9P107 bacillus su	483	24	75.0	7.15	1	0501_HUMAN	Q06K10 homo sapien
411	24	75.0	5.52	1	0501_HUMAN	P70312 mus musculus	484	24	75.0	7.20	1	0501_HUMAN	Q06K10 homo sapien
412	24	75.0	5.52	1	0501_HUMAN	Q57424 gallus gall	485	24	75.0	7.20	1	0501_HUMAN	Q06K10 homo sapien
413	24	75.0	5.53	1	0501_HUMAN	Q50219 homo sapien	486	24	75.0	7.20	1	0501_HUMAN	Q06K10 homo sapien
414	24	75.0	5.54	1	0501_HUMAN	Q06650 mus musculus	487	24	75.0	7.31	1	0501_HUMAN	Q06K10 homo sapien
415	24	75.0	5.57	1	0501_HUMAN	P45157 quercus max	488	24	75.0	7.31	1	0501_HUMAN	Q06K10 homo sapien
416	24	75.0	5.59	1	0501_HUMAN	P45456 quercus max	489	24	75.0	7.49	1	0501_HUMAN	Q06K10 homo sapien
417	24	75.0	5.60	1	0501_HUMAN	P13101 influenza a	490	24	75.0	7.56	1	0501_HUMAN	Q06K10 homo sapien
418	24	75.0	5.65	1	0501_HUMAN	P16060 influenza a	491	24	75.0	7.59	1	0501_HUMAN	Q06K10 homo sapien
419	24	75.0	5.66	1	0501_HUMAN	P03454 influenza a	492	24	75.0	7.61	1	0501_HUMAN	Q06K10 homo sapien
420	24	75.0	5.67	1	0501_HUMAN	P18159 bacillus su	493	24	75.0	7.73	1	0501_HUMAN	Q06K10 homo sapien
421	24	75.0	5.66	1	0501_HUMAN	P26562 bacillus su	494	24	75.0	7.75	1	0501_HUMAN	Q06K10 homo sapien
422	24	75.0	5.66	1	0501_HUMAN	P13103 influenza a	495	24	75.0	7.75	1	0501_HUMAN	Q06K10 homo sapien
423	24	75.0	5.66	1	0501_HUMAN	P18875 influenza a	496	24	75.0	7.78	1	0501_HUMAN	Q06K10 homo sapien
424	24	75.0	5.66	1	0501_HUMAN	P18876 influenza a	497	24	75.0	7.78	1	0501_HUMAN	Q06K10 homo sapien
425	24	75.0	5.66	1	0501_HUMAN	P13102 influenza a	498	24	75.0	7.79	1	0501_HUMAN	Q06K10 homo sapien
426	24	75.0	5.67	1	0501_HUMAN	P03452 influenza a	499	24	75.0	7.80	1	0501_HUMAN	Q06K10 homo sapien
427	24	75.0	5.66	1	0501_HUMAN	P03448 influenza a	500	24	75.0	7.81	1	0501_HUMAN	Q06K10 homo sapien
428	24	75.0	5.66	1	0501_HUMAN	P03453 influenza a	501	24	75.0	7.83	1	0501_HUMAN	Q06K10 homo sapien
429	24	75.0	5.66	1	0501_HUMAN	P26140 influenza a	502	24	75.0	7.83	1	0501_HUMAN	Q06K10 homo sapien
430	24	75.0	5.66	1	0501_HUMAN	P03455 influenza a	503	24	75.0	7.84	1	0501_HUMAN	Q06K10 homo sapien
431	24	75.0	5.66	1	0501_HUMAN	P04283 borrelia bu	504	24	75.0	7.85	1	0501_HUMAN	Q06K10 homo sapien
432	24	75.0	5.67	1	0501_HUMAN	Q42589 brassica ca	505	24	75.0	7.85	1	0501_HUMAN	Q06K10 homo sapien
433	24	75.0	5.67	1	0501_HUMAN	Q95626 dendratum	506	24	75.0	7.86	1	0501_HUMAN	Q06K10 homo sapien
434	24	75.0	5.68	1	0501_HUMAN	P46237 lysoperidum	507	24	75.0	7.86	1	0501_HUMAN	Q06K10 homo sapien
435	24	75.0	5.68	1	0501_HUMAN	P58131 astasia ion	508	24	75.0	7.87	1	0501_HUMAN	Q06K10 homo sapien
436	24	75.0	5.68	1	0501_HUMAN	P28297 aradopsis	509	24	75.0	7.87	1	0501_HUMAN	Q06K10 homo sapien
437	24	75.0	5.68	1	0501_HUMAN	P25348 brassica na	510	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
438	24	75.0	5.68	1	0501_HUMAN	P25318 brassica na	511	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
439	24	75.0	5.68	1	0501_HUMAN	P49296 cucumis sat	512	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
440	24	75.0	5.68	1	0501_HUMAN	P17069 gossypium h	513	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
441	24	75.0	5.68	1	0501_HUMAN	P15479 ricinus com	514	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
442	24	75.0	5.68	1	0501_HUMAN	P32384 newcastle d	515	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
443	24	75.0	5.68	1	0501_HUMAN	P12559 newcastle d	516	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
444	24	75.0	5.68	1	0501_HUMAN	P35743 newcastle d	517	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
445	24	75.0	5.68	1	0501_HUMAN	P12553 newcastle d	518	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
446	24	75.0	5.68	1	0501_HUMAN	P11071 escherichia	519	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
447	24	75.0	5.68	1	0501_HUMAN	Q92819 homo raption	520	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
448	24	75.0	5.68	1	0501_HUMAN	Q94975 salmonella	521	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
449	24	75.0	5.68	1	0501_HUMAN	P11097 sirius taeda	522	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
450	24	75.0	5.68	1	0501_HUMAN	P11097 sirius taeda	523	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
451	24	75.0	5.68	1	0501_HUMAN	Q61647 mus musculus	524	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
452	24	75.0	5.68	1	0501_HUMAN	Q57428 xenopus lae	525	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
453	24	75.0	5.68	1	0501_HUMAN	P41510 brassica na	526	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
454	24	75.0	5.68	1	0501_HUMAN	P34458 e agna prot	527	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
455	24	75.0	5.68	1	0501_HUMAN	Q20759 caenorhabdit	528	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
456	24	75.0	5.68	1	0501_HUMAN	P13570 xenopus lae	529	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
457	24	75.0	5.68	1	0501_HUMAN	P41582 corynebacte	530	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
458	24	75.0	5.68	1	0501_HUMAN	P14236 gallus gall	531	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
459	24	75.0	5.68	1	0501_HUMAN	P58233 aradopsis	532	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
460	24	75.0	5.68	1	0501_HUMAN	Q42968 cryza glabo	533	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
461	24	75.0	5.68	1	0501_HUMAN	P12565 newcastle d	534	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
462	24	75.0	5.68	1	0501_HUMAN	P12555 newcastle d	535	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
463	24	75.0	5.68	1	0501_HUMAN	P13850 newcastle d	536	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
464	24	75.0	5.68	1	0501_HUMAN	P12558 newcastle d	537	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
465	24	75.0	5.68	1	0501_HUMAN	Q96K13 homo sapien	538	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
466	24	75.0	5.68	1	0501_HUMAN	P10775 mycobacteri	539	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
467	24	75.0	5.68	1	0501_HUMAN	P13429 pseudomonas	540	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
468	24	75.0	5.68	1	0501_HUMAN	Q50614 mycobacteri	541	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
469	24	75.0	5.68	1	0501_HUMAN	P52462 human hepte	542	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
470	24	75.0	5.68	1	0501_HUMAN	P127095 methanobac	543	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien
471	24	75.0	5.68	1	0501_HUMAN	P09662 bacillus th	544	24	75.0	7.88	1	0501_HUMAN	Q06K10 homo sapien

[illegible]

691	24	71.9	704	1	PHIL_SULPH	Q7096	sulfobins	764	22	68.8	192	1	Y345_NEVAP	P41450	antioxiapha
692	24	71.9	716	1	GALE_HIND	P2627	theromayer	765	22	68.8	195	1	IGFB_HUMAN	P05019	homo sapien
693	24	71.9	740	1	CAIR_SALMON	Q9189	streptomyce	766	22	69.9	202	1	MYO17A_HUMAN	P05117	homo sapien
694	24	71.9	749	1	Y311_YEAST	P08364	streptomyce	767	22	69.8	221	1	SRGA_HUMAN	P24286	homo sapien
695	24	71.9	764	1	Y311_YEAST	P08368	saccharomyce	768	22	68.8	234	1	K515_FYB1	P24286	saccharomyce
696	24	71.9	782	1	CHAO_DRAVA	P08368	tritolium	769	22	68.8	246	1	K515_FYB1	P41442	homo sapien
697	24	71.9	784	1	OUT_CASHEL	Q91219	caenorhabdi	770	22	68.8	249	1	K515_FYB1	P07974	caenorhabdi
698	24	71.9	808	1	PHIL_HIND	P46337	barkey help	771	22	68.8	249	1	TRIA_MYD88	Q06291	mycoplasma
699	24	71.9	858	1	PHIL_HUMAN	Q95052	homo sapien	772	22	69.8	249	1	PHIL_HUMAN	Q06291	mycoplasma
700	24	71.9	858	1	PHIL_HUMAN	Q95052	homo sapien	773	22	69.8	249	1	PHIL_HUMAN	Q06291	mycoplasma
701	24	71.9	858	1	PHIL_HUMAN	Q95052	homo sapien	774	22	69.8	249	1	PHIL_HUMAN	Q06291	mycoplasma
702	24	71.9	859	1	PHIL_HUMAN	Q95052	homo sapien	775	22	68.8	247	1	Y345_NEVAP	Q06291	mycoplasma
703	24	71.9	859	1	PHIL_HUMAN	Q95052	homo sapien	776	22	68.8	247	1	Y345_NEVAP	Q06291	mycoplasma
704	24	71.9	997	1	PHIL_HUMAN	Q95052	homo sapien	777	22	68.8	252	1	SHIB_AAVP	Q06291	mycoplasma
705	24	71.9	1019	1	PHIL_HUMAN	Q95052	homo sapien	778	22	68.8	252	1	SHIB_AAVP	Q06291	mycoplasma
706	24	71.9	1024	1	PHIL_HUMAN	Q95052	homo sapien	779	22	68.8	252	1	SHIB_AAVP	Q06291	mycoplasma
707	24	71.9	1176	1	PHIL_HUMAN	Q95052	homo sapien	780	22	69.8	276	1	Y345_NEVAP	Q06291	mycoplasma
708	24	71.9	1203	1	ATB4_PAT	Q44542	rattus norv	781	22	69.8	293	1	Y345_NEVAP	P47449	mycoplasma
709	24	71.9	1207	1	PHIL_HUMAN	Q95052	homo sapien	782	22	68.8	291	1	ATP6_GENIE	Q94654	elicia labia
710	24	71.9	1303	1	PHIL_HUMAN	Q95052	homo sapien	783	22	68.8	296	1	ATP6_GENIE	Q94654	elicia labia
711	24	71.9	1395	1	PHIL_HUMAN	Q95052	homo sapien	784	22	68.8	296	1	ATP6_GENIE	Q94654	elicia labia
712	24	71.9	1429	1	PHIL_HUMAN	Q95052	homo sapien	785	22	68.8	309	1	ATP6_GENIE	Q94654	elicia labia
713	24	71.9	1492	1	PHIL_HUMAN	Q95052	homo sapien	786	22	68.8	309	1	ATP6_GENIE	Q94654	elicia labia
714	24	71.9	1514	1	PHIL_HUMAN	Q95052	homo sapien	787	22	68.8	313	1	ATP6_GENIE	Q94654	elicia labia
715	24	71.9	1518	1	PHIL_HUMAN	Q95052	homo sapien	788	22	68.8	316	1	ATP6_GENIE	Q94654	elicia labia
716	24	71.9	1581	1	PHIL_HUMAN	Q95052	homo sapien	789	22	68.8	316	1	ATP6_GENIE	Q94654	elicia labia
717	24	71.9	1587	1	PHIL_HUMAN	Q95052	homo sapien	790	22	68.8	321	1	ATP6_GENIE	Q94654	elicia labia
718	24	71.9	1639	1	PHIL_HUMAN	Q95052	homo sapien	791	22	68.8	323	1	ATP6_GENIE	Q94654	elicia labia
719	24	71.9	2244	1	PHIL_HUMAN	Q95052	homo sapien	792	22	68.8	345	1	ATP6_GENIE	Q94654	elicia labia
720	24	71.9	3718	1	PHIL_HUMAN	Q95052	homo sapien	793	22	68.8	349	1	ATP6_GENIE	Q94654	elicia labia
721	24	71.9	3947	1	PHIL_HUMAN	Q95052	homo sapien	794	22	68.8	349	1	ATP6_GENIE	Q94654	elicia labia
722	24	71.9	4449	1	PHIL_HUMAN	Q95052	homo sapien	795	22	68.8	349	1	ATP6_GENIE	Q94654	elicia labia
723	24	71.9	4451	1	PHIL_HUMAN	Q95052	homo sapien	796	22	68.8	341	1	ATP6_GENIE	Q94654	elicia labia
724	24	68.8	56	1	PHIL_HUMAN	Q95052	homo sapien	797	22	68.8	341	1	ATP6_GENIE	Q94654	elicia labia
725	24	68.8	74	1	PHIL_HUMAN	Q95052	homo sapien	798	22	68.8	349	1	ATP6_GENIE	Q94654	elicia labia
726	24	68.8	81	1	PHIL_HUMAN	Q95052	homo sapien	799	22	68.8	350	1	ATP6_GENIE	Q94654	elicia labia
727	24	68.8	91	1	PHIL_HUMAN	Q95052	homo sapien	800	22	68.8	350	1	ATP6_GENIE	Q94654	elicia labia
728	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	801	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
729	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	802	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
730	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	803	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
731	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	804	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
732	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	805	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
733	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	806	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
734	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	807	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
735	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	808	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
736	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	809	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
737	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	810	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
738	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	811	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
739	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	812	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
740	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	813	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
741	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	814	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
742	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	815	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
743	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	816	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
744	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	817	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
745	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	818	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
746	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	819	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
747	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	820	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
748	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	821	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
749	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	822	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
750	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	823	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
751	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	824	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
752	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	825	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
753	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	826	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
754	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	827	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
755	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	828	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
756	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	829	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
757	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	830	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
758	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	831	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
759	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	832	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
760	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	833	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
761	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	834	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
762	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	835	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia
763	24	68.8	100	1	PHIL_HUMAN	Q95052	homo sapien	836	22	68.8	351	1	ATP6_GENIE	Q94654	elicia labia

[illegible]

983 21 65.6 126 1 ACB1_BCCAL
984 21 65.6 126 1 YP61_XYLFIA
985 21 65.6 128 1 AR21_ENTHT
986 21 65.6 129 1 KAP1_BACSU
987 21 65.6 132 1 C563_GVACA
988 21 65.6 132 1 IAT3_M03SU
989 21 65.6 144 1 RE15_HUMAN
990 21 65.6 149 1 MAB1_SCHJA
991 21 65.6 149 1 MAB1_SCHJA
992 21 65.6 149 1 ZG29_XENLA
993 21 65.6 142 1 CYPE1_P0V1
994 21 65.6 143 1 R135_M03VA
995 21 65.6 145 1 YJAR_SALTY
996 21 65.6 146 1 HABC_VITSI
997 21 65.6 146 1 HABC_VITSI
998 21 65.6 147 1 YPAR_YEAST
999 21 65.6 149 1 RL9_HAETN
1000 21 65.6 149 1 RL9_PASMU

ALIGNMENTS

RESULT 1

MIR3_MOUSE
ID MIR3_MOUSE STANDARD: PRG: 121 AA.
AC G42210;
DT 16-OCT-2001 (Ref.: 40, Created)
DT 16-OCT-2001 (Ref.: 40, Last sequence update)
DT 16-OCT-2001 (Ref.: 40, Last annotation update)
DE Myotubularin-related protein 3 (Fragment).
GN MIR3.
GS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_taxonomy:100960;
FN 111
FP SEQUENCE FROM N.A.
EX MEDLINE 98409499; PubMed 9746772;
KA Laporte J., Blondeau F., Bu-Bello A., Tentler D., Kretz C., Dahl N.,
Mandel J.-L.;
KI "Characterization of the myotubularin dual specificity phosphatase
gene family from yeast to human."
KL Hum. Mol. Genet. 7:1703-1712(1998).
CC -1- FUNCTION: NOT KNOWN. COULD BE A TYROSINE PHOSPHATASE.
CC -1- SIMILARITY: PROTEIN TO THE MYOTUBULARIN TYPE FAMILY.
CC
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/ncn000000>
CC or send an email to license@isb-sib.ch).

EMBL: A0074881; AA080003.1;
InterPro: IPR000387; TYR-phosphatase.
PROSITE: PS00484; TYR-phosphatase_1; PARTIAL
PROSITE: PS00056; TYR-phosphatase_2; PARTIAL.
KW Hydrolase.
FI NON_TER
SQ SEQUENCE 121 AA: 14292 MW: 097A0749;ABBP98 QRC64.

Query Match 93.8%; Score 30; DB 1; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 5; Conservative 0; Mismatch 0; Indels 0; Gaps 0.
QY 3 GYRN 7
11111
DB 105 GYRN 109

RESULT 2

HPST_MYCE
ID HPST_MYCE STANDARD: PRG: 175 AA.
AC P47696;
DT 01 FEB 1996 (Ref.: 33, Created)
DT 01 FEB 1996 (Ref.: 33, Last sequence update)
DT 15 JUN 2002 (Ref.: 41, Last annotation update)
DE Hypoxanthine-phosphoribosyltransferase (EC 2.4.2.8) (HPRF)
DE (HPRF).
DE (HPRF).
GN HPI OR M0458.
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmales; Mycoplasma.
OX NCBI_taxonomy:2047;
FN 111
FP SEQUENCE FROM N.A.
EX STRAIN ATCC 35030 / G-37;
EX MEDLINE 96026446; PubMed 7569993;
EX Fraser C.M., Gervayne J.D., White O., Adams M.D., Clayton R.A.,
PA Fleischman K.B., Pitt C.J., Kervayne A.R., Sutton G., Kelley J.M.,
KA Fritchman J.L., Weidman J.F., Small K.V., Sandusky M., Fuhrmann J.L.,
KA Rayon R.T., Osterback I.K., Saubek D.M., Phillips C.A., Patrick J.M.,
RA Tomb J.F., Dougherty B.A., Bolt K.F., Hu P.-C., Loefer T.S.,
RA Peterson S.N., Smith H.O., Hutchison C.A. III, Venter J.C.;
RT "The minimal gene complement of Mycoplasma genitalium."
KL Science 270:397-403(1995).
FN 121
FP SEQUENCE OF 9-98 FROM N.A.
EX STRAIN ATCC 35030 / G-37;
EX MEDLINE 94075240; PubMed 825680;
KA Peterson S.N., Hu P.-C., Bolt K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
RT sequencing."
KL J. Bacteriol. 175:7918-7930(1993).
CC -1- CATALYTIC ACTIVITY: IMP + PYROPHOSPHATE -> HYPOXANTHINE +
CC 5-PYRIBOSYL-ALPHA-D-RIBOSE 1-PYRIBOSYL-ATP
CC HYPOXANTHINE TO PHOSPHO-GMP.
CC -1- PATHWAY: Purine salvage.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO THE PPK/RE/TYP/IMINE
CC PHOSPHORIBOSYLTRANSFERASE FAMILY.
CC
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.isb-sib.ch/ncn000000>
CC or send an email to license@isb-sib.ch).

EMBL: U09727; AA72478.1;
EMBL: 002193; AA012474.1;
DB ISSP: P51900; IIRX.
DB TIGR: M0458.
DB InterPro: IPR000836; PRTransferase.
DB InterPro: IPR002875; P/PP_PP_Transf.
DB Pfam: PF00156; PRibosyltran_1.
DB TIGREMS: TIGR01203; HPRFase; 1.
DB PROSITE: PS00103; PPR-PYR-PP-TRANSFER; 1.
KW Transferase, glycosyltransferase, Purine salvage, Mammalian,
KW Complete proteome.
FI METAL 96
FI METAL 97
SQ SEQUENCE 175 AA: 19759 MW: 96473324;PRF04880 QRC64.
Query Match 93.8%; Score 30; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 9.9;
Matches 5; Conservative 0; Mismatch 0; Indels 0; Gaps 0.
QY 3 GYRN 7
11111
DB 159 GYRN 163

DI 01-OCT-1992 (Rel. 27, Last sequence update)
 DI 15-JUN-2002 (Rel. 41, Last annotation update)
 DE (tryptophanyl-trna synthetase (EC 6.1.1.2) (tryptophan: tRNA ligase)
 DF (TrpS).
 GN WAYS OF WPS
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2)
 EX MEDLINE 9019226, PubMed 793716,
 PA Pajot B., Sarger C., Bonnet J., Garnet M.;
 RT "An alternative splicing modifies the C-terminal end of tryptophanyl-
 trna synthetase in murine embryonic stem cells.";
 RL J. Mol. Biol. 243:559-563(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) -> AMP +
 CC diphosphate + L-tryptophanyl-tRNA(Trp).
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- ALTERNATIVE PRODUCTS: 2 isoforms, a long form (shown here) and a
 CC short form; are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: the short isoform is widely expressed, the
 CC long form is found only in embryonic stem cells.
 CC -1- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
 CC -1- SIMILARITY: CONTAINS 1 WHEP-TRS DOMAIN.
 CC
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.ebi.ac.uk/infocentre>,
 CC or send an email to license@lsb.scrib.ch).
 CC
 DR EMBL: X69656; CAA49347.1; 1;
 DE EMBL: X69657; CAA49348.1; 1;
 DR FIR: S31461; S31461;
 DR PIR: S31462; S31462;
 DR MG0: M0104630; WARS
 DE InterPro: IPR000706, Trp-trna-synth_1b
 DR InterPro: IPR000738; WHEP-TRS;
 DE InterPro: IPR002205; tRNA-synt_1b.
 DR InterPro: IPR001412; tRNA-synt_1.
 DR Pfam: PF0045H; WHEP-TRS; 1;
 DR Pfam: PF00579; tRNA-synt_1b; 1;
 DR PRINTS: PK01039; TRNASYNTHTRP.
 DR TIGRFAMs: TIGR00232; TrpS; 1;
 DR PROSITE: PS00178; AA-TRNA-LIGASE_I; 1;
 DR PROSITE: PS00762; WHEP-TRS; 1;
 FW Aminoacyl-tRNA synthetase; Protein biosynthesis, Ligation, ATP binding,
 KW Alternative splicing.
 FT DOMAIN 23 68
 FT SITE 168 177 "HIGH" REGION.
 FT SITE 353 357 "KMSKS" REGION.
 FT VARSPLIC 476 481 MISSING (IN ISOFORM 2).
 SQ SEQUENCE 481 AA: 54292 MW: 805445203074152 CRG64;
 Query Match 93.88; Score 30; DB 1; Length 481;
 Best Local Similarity 100.00; Pred. Rel. 27.
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
 QY 3 GYRN 7
 DI 1111
 DI 250 GYRN 254
 RESULT 8
 TYRO_MOUSE
 ID TYRO_MOUSE STANDARD; PPI; 533 AA.
 AC P11344;
 DI 01-JUL-1989 (Rel. 11, Created)
 DI 01-AUG-1990 (Rel. 15, Last sequence update)
 DI 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tyrosinase precursor (EC 1.14.16.1) (Monophenol monooxygenase)
 DE (Albino locus protein).
 GN TYR.
 OS Mus musculus (Mouse).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
 OX NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 EX STRAIN DBA/2J; PubMed 314020;
 EX MEDLINE 9826913, PubMed 314020;
 PA Kato K., Watanabe H., Bai A.P., Balaban R., Resler D.;
 RT "Sequence analysis of mouse tyrosinase cDNA and the effect of
 melanotropin on its gene expression.";
 RL Biochem. Biophys. Res. Commun. 153:1301-1309(1988).
 CC [2]
 RP SEQUENCE FROM N.A.
 EX STRAIN-Himalayan;
 EX MEDLINE 9927464; PubMed 2667165;
 PA Kwon B.S., Balaban R., Chintamaneni C.;
 RT "Molecular basis of mouse Himalayan mutation.";
 RL Biochem. Biophys. Res. Commun. 161:252-260(1989).
 CC [3]
 RP SEQUENCE FROM N.A.
 EX MEDLINE 9903066; PubMed 3141148;
 PA Mueller G., Koppert S., Schmid E., Schuetz G.;
 RT "Functional analysis of alternatively spliced tyrosinase gene
 transcripts.";
 RL EMBO J. 7:2723-2730(1988).
 CC [4]
 RP SEQUENCE FROM N.A.
 EX MEDLINE 9000000, PubMed 144997;
 PA Terao M., Take H., Garattini E., Sartori B., Mintz B.;
 RT "Isolation and characterization of variant cDNAs encoding mouse
 tyrosinase.";
 RL Biochem. Biophys. Res. Commun. 159:848-854(1989).
 CC [5]
 RP SEQUENCE FROM N.A.
 EX STRAIN-C57BL/6J;
 PA Takahashi T., Takahashi T., Nakai T., Tanaka A., Shinoda T.;
 RT "Isolation and sequencing of mouse tyrosinase cDNA.";
 RL Jpn. J. Genet. 62:271-274(1987).
 CC [6]
 RP SEQUENCE OF 1-273 FROM N.A.
 EX MEDLINE 9021994, PubMed 2617217;
 PA Yamanishi H., Takahashi T., Nakai T., Takahashi T.;
 RT "Melanin production in cultured albino melanocytes transfected with
 mouse tyrosinase cDNA.";
 RL Jpn. J. Genet. 64:121-135(1989).
 CC [7]
 RP VARIANT ALBINO.
 EX STRAIN-BALB/c;
 EX MEDLINE 9024949; PubMed 2110899;
 PA Takahashi T., Takahashi T., Tanaka A., Takahashi T., Takahashi T.;
 RT "A point mutation in the tyrosinase gene of BALB/c albino mouse
 causes the cysteine residue substitution at position 85.";
 RL Jpn. J. Biochem. 139:455-461(1990).
 CC [8]
 RP VARIANT CHINCHILLA MICE.
 EX MEDLINE 9036093; PubMed 2118105;
 PA Boermann F., Koppert S., Hummel E., Boschi F.X., Mueller G.,
 Koppert G., Schuetz G.;
 RT "Rescue of the albino phenotype by introduction of a functional
 tyrosinase gene into mice.";
 RL EMBO J. 9:2819-2825(1990).
 CC [9]
 CC FUNCTION: THIS IS A G-THREE CONTAINING OXIDASE THAT FUNCTIONS IN
 CC THE FORMATION OF PIGMENTS SUCH AS MELANINS AND OTHER POLYPHENOLIC
 CC COMPOUNDS. CATALYZES THE RATE LIMITING CONVERSION OF TYROSINE TO
 CC DOPA, DOPA TO DOPA QUINONE AND POSSIBLY 5,6-DIHYDROXYINDOLE TO
 CC INDOLE-5,6-DIOL.
 CC [10]
 CC CATALYTIC ACTIVITY: L-tyrosine + O2 -> L-DOPA + H2O + H2O2


```

DR Genbank: BCN0112816; XPR.
DR MIM: 278720;
DR InterPro: IPR004583; Rad4.
DR TIGRfam: TIGR00005; Rad4.1.
DR PRA RefSeq: CNA binding, Rad4.1 protein, Xorishoma pigmentosum.
KW disease mutation.
FT INIT MET 0
FT DOMAIN 29 176 OLD RICH (ACIDIC).
FT DOMAIN 308 394 LYS-RICH (BASIC).
FT DOMAIN 489 494 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
FT DOMAIN 407 430 ARG/LYS-RICH (BASIC).
FT DOMAIN 441 460 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 465 492 ARG/LYS-RICH (BASIC).
FT DOMAIN 29 43 POLY-GLU.
FT DOMAIN 123 129 POLY-GLU.
FT DOMAIN 506 POLY-SER.
FT VARIANT 333 333 P -> H (IN XP-C; SEVERE).
FT VARIANT 656 656 /FTID-VAR_005846.
FT VARIANT 938 938 V -> VV (IN XP-C; MILD).
FT VARIANT 938 938 K -> Q (IN XP-C; MILD).
FT CONFLICT 498 498 V -> A (IN REF. 3).
SQ SEQUENCE 430 AA: 100049 MW: 2505222121212121 CPE61.
Query Match 93.8% Score 30; ID 1; Length 929;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 5; Conservations 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GYRN 7
DB 216 GYRN 220
RESULT 12
PRA_YEAST
ID PRA_YEAST STANDARD; PRT; 1564 AA.
AC P51533;
DI 01-OCT-1996 (Ref. 34, Created)
DI 01-OCT-1996 (Ref. 34, Last sequence update)
DI 16-OCT-2001 (Ref. 40, Last annotation update)
DE ATP-dependent permease PDR10.
GN PDR10 OR YOR328W.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI TaxID: 4932;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97051586; PubMed: 8894263;
RA Paré-Rechmont A.G., Rand N.D., Goulding S.G., Wolfe K.H.;
RT "Sequence of 26 kb around the PDR10 locus on the right arm of
RT Saccharomyces cerevisiae chromosome XV: similarity to part of
RT chromosome I."
RC Yeast 17:969-1004 (1996)
CC 1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC 1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
CC This SWISS-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ssi.ch/sequence/
CC or send an email to license@ssi.ch).

```

```

DR Pfam: PF00005; ABC_tran; 2.
DR Prodom: PD00006; ABC_Transport; 2.
DR SMART: SM00482; AAA; 1.
DR TIGRfam: TIGR00005; Rad4.1.
DR PRA RefSeq: CNA binding, Rad4.1 protein, Xorishoma pigmentosum.
KW ATP-binding; Transmembrane; Glycoprotein; Transport.
FT DOMAIN 1 587 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 588 608 POTENTIAL.
FT TRANSMEM 624 634 POTENTIAL.
FT TRANSMEM 674 694 POTENTIAL.
FT TRANSMEM 699 719 POTENTIAL.
FT TRANSMEM 742 752 POTENTIAL.
FT TRANSMEM 841 961 POTENTIAL.
FT DOMAIN 862 1404 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 1405 1425 POTENTIAL.
FT TRANSMEM 1440 1460 POTENTIAL.
FT TRANSMEM 1490 1410 POTENTIAL.
FT TRANSMEM 1426 1446 POTENTIAL.
FT TRANSMEM 1459 1479 POTENTIAL.
FT TRANSMEM 1491 1511 POTENTIAL.
FT DOMAIN 1512 1564 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 73 80 POLY-SER.
FT DOMAIN 568 572 POLY-SER.
FT DOMAIN 845 848 POLY-LYS.
FT NP_BIND 959 966 ATP (POTENTIAL).
FT CARBOHYD 754 754 N-LINKED GLYCAN. (POTENTIAL).
SQ SEQUENCE 1564 AA: 176440 MW: 708570914080A01 C8C64.
Query Match 93.8% Score 30; ID 1; Length 1564;
Best Local Similarity 100.0%; Pred. No. 89;
Matches 5; Conservations 0; Mismatches 0; Indels 0; Gaps 0;
QY 4 GYRN 7
DB 1363 GYRN 1467
RESULT 13
ID R13260R00 STANDARD; PRT; 59 AA.
AC 051646;
DI 15-DEC-1998 (Ref. 47, Created)
DI 15-DEC-1998 (Ref. 47, Last sequence update)
DI 16-OCT-2001 (Ref. 40, Last annotation update)
DE 50S ribosomal protein L12.
GN RMPF OR BR0703.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI TaxID: 119;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE: 97051586; PubMed: 8894263;
RA Fraser C.M., Casjens S., Hand W.M., Sutton G.G., Clayton R.A.,
RA Lathia C.M., Whiteley K.A., Dodson R., Blackey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Evanson T., Karpman A., Adams M.D., Gocayne J.D., Johnson M.,
RA Venter K., Palmer N., Whiteley K.A., Peterson J., Smith T.,
RA Osterback L., Watheny L., McDonald L., Artiach P., Bowman C.,
RA Garland S., Fujii O., Cotton M.D., Beist K., Roberts K., Hatch K.,
RA Smith H.O., Venter J.C.;
RT "Genomic sequence of a Lyme disease spirochete, Borrelia
RT burgdorferi."
RC Yeast 17:969-1004 (1996)
CC 1- SIMILARITY: BELONGS TO THE ABC FAMILY OF TRANSPORTERS.
CC This SWISS-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation at
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ssi.ch/sequence/
CC or send an email to license@ssi.ch).

```

```

CC EMBL: AF001170; AAC67042.1; -.
DR TIGR: BB0703; -.
DR InterPro: IPR002677; Euk_sacchar_L32p.
DR Pfam: PF01783; Ribosomal_L32p; 1.
DR TrEMBL: I1100101; rfmf_bact; 1.
KW Ribosomal protein; Complete proteome.
FT INIT_MET 0
FT INI_MET 0
SQ SEQUENCE 59 AA; 6445 MW; 959P03FE0F0E1D07E C5C6A.

Query Match 84.4%; Score 27; DB 1; Length 59;
Best Local Similarity 80.0%; Pred. No. 15;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYFVN 7
DQ 47 GYFVN 51

RESULT 14
ID YAJF_LACIA STANDARD; PRT; 201 AA.
AC Q9CIB0;
DT 15-JUN-2002 (Rel. 41, Created)
DI 15-JUN-2002 (Rel. 41, Last sequence update)
DE Hypothetical protein yajf.
GN YAJF OR L10089.
CS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
CC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus
OX NCBI_TaxID=1360;
FN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=111403.
EX MEDLINE=21245186; PubMed=11337471;
RA Bolotin A., Winkler P., Mauger S., Jaillon O., Malarne K.,
RA Weissbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis ssp. lactis Il1403."
RL Genome Res. 11:731-753(2001).
CC -1- SURCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO THE Q9F0177 FAMILY.
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/edl/terms/
CC or send an email to license@sib-swiss.ch).
CC EMBL: AE006247; AAK04187.1; -.
DR TrEMBL: IPR003675; Abi.
DR Pfam: PF02517; Abi; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 44 64 POTENTIAL.
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 119 139 POTENTIAL.
FT TRANSMEM 159 179 POTENTIAL.
SQ SEQUENCE 201 AA; 23173 MW; B8C1E5495030E3B8 C8F64.

Query Match 84.4%; Score 27; DB 1; Length 201;
Best Local Similarity 80.0%; Pred. No. 51;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYFVN 7
DQ 67 GYFVN 71

RESULT 15
ID YAJF_LACIA

```

```

ID DECO_BUCAI STANDARD; PRT; 234 AA.
AC P57606;
DT 16-OCT-2001 (Rel. 40, Created)
DI 16-OCT-2001 (Rel. 40, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE Purine nucleoside phosphorylase (EC 2.4.2.1) (Inosine phosphorylase)
DE (PNP).
GN PNP OR P0541.
CS Escherichia aphidivora (subsp. de aphidivora) (A-phidivora) (Pisum
CC symbiotic bacterium).
CC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
OX NCBI_TaxID=118099;
FN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13470 1998;
EX MEDLINE=20445173; PubMed=10994077;
RA Shigenori S., Watanabe H., Harperi M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. APS."
RL Nature 407:81-86(2000).
CC -1- FUNCTION: CLEAVAGE OF GUANOSINE OR INOSINE TO RESPECTIVE BASES AND
CC SUGAR-1-PHOSPHATE MOLECULES (BY SIMILARITY).
CC -1- CATALYTIC ACTIVITY: Purine nucleoside + phosphate -> purine +
CC alpha-D-ribose 1-phosphate.
CC SUBUNIT: HOMODIMER (BY SIMILARITY).
CC SIMILARITY: BELONGS TO THE PNP FAMILY 1 or INOSINPHOSYLASES.
CC THIS SWISS-PROT entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.ebi.ac.uk/edl/terms/
CC or send an email to license@sib-swiss.ch).
CC EMBL: AP001119; BAB13233.1; -.
DR TrEMBL: P05743; IAG9.
DR InterPro: IPR004402; D000;
DR InterPro: IPR003845; PNP_HBP.
DR Pfam: PTC0348; PNP_HBP; 1.
DR TrEMBL: P000424; PNP_HBP; 1.
DR TrEMBL: ITC00107; deob; 1.
DR TrEMBL: P01232; PNP_HBP; 1; FALSE NEG.
RW Database: 21245186; PubMed=11337471;
SQ SEQUENCE 234 AA; 26425 MW; 676P041B0E0B41FA C8F64.

Query Match 84.4%; Score 27; DB 1; Length 234;
Best Local Similarity 80.0%; Pred. No. 60;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYFVN 7
DQ 51 GYFVN 66

RESULT 16
ID SOLR_CICAB STANDARD; PRT; 318 AA.
AC P33746;
DT 01-FEB-1994 (Rel. 28, Created)
DI 01-FEB-1994 (Rel. 28, Last sequence update)
DE 15-JUN-2002 (Rel. 41, Last annotation update)
DE Sol locus transcriptional repressor.
GN SOLR OR CAP0161.
CS Clostridium acetobutylicum.
CC Plasmid pSOL.
CC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
CC Clostridium.
OX NCBI_TaxID=1488;
FN [1]
RP SEQUENCE FROM N.A.
RC STRAIN ATCC 821 / LEW 732 / VPM b 1787;
EX MEDLINE=94042861; PubMed=8226049;

```


CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in the
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.ebi.ac.uk/infocentre>
CC or send an email to license@ebi.ac.uk).

DR EMBL: U67509; AAB28606.1; -
DR RSP: P20625; ZABK.
DR TIGR: M10613; -
DR InterPro: IPR002847; DUF123.
DR InterPro: IPR004045; Endo111_FGL.
DR InterPro: IPR004046; Endo111_mh.
DR InterPro: IPR003265; Endo_3c.
DR InterPro: IPR002451; FcG_L113.
DR InterPro: IPR003583; HHH_L1.
DR InterPro: IPR000305; nvrC_N
DR Pfam: PF00710; HhH-GPD; 1.
DR Pfam: PF01486; DUF123; 1.
DR Pfam: PF01567; DUF124; 1.
DR SMART: SM00478; END03c; 1.
DR SMART: SM00525; FES; 1.
DR SMART: SM00455; GIVC; 1.
DR SMART: SM00278; HHH1; 1.
DR PROSITE: PS00764; ENDONUCLEASE_IL11; FALSE_NEG.
DR PROSITE: PS01155; ENDONUCLEASE_IL12; 1.
KW Hypothetical protein, Hydrolyase, Glycosidase, 1; a saltin, 4Fe 4S,
KW Complete Proteome.
FT METAL 184 184 IRON-SULFUR (AFE-4S) (BY SIMILARITY).
FT METAL 190 190 IRON-SULFUR (AFE-4S) (BY SIMILARITY).
FT METAL 193 193 IRON-SULFUR (AFE-4S) (BY SIMILARITY).
FT METAL 201 201 IRON-SULFUR (4Fe 4S) (BY SIMILARITY).
SQ SEQUENCE 344 AA; 40567 MW; BC3BEFED778B85 CRC64;

Query Match 84.4%; Score 27; DB 1; Length 344;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 3 GYKRN 7
DB 77 GYKRN 81

RESULT 19
ID YCJX_ECOLI STANDARD; EBI; 465 AA.
AC P76046; P77411;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein ycjx.
GN YCJX OR 91321.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae,
OC Escherichia.
OX NCBI_Taxid:562;
RN [1]
RF SEQUENCE FROM N.A.
RC STRAIN=K12; PubMed 9278503;
RX MEDLINE=97456617; PubMed 9278503;
RA Blattner F.B., Plunkett G. III, Bloch C.A., Borna N.T., Burland V.,
RA Riley M., Gillis V., Glasner J.D., Rode C.K., Mayhew G.P.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K12.";
RL Science 277:1232-1244(1997).
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97251357; PubMed 9607030;
RA Aiba H., Baba T., Fujita K., Hayashi K., Inada T., Isoko K.,
RA Itoh T., Kasai H., Kashiwagi K., Kimura S., Kitakawa M.,
RA Kitajima M., Makino K., Miki T., Mizubuchi K., Mori H., Mori T.,

KA Matsuda F., Kubota E., Nakamura Y., Hashimoto H., Hishio Y.,
KA Ashina T., Saito N., Sampei G., Saki Y., Sivasubraman S.,
KA Taira H., Takeda T., Tabei T., Tate H., Y. Wada C.,
KA Yamamoto Y., Horiochi T.;
RT "A 1.7 kb DNA sequence of the *Escherichia coli* K12 genome
RT corresponding to the 28.0-40.1 min region on the linkage map.";
KL DNA RES. 4:393-397(1996).
CC 1. SIMILARITY: STRCS; TO H. INFERREAE H11637.
CC This SWISS-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in the
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see <http://www.ebi.ac.uk/infocentre>
CC or send an email to license@ebi.ac.uk).

Query Match 84.4%; Score 27; DB 1; Length 465;
Best Local Similarity 80.0%; Pred. No. 88;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0.

QY 3 GYKRN 7
DB 270 GYKRN 274

RESULT 20
ID YCJX_HUMAN STANDARD; EBI; 471 AA.
AC P23381; P78535; Q90014;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE tryptophanyl tRNA synthetase (E.C.2.3.1.2) (tryptophan tRNA idase)
DE (trpS) (trpS) (trpS).
GN WARS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid:9606;
RN [1]
RF SEQUENCE FROM N.A.
RC MEDLINE 92100711; PubMed 1761529;
RX Rubin B.V., Anderson S.L., Xing L., Powell R.J., Tate W.P.;
KA "Interferon induces tryptophanyl tRNA synthetase expression in human
KA fibroblasts.";
KL J. Biol. Chem. 266:24245-24248(1991).
RP [2]
RF SEQUENCE FROM N.A.
RC MEDLINE 92107062; PubMed 1763065;
RX Eickholt J., Boshuizen H.B., Justesen J.;
KA "Human interferon gamma potently induces the synthesis of a 55 kDa
KA protein (gamma 2) highly homologous to rabbit peptide chain release
KA factor and bovine tryptophanyl tRNA synthetase.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:11523-11524(1996).
RN [3]
RF SEQUENCE FROM N.A.
RC MEDLINE 92100711; PubMed 1761529;
KA Eickholt J., Boshuizen H.B., Justesen J.;
KA "Cloning and nucleotide sequence of the structural gene encoding for
KA human tryptophanyl tRNA synthetase.";
RL Gene 199:291-296(1994).
RN [4]
RF SEQUENCE FROM N.A.

CC (omega-0).

CC 1. SIMILARITY. BELONGS TO THE CYCLOPHANYL-TYPE EFASE FAMILY.

CC This SWISS-prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation.

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Please send an email to

CC or send an email to license@isb-sib.ch).

CC edit requires a license agreement (see <http://www.isb-sib.ch>).

DR EMU: 267944; CAA91964 1;

DR HSSP: 027450; ICSEF;

DR InterPro: IPR002130; CSA_PPase;

DR InterPro: IPR002130; Znf_modifng;

DR Pfam: PF00160; pro_isomerase; 1;

DR PRINTS: PR00153; CSNPISMRASE;

DR SMART: SM00594; Ubox; 1;

DR PROSITE: PS00170; CSA_PPase; 1;

DR PROSITE: PS00072; CSA_PPase; 2;

KW Hypothetical protein; Isomerase; Rofamide;

FT DOMAIN 237 293 PPase; CYCLOPHANYL-TYPE;

SQ SEQUENCE 471 AA: 53573 MW: 66156620390608 CR644;

Query Match 84.4%; Score 27; BB 1; Length 471;

Best local Similarity 80.0%; Pred. No. 120-02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYEN 7

DB 245 GYEN 269

RESULT 22

ID SWV_BOVIN STANDAPP: PPT: 475 AA.

AC P17248;

DT 01-AUG-1990 (Rel. 15, Created)

DT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)

DE (TPRS).

CN WARS

OS Bos taurus (Bovine).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Cetartiodactyla; Perissodactyla; Bovidae;

CC Bovidae; Bovinae; Bos.

OX NCBI_TaxID=9913;

RN [1]

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE

RC TISSUE=Retina;

RX MEDLINE=91329348; PubMed=1907847;

RA Garret M., Pajot B., Trezequet V., Labrousse J., Merle M.,

RA Gaudier J.-C., Benedetto J.-P., Sallafranque M.-L., Allierio J.,

RA Guenou M., Sarger C., Labrousse B., Boucet J.,

RT "A mammalian tryptophanyl-tRNA synthetase shows high homology to

RT prokaryotic synthetases but near identity with mammalian peptide

RT chain release factor.";

RL Biochemistry 30:7809-7817(1991).

RN [2]

RP SEQUENCE OF 17-475 FROM N.A.

RC TISSUE=Pancreas;

PA Garret M., Trezequet V., Pajot B., Gaudier J.-C., Merle M.,

PA Guenou M., Benedetto J.-P., Sarger C., Allierio J., La Porcesse P.,

RA Labrousse J., Boucet J.,

RL Submitted (MAR-1990) to the EMBL/Genbank/DDB databases.

CC 1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) -> AMP +

CC diphosphate + L-tryptophanyl-tRNA(Trp);

CC 1- SIMULTANEOUS HOMODIMER

CC 1- SIMILARITY: BELONGS TO CLASS-1 AMINOACYL-TRNA SYNTHETASE FAMILY.

CC 1- SIMILARITY: CONTAINS 1 WHIP-TRS DOMAIN.

CC This SWISS-prot entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation.

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Please send an email to

CC or send an email to license@isb-sib.ch).

CC edit requires a license agreement (see <http://www.isb-sib.ch>).

DR EMU: 267944; CAA91964 1;

DR HSSP: 027450; ICSEF;

DR InterPro: IPR002130; CSA_PPase;

DR InterPro: IPR002130; Znf_modifng;

DR Pfam: PF00160; pro_isomerase; 1;

DR PRINTS: PR00153; CSNPISMRASE;

DR SMART: SM00594; Ubox; 1;

DR PROSITE: PS00170; CSA_PPase; 1;

DR PROSITE: PS00072; CSA_PPase; 2;

KW Hypothetical protein; Isomerase; Rofamide;

FT DOMAIN 237 293 PPase; CYCLOPHANYL-TYPE;

SQ SEQUENCE 471 AA: 53573 MW: 66156620390608 CR644;

Query Match 84.4%; Score 27; BB 1; Length 475;

Best local Similarity 80.0%; Pred. No. 120-02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYEN 7

DB 245 GYEN 264

RESULT 24

ID SWV_RABBIT STANDAPP: PPT: 475 AA.

AC P24612; Q28607;

DT 01-NOV-1991 (Rel. 20, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-JUL-1998 (Rel. 36, Last annotation update)

DE Tryptophanyl-tRNA synthetase (EC 6.1.1.2) (Tryptophan-tRNA ligase)

DE (TPRS).

CN WARS

OS Oryctolagus cuniculus (Rabbit).

CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.

OX NCBI_TaxID=9986;

RN [1]

RP SEQUENCE FROM N.A.

RC MEDLINE=9024994; PubMed=2185172;

RA Garret M., Trezequet V., Pajot B., Gaudier J.-C., Merle M.,

RA Guenou M., Sarger C., Labrousse B., Boucet J.,

RT "Cloning and expression of a mammalian peptide chain release factor

RT with sequence similarity to tryptophanyl tRNA synthetases.";

RL Proc. Natl. Acad. Sci. U.S.A. 87:3508-3512(1990).

RN [2]

RP SEQUENCE OF 17-475 FROM N.A.

RC MEDLINE=94009008; PubMed=8404867;

PA Garret M., Trezequet V., Pajot B., Gaudier J.-C., Merle M.,

PA Guenou M., Benedetto J.-P., Sarger C., Allierio J., La Porcesse P.,

RA Labrousse J., Boucet J.,

RL Submitted (MAR-1990) to the EMBL/Genbank/DDB databases.

CC 1- CATALYTIC ACTIVITY: ATP + L-tryptophan + tRNA(Trp) -> AMP +

CC diphosphate + L-tryptophanyl-tRNA(Trp);

CC 1- SIMULTANEOUS HOMODIMER

CC 1- SIMILARITY: BELONGS TO CLASS-1 AMINOACYL-TRNA SYNTHETASE FAMILY.

CC 1- SIMILARITY: CONTAINS 1 WHIP-TRS DOMAIN.

CC This SWISS-prot entry is copyright. It is produced through a collaboration

RELEASE FACTOR (RFF)

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcements/>
CC or send an email to license@isb-sib.ch).

DR EMBL: M33460; AAA4246.1; ALL_SEQ.
DR EMBL: 002595; AAF60257.1;
DR PIR: A5504; YWRNRK.
DR InterPro: IPR002305; TRF_PRR-synt_lb.
DR InterPro: IPR000748; WHEP-TRS.
DR InterPro: IPR002306; PRR_PRR_1.
DR InterPro: IPR001412; TRF-synt_1.
DR Pfam: PF00458; WHEP-TRS; 1.
DR Pfam: PF00679; TRF-synt_lb; 1.
DR Pfam: PF01049; TRNASYNTHRP.
DR Tricore: TIGR00243; TRS; 1.
DR ProSITE: PS00178; AA_TPNA_TICASE_1; 1.
DR ProSITE: PS00762; WHEP-TRS; 1.
KW Anticatalytic RNA synthetase, protein biosynthesis, ligase, ATP binding.
FT DOMAIN 23 68 WHEP-TRS.
FT SITE 168 177 "HIGH" REGION.
FT SITE 453 457 "KMSK" REGION.
SQ SEQUENCE 475 AA; 53799 MW; 338C9E719FF45D94 CRC64;

Query Match 84.4%, Score 27, DB 1, Length 175.

Best Local Similarity 80.0%; Prod. No. 1.2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

DB 250 GYRN 254

RESULT 24

DR ANKH_MOUSE STANF25, PFI, 492 AA.
AC Q9HJ2; G6319; G63140;
DI 15-JUN-2002 (Rel. 41, Created)
DI 15-JUN-2002 (Rel. 41, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Progressive ankylosis protein (Pn54 protein).
GN ANKH OR ANK.
OS Mus musculus (Mouse).
CC Fukuyama; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus;
CC NCBI_TaxID 10090;
CC [1]
CC SEQUENCE FROM N.A. AND VARIANT VAL 201.
CC SIKAIN (S796/6; TISSUE-BRAIN;
CC MEDLINE 2945194; PubMed 13894769;
CC Bo A.M., Johnson M.D., Kinsley D.M.;
CC "Role of the mouse ank gene in control of tissue calcification and
CC arthritis."
CC Science 289:265-270 (2000).
CC [2]
CC SEQUENCE FROM N.A.
CC SIKAIN R646/5;
CC Guo Y., Hsu D.K.W., Alberts G.F., Ford S.L., Copeland N.G.,
CC Gilbert D.L., Jenkins R.A., Peifley R.A., Whittes J.A.;
CC "Molecular cloning and characterization of a mouse inducible gene
CC differentially expressed in androgen-dependent and independent
CC prostate carcinoma cell lines."
CC Submitted (2000) to GenBank, EMBL, and SwissProt databases.
CC [3]
CC FUNCTION: Regulates intra- and extracellular levels of inorganic
CC pyrophosphate (PPi), probably functioning as Ppi transporter
CC in SKELETON formation. Intra- and extracellular levels of inorganic
CC pyrophosphate (PPi) are important for bone formation. It is
CC a TISSUE SPECIFIC gene, expressed in heart, brain, liver, spleen,
CC lung, muscle, and kidney of adult animals. Strongly expressed in

the developing articular cartilage of joints in the shoulder,
elbow, wrist, and digits of the embryo.

DI MISAGE: Entries in ANKH are the range of a generalized,
progressive form of arthritis. In ank mice hypophosphatase crystals
develop in articular surfaces and synovial fluid leading to joint
space narrowing, cartilage erosion, and formation of bony
outgrowths or osteophytes that cause fusion and joint immobility
and destruction.

SIMILARITY: BELONGS TO THE ANKH FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announcements/>
CC or send an email to license@isb-sib.ch).

DR EMBL: A5274752; AAF88048.1;
DR EMBL: AF001542; AAB65653.1;
DR EMBL: AF001543; AAB65654.2;
DR X25; MCI:99024; JCK.
KW Transport; Phosphate transport; Transmembrane; Polymorphism.
FT DOMAIN 1 95 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 86 106 POTENTIAL.
FT DOMAIN 107 131 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 132 152 POTENTIAL.
FT EXMAIN 153 156 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 159 179 POTENTIAL.
FT TRANSMEM 180 189 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 190 210 POTENTIAL.
FT DOMAIN 211 426 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 427 447 POTENTIAL.
FT DOMAIN 448 450 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 451 471 POTENTIAL.
FT DOMAIN 472 483 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 404 426 POTENTIAL.
FT DOMAIN 427 429 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 430 452 POTENTIAL.
FT DOMAIN 453 492 CYTOPLASMIC (POTENTIAL).
FT VARIANT 251 251 V (IN EXMAIN 10).
SQ SEQUENCE 492 AA; 54297 MW; 93029248C876088E CRC64;

Query Match 84.4%, Score 27, DB 1, Length 492.

Best Local Similarity 80.0%; Prod. No. 1.2e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

DB 211 GYRN 215

RESULT 25

DR ANKH_RAI
AC P58466;
DI 15-JUN-2002 (Rel. 41, Created)
DI 15-JUN-2002 (Rel. 41, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Progressive ankylosis protein homolog (AMK).
GN ANKH.
OS Rattus norvegicus (Rat).
CC Fukuyama; Metazoa; Chordata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus;
CC NCBI_TaxID:10116;
CC [1]
CC SEQUENCE FROM N.A.
CC SIKAIN R646/5; Guo Y., Hsu D.K.W., Alberts G.F., Ford S.L., Copeland N.G.,
CC Gilbert D.L., Jenkins R.A., Peifley R.A., Whittes J.A.;
CC "Molecular cloning and characterization of a mouse inducible gene
CC differentially expressed in androgen-dependent and independent
CC prostate carcinoma cell lines."
CC Submitted (2000) to GenBank, EMBL, and SwissProt databases.
CC [3]
CC FUNCTION: Regulates intra- and extracellular levels of inorganic
CC pyrophosphate (PPi), probably functioning as Ppi transporter
CC in SKELETON formation. Intra- and extracellular levels of inorganic
CC pyrophosphate (PPi) are important for bone formation. It is
CC a TISSUE SPECIFIC gene, expressed in heart, brain, liver, spleen,
CC lung, muscle, and kidney of adult animals. Strongly expressed in


```

US Giardia lamblia (Giardia intestinalis).
CX Enkaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
RN NCBI_TaxID 5741;
RP SEQUENCE FROM N.A.
RC STRAIN AD-1;
RX MEDLINE 9241215; PubMed 8479449;
RA By P.L., Klumpp K., Manning P.A., Mayrhofer G.;
RT "A gene encoding a 69-kilodalton major surface protein of Giardia
RI intestinalis trophozoites."
RL Mol. Biochem. Parasitol. 58:247-252(1994).
CC -1- SURFACELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN. ANCHORED TO THE
CC PLASMA MEMBRANE.
CC -1- DOMAIN: CONTAINS 27 REPEATS OF A CXXC MOTIF.
CC -1- SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announcements
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M95814; AAA02687.1; -.
DR PIR: A48579; A48579.
DR BSSP: po2468; 1875.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR005127; Giardia_VSP.
DR Pfam: PF03402; VSP; 1.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00261; PD; 3.
DR SMART: SM00261; PD; 5.
KW Antigen; Repeat; Transmembrane; Signal.
FT SIGNAL 1 17
FT CHAIN 18 667 MAJOR SURFACE TROPHOZOITE ANTIGEN 11.
FT DOMAIN 18 667 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 644 667 POTENTIAL.
FT DOMAIN 663 667 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 591 591 N-LINKED GLYCANS (POTENTIAL).
FT CARBOHYD 640 640 N-LINKED GLYCANS (POTENTIAL).
SQ SEQUENCE 667 AA: 6647 MW: 119572.7322 Da: G6V64.

Query Match 84.4%; Score 27; DB 1; Length 667;
Best Local Similarity 80.0%; Pred. No. 1; 70:92;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 GFYKN 7
ID 362 GFYKN 465
III:1

RESULT 28
ISAA_GIALA
ID ISAA_GIALA STANDARD: PRT: 713 AA.
AC P21849;
DI 01 MAY-1991 (Rel. 18, Created)
DI 01 MAY-1991 (Rel. 18, Last sequence update)
DI 16 OCT-2001 (Rel. 43, Last annotation update)
DE Major surface labeled trophozoite antigen 417 precursor.
GN TSA 417.
OS Giardia lamblia (Giardia intestinalis).
CX Enkaryota; Diplomonadida; Hexamitidae; Giardiinae; Giardia.
RN NCBI_TaxID 5741;
RP SEQUENCE FROM N.A.
RC STRAIN AD-1;
RX MEDLINE 90280495; PubMed 2352929;
RA Gillin F.D., Hasplom P., Harwood J., Alley S.B., Reiner D.S.,
RT "Isolation and expression of the gene for a major surface protein of
RT Giardia lamblia."
RL Proc. Natl. Acad. Sci. U.S.A. 87:4463-4467(1990).

```

```

RN RP SEQUENCE OF 480-620 FROM N.A.
RC STRAIN AD-1;
RX MEDLINE 93341970; PubMed 8425510;
RA By P.L., Mayrhofer G.;
RT "Two genes encoding homologous 70-kDa surface proteins are present
RT within individual trophozoites of the binucleate protozoan parasite
RT Giardia intestinalis."
RL Gene 129:257-262(1993).
CC -1- SURFACELLULAR LOCATION: TYPE 1 MEMBRANE PROTEIN. ANCHORED TO THE
CC PLASMA MEMBRANE.
CC -1- DOMAIN: CONTAINS 29 REPEATS OF THE CXXC MOTIF.
CC -1- SIMILARITY: BELONGS TO THE GIARDIA VARIANT SURFACE PROTEIN FAMILY.
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC at the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb.ch/announcements
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M33641; AAA02688.1; -.
DR EMBL: M97488; AAA02581.1; -.
DR PIR: A35502; A35502.
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002174; Furin-like.
DR InterPro: IPR005127; Giardia_VSP.
DR Pfam: PF03402; VSP; 2.
DR SMART: SM00181; EGF; 1.
DR SMART: SM00061; EGF-like; 1.
DR SMART: SM00261; PD; 3.
KW Signal; Antigen; Glycoprotein; Transmembrane; Repeat.
FT SIGNAL 1 17
FT CHAIN 18 713 MAJOR SURFACE-LABELLED TROPHOZOITE
FT DOMAIN 18 679 ANTIGEN 417.
FT TRANSMEM 699 713 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 709 713 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 679 679 N-LINKED GLYCANS (POTENTIAL).
FT CARBOHYD 679 679 N-LINKED GLYCANS (POTENTIAL).
FT VARIANT 692 682 A -> T (IN STRAIN ADELALDE-1).
FT VARIANT 696 696 A -> S (IN STRAIN ADELALDE-1).
FT VARIANT 713 AA: 72510 MW: 940719584 Da: E5601 CR684.

Query Match 84.4%; Score 27; DB 1; Length 713;
Best Local Similarity 80.0%; Pred. No. 1; 60:02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYKN 7
ID 414 GFYKN 418
III:1

RESULT 29
V179_FOWPV
ID V179_FOWPV STANDARD: PRT: 91 AA.
AC Q90554;
DI 16 OCT-2001 (Rel. 40, Created)
DI 16 OCT-2001 (Rel. 40, Last sequence update)
DI 16 OCT-2001 (Rel. 40, Last annotation update)
DE Virion envelope protein FV179.
GN FV179.
OS Fowlpox virus (FV).
CX Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae.
CX Avipoxvirus.
GX NCBI_TaxID 10261;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE 20191920; PubMed 10729150;
RA "The genome of fowlpox virus."
RT J. Virol. 74:4815-4831(2000).

```

CC -1- SIMILARITY: BELONGS TO THE POXVIRUSES A14 FAMILY.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement. (See <http://www.ebi.ac.uk/infocentre/licenses>)

CC or send an email to license@isb-sib.ch.

DR EMBL: AF198100; AAF44523.1; -

KW Envelope protein.

SW SEQUENCE 91 AA; 9950 MW; 64FE7AECEED3849D CPE64;

Query Match 81.28; Score 26; DB 1; Length 91;

Best Local Similarity 80.08; Pred NS: 92;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYEN 7

DB 5 GFYEN 9

RESULT 30

RK9_PEA STANDARD; PRT; 194 AA.

AC PL1894;

DI 01-02V-1989 (Rel. 12, Created)

LT 01-NV-1996 (Rel. 22, Last sequence update)

DT 01-FEB-1996 (Rel. 34, Last annotation update)

DE 50S ribosomal protein L9, chloroplast precursor (CL19).

GN RPL9.

CS Pisum sativum (Garden pea)

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Eudicotyledons; Ericales; Fagales;

OC Eucuriales 1; Fagales; Fagaceae; Fagitionoideae; Vireoideae; Fagum

OX NCBI_TaxID:3888;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN:cv. Little Marvel; TISSUE:Seedling;

PX MEDLINE:8913671; PubMed:3066512;

RA Gant J.S.;

FT "Nucleotide sequence of cDNA encoding four complete nuclear-encoded

FT plastid ribosomal proteins";

RL Curr. Genet. 14:519-528(1988).

CC -1- FUNCTION: BINDS TO THE 23S rRNA (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Chloroplast.

CC -1- SIMILARITY: BELONGS TO THE LRP FAMILY OF RIBOSOMAL PROTEINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement. (See <http://www.ebi.ac.uk/infocentre/licenses>)

CC or send an email to license@isb-sib.ch.

CC EMBL: X14019; CAA32184.1;

DR PIR: S04684; R5PM9.

DP R5SP: P02417; 1DIV.

DP ITC:FCR1 PFO00344; Ribosomal_L9.

DP Pfam: PF01381; Ribosomal_L9; 1.

DP TIGR:PF01381; Ribosomal_L9; 1.

DR PROSITE: PS00651; RIBOSOMAL_L9; 1.

KW Ribosomal protein, rRNA-binding, Chloroplast, Transit peptide.

FT TRANSIT 1 34 CHLOROPLAST.

FT CHAIN 35 194 50S RIBOSOMAL PROTEIN L9.

SW SEQUENCE 194 AA; 21766 MW; 2F624C3E49A9444 3C924;

Query Match 81.28; Score 26; DB 1; Length 194;

Best Local Similarity 80.08; Pred NS: 92;

Matches 4; Conservative 1; Mismatches 0; Indels 9; Gaps 0;

QY 3 GFYEN 7

DB 70 GFYEN 74

PS9131 31

RK9_AWATH

AC PL2964;

DI 01-MAY-1992 (Rel. 22, Created)

LT 01-MAY-1992 (Rel. 22, Last sequence update)

DT 15-JUN-2002 (Rel. 41, Last annotation update)

DE 50S ribosomal protein L9, chloroplast precursor (CL9).

GN RPL9 OR AT1G344890 OR F28D10_80.

CS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

OC Spermatophyta; Magnoliophyta; Eudicotyledons; Ericales; Rosidae;

OC Eucuriales 1; Brassicales; Brassicaceae; Arabidopsids.

OX NCBI_TaxID:3702;

RN [1]

RP SEQUENCE FROM N.A.

RX STRAIN:cv. Columbia;

PX MEDLINE:9255911; PubMed:1591570;

RA Thompson M.D., Jacks C.M., Lemvik T.P., Gantt J.S.;

FT "Characterization of rpl7, rpl9 and rpl15: three nuclear-encoded

FT plastid ribosomal protein genes";

RL Plant Mol. Biol. 18:931-944(1992).

RN [2]

RP SEQUENCE FROM N.A.

RX STRAIN:cv. Columbia;

PX MEDLINE:21016720; PubMed:11130713;

RA Saitohkai M., Lemke K., Kiefer H., Peter Alonso, M., Schmaier B.,

RA Erdmann R., Valle G., Plecker H., Michel R., Polakowicz P.,

PA Sledge V., Chisholm R., Artzner T., Edler C., Brattier P.,

FA Winkler P., Gattling T., Weissenbach J., Saurin W., Queller F.,

RA Schaefer M., Mueller-Auer S., Gabel C., Fuchs M., Bous V.,

RA Wundbach E., Drzonek H., Erle H., Jordan N., Banert S.,

RA Wiedemann P., Franz H., Voss H., Holland S., Brandt P., Nakamura G.,

RA Vozel A., D'Amelio M., Pallavicini A., Poppe S., Simonati R.,

RA Conrad A., Hentscher K., Kauer C., Lambert J. B., Hefisch G.,

RA Reichelt J., Scharfe M., Schoen O., Barques M., Terol J., Clement J.,

RA Navarro P., Collado C., Iezzi-Felze A., Offenkordt R., Buchlein D.,

RA Cooke P., Lande M., Berger-Hellau C., Purnelle B., Masny D.,

RA de Haan M., Maarse A.C., Alcaraz J.-P., Cotter A., Casaubert E.,

RA Monfort A., Arriou A., Flores M., Linares R., Vitale D.,

RA Manhaupt G., Haase D., Schott H., Rudi S., Zaccaria P., Meves H.W.,

RA Mayer E.T.X., Paul S., Pown C.B., Koo H.L., Tallon B.J., Shea T.P.,

RA Rooney T.B., Rizzo M., Walts A., Unterbark T., Fujii P.Y., Shea T.P.,

FA Greary T.B., Ghar R., Bittler P., Wu C., Peters A., Van Wijk R.,

RA Bai G., Mills-Hor J., Sellers P., Gill J.B., Feldblum T.V.,

RA Fieuss B., Lin X., Nicman W.C., Salzberg S.L., White O., Venter J.C.,

FA Brandt P., Erle H., Nakamura Y., Valle G., Kato T., Asanaka E.,

RA Saitohkai M., Kiefer H., Plecker H., Schmaier B., Fiedler T.,

FA Fieuss B., Nakamura H., Nakazaki H., Shinozaki T., Hara K.,

RA Sakayama A., Yamada M., Yasuda M., Tabata S.;

RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis

RT thaliana";

RL Nature 409:820-823(2000).

CC -1- FUNCTION: BINDS TO THE 23S rRNA (BY SIMILARITY).

CC -1- SUBCELLULAR LOCATION: Chloroplast.

CC -1- SIMILARITY: BELONGS TO THE LRP FAMILY OF RIBOSOMAL PROTEINS.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration

CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its

CC use by non-profit institutions as long as its content is in no way

CC modified and this statement is not removed. Usage by and for commercial

CC entities requires a license agreement. (See <http://www.ebi.ac.uk/infocentre/licenses>)

CC or send an email to license@isb-sib.ch.

CC EMBL: Z11129; CAA77480.1;

```

DR EMBL: Z11509; CAA77594.1;
DR EMBL: AL391254; CAC04549.1;
DR EMBL: S20943; B5M019.
DR BSSP: F02417; L1V1.
DR InterPro: IPR009244; Ribosomal_L9.
DR Pfam: PF01281; Ribosomal_L9; 1.
DR TIGFAMS: TIGR00158; L9; 1.
DR PROSITE: PS00651; RIBOSOMAL_L9; 1.
KW Ribosomal protein; rRNA-binding; chloroplast; Transl: peptide.
FT TRANSIT 1 47 CHLOROPLAST (POTENTIAL).
FT CHAIN 48 197 56S RIBOSOMAL PROTEIN L9.
SQ SEQUENCE 197 AA: 22174 MW: 25539.96 kDa; CD044.

Query Match
Best Local Similarity 80.08; Score 26; DB 1; Length 197;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 GYRN 7
DB 73 GYRN 77

RESULT 32
YALF_LACLA
ID YALF_LACLA STANDARD: PRT: 218 AA.
AC Y9CJH5;
DI 15-JUN-2002 (rel. 41, Created)
DI 15-JUN-2002 (rel. 41, Last sequence update)
DI 15-JUN-2002 (rel. 41, Last annotation update)
DE Hypothetical protein yalF.
GN YalF ORF L10092.
OS Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI TaxID 1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 111403;
RX M011NP-212 c146; b1964-110747.
RA Molot in A.; Wincker P.; Mauger S.; Jallion G.; Malarum K.;
RA Weissbach J.; Ehrlich S.P.; Sorokin A.;
RA "The complete genome sequence of the lactic acid bacterium Lactococcus
RA lactis ssp. lactis 111403."
RL Genome Res. 11:741-753(2001).
CC -! SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -! SIMILARITY: BELONGS TO THE YALF/Y7 FAMILY
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch) or
CC send an email to license@sib-sib.ch).
DR EMBL: AF006247; AAK04180.1;
DR InterPro: IPR003675; Abi.
DR Pfam: PF02517; Abi; 1.
KW Hypothetical protein; Transmembrane; Complete proteome.
FT TRANSMEM 8 28 POTENTIAL.
FT TRANSMEM 48 68 POTENTIAL.
FT TRANSMEM 81 101 POTENTIAL.
FT TRANSMEM 124 143 POTENTIAL.
FT TRANSMEM 163 183 POTENTIAL.
SQ SEQUENCE 218 AA: 25414 MW: 95786.49 kDa; CD044.

Query Match
Best Local Similarity 80.08; Score 26; DB 1; Length 218;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 GYRN 7
DB 67 GYRN 71

```

```

RESULT 33
ENDS_SYN4
ID ENDS_SYN4 STANDARD: PRT: 219 AA.
AC P73715;
DI 15-JUN-1998 (rel. 36, Created)
DI 15-JUN-1998 (rel. 36, Last sequence update)
DI 16-OCT-2001 (rel. 40, Last annotation update)
DE Endonuclease III (5'-3',5'-phosphate dependent) (DNA dependent on pyrimidine site)
GN ENDS_SYN4
GN NTH OR SLK1822.
OS Synechocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chlorococcales; Synechocystis.
OX NCBI TaxID 1148;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-97061201; PubMed-8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirosewa M., Suda M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuo A., Muraki A., Nakazaki N., Nishio K.,
RA Okumura S., Shimizu S., Takagishi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RA "Sequence analysis of the genome of the unicellular cyanobacterium
RA Synechocystis sp. strain PCC6803. II. Sequence determination of the
RA entire genome and assignment of potential protein-coding regions."
RL DNA RES. 3:109-136(1996).
CC -! FUNCTION: HAS BOTH AN ATP-DEPENDENT 5'-3' EXONUCLEASE
CC ACTIVITY AND A DNA N-GLYCOSYLASE ACTIVITY. INCISES DAMAGED DNA AT
CC CYTOSINES, THYMINES AND GUANINES, AS WELL AS A DAMAGED CHARGED, 5'
CC FROM THE DAMAGED SITE (BY SIMILARITY).
CC -! CATALYTIC ACTIVITY: The c-c-p bond 3' to the apurinic or
CC apyrimidinic site in DNA is broken by a beta-elimination reaction,
CC leaving a 3'-terminal unsaturated sugar and a product with a
CC terminal 5'-phosphate.
CC -! COFACTOR: BINDS A 4FE-4S CLUSTER WHICH IS NOT RELEASED FOR THE
CC CATALYTIC ACTIVITY, BUT WHICH IS PREPARY INVOLVED IN THE PROPER
CC POSITIONING OF THE ENZYME ALONG THE DNA STRAND (BY SIMILARITY).
CC -! SIMILARITY: BELONGS TO THE RIBREX1 FAMILY.
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed, usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch) or
CC send an email to license@sib-sib.ch).
DR EMBL: D90908; BAA17762.1;
DR BSSP: P20625; ZAKK.
DR InterPro: IPR004035; EndonIII_FCH.
DR InterPro: IPR004036; EndonIII_HH.
DR PROSITE: PS003265; Endo_3c.
DR InterPro: IPR003651; FeS_Bind.
DR InterPro: IPR003583; HHH_1.
DR Pfam: PF00740; HHH-GP05; 1.
DR SMART: SM00478; HHH030; 1.
DR SMART: SM00525; HHH; 1.
DR SMART: SM00273; HHH; 1.
DR TIGFAMS: TIGR01083; Hhh; 1.
DR PROSITE: PS00764; ENDONUCLEASE_III_L1; 1.
DR PROSITE: PS01155; ENDONUCLEASE_III_L2; 1.
KW Hydroxylase; Nuclease; Endonuclease; Multifunctional enzyme; DNA repair;
KW Glycosylase; Lyase; Iron sulfur; 4FE-4S; Complete proteome.
FT METAL 197 197 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 204 204 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 207 207 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
FT METAL 213 213 IRON-SULFUR (4FE-4S) (BY SIMILARITY).
SQ SEQUENCE 219 AA: 24377 MW: 28456.16 kDa; CD044.

Query Match
Best Local Similarity 80.08; Score 26; DB 1; Length 219;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```


[illegible]

RX MEDLINE=87057483; PubMed=3021364;
 RA Shull G.P., Lingrel J.B.;
 RL "Molecular cloning of the rat stomach. (H⁺ + K⁺)-ATPase.";
 RI J. Biol. Chem. 261:16788-16791(1986)
 RP REVISIONS.
 RN Shull G.E.
 RL Submitted (FEB-1987) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 53-506 FROM N.A.
 RX MEDLINE=95142238; PubMed 7840253,
 RA Ahn K.Y., Kone B.C.;
 RL "Expression and cellular localization of mRNA encoding the 'gastric' isoenzyme of H⁺ K⁺-ATPase alpha-subunit in rat kidney.";
 RI Am. J. Physiol. 268:F99-F103(1995).
 RN [4]
 RP SEQUENCE OF 1-49 FROM N.A.
 RX ISSUP=Liver;
 RA Song I., Mortell M.P., Gantz L., Marino L.F., Yamada T.;
 RL Submitted (FEB 1993) to the EMBL/GenBank/DBJ databases
 RN [5]
 RP SEQUENCE OF 176-259 AND 435-465 FROM N.A.
 RX STRAIN=Sprague-Dawley;
 RA Oshiman K.-I., Motajima K., Mahmood S., Shimada A., Tamura S., Maeda M., Futai M.;
 RL "Control region and gastric specific transcription of the rat H⁺ K⁺-ATPase alpha subunit gene.";
 RI FEBS Lett. 281:250-254(1991).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF H⁺ AND K⁺ IONS ACROSS THE PLASMA MEMBRANE. RESPONSIBLE FOR ACID PRODUCTION IN THE STOMACH.
 CC -2- CATALYTIC ACTIVITY: ATP + H₂O + H⁺(In) + K⁺(Out) = ADP + phosphate + H⁺(Out) + K⁺(In).
 CC -3- SUBUNIT: COMPOSED OF TWO SUBUNITS: ALPHA (CATALYTIC) AND BETA.
 CC -4- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -5- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IIC
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch> or send an email to license@sib-sib.ch).
 CC
 DR EMBL: J02649; AAA66036.1; ..
 DR EMBL: S74801; .. NOT_ANNOTATED_CDS.
 DR EMBL: L11569; AAA72454.1; ..
 DR EMBL: X61934; CAA43938.1; ..
 DR EMBL: X61935; CAA43939.1; ..
 DR PIR: A25344; A25344
 DR HSSP: P04191; IEUL.
 DR InterPro: IP0001757; ATPase.F1-E2.
 DR InterPro: IP0004014; Cation_ATPase.
 DR InterPro: I0606661; H⁺K⁺ATPase.
 DR InterPro: I06091454; HgATase/hydrolase.
 DR Pfam: PF00132; F1-E2_ATPase; 2.
 DR Pfam: PF00689; Cation_ATPase; 1.
 DR Pfam: PF00702; Hydrolase; 1.
 DR Pfam: PF00702; Hydrolase; 1.
 DR TIGRfams: TIGR01106; X_K_ATPasealp; 1.
 DR PROSITE: PS00154; ATPase.F1-P2; 1.
 DR Hydrolase; Potassium transport; Hydrolase iso. transport; Transmembrane.
 KW Phosphorylation; ATP-binding; Magnesium; Metal binding.
 FT INIT_MET 0 0 BY SIMILARITY.
 FT DOMAIN 1 95 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 96 116 POTENTIAL.
 FT DOMAIN 117 139 LUMENAL (POTENTIAL).
 FT TRANSMEM 140 160 POTENTIAL.
 FT DOMAIN 161 236 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 237 316

FT DOMAIN 317 328 LUMENAL (POTENTIAL).
 FT TRANSMEM 329 345 POTENTIAL.
 FT DOMAIN 347 380 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 381 400 POTENTIAL.
 FT DOMAIN 401 410 LUMENAL (POTENTIAL).
 FT TRANSMEM 411 431 POTENTIAL.
 FT DOMAIN 432 451 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 452 474 POTENTIAL.
 FT DOMAIN 475 526 LUMENAL (POTENTIAL).
 FT TRANSMEM 527 546 POTENTIAL.
 FT DOMAIN 547 599 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 600 629 POTENTIAL.
 FT DOMAIN 630 654 LUMENAL (POTENTIAL).
 FT TRANSMEM 655 674 POTENTIAL.
 FT DOMAIN 675 703 CYTOPLASMIC (POTENTIAL).
 FT TRANSMEM 704 725 PHOSPHORYLATION (BY SIMILARITY).
 FT METAL 726 725 PHOSPHORYLATION (BY PRA) (BY SIMILARITY).
 FT METAL 726 725 MAGNESIUM (BY SIMILARITY).
 FT METAL 726 725 MAGNESIUM (BY SIMILARITY).
 FT CATALYTIC ACTIVITY: ATP + H₂O + H⁺(In) + K⁺(Out) = ADP + phosphate + H⁺(Out) + K⁺(In).
 RN SEQUENCE 1032 AA; 113906 MW; 564E91A8276987E CWC64;
 Query Match 81.2%; Score 26; DB 1; Length 1042;
 Best Local Similarity 85.0%; Pred. Rev. 4.4e-02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 27 3 CYPRN 7
 10 956 GFFRN 960
 11 1111
 12 956 GFFRN 960
 RESULT 42
 ALPHA_CANFA
 ID ALPHA_CANFA STANDARD; PRI: 1033 AA.
 AC P50996;
 DT 01 OCT 1996 (Ref. 34, Created)
 DT 15 JUN 2002 (Ref. 41, Last sequence update)
 DT 15 JUN 2002 (Ref. 41, Last annotation update)
 DE Potassium-transporting ATPase alpha chain 1 (EC 3.6.4.10) (Proton pump) (Gastric H⁺/K⁺ ATPase alpha subunit).
 GN ATP4A.
 OS Canis familiaris (Dog).
 EC Enkaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
 Y N-1_1270-3915;
 RN
 RP SEQUENCE FROM N.A.
 RC TISSUE=Stomach;
 RX MEDLINE=94071880; PubMed 8250881;
 RA Song I., Mortell M.P., Gantz L., Brown D.K., Yamada T.;
 RI "Molecular cloning and structural analysis of canine gastric H⁺ K⁺-ATPase.";
 RL Biochem. Biophys. Res. Commun. 196:1240-1247(1993).
 CC -1- FUNCTION: CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF H⁺ AND K⁺ IONS ACROSS THE PLASMA MEMBRANE. RESPONSIBLE FOR ACID PRODUCTION IN THE STOMACH.
 CC -2- CATALYTIC ACTIVITY: ATP + H₂O + H⁺(In) + K⁺(Out) = ADP + phosphate + H⁺(Out) + K⁺(In).
 CC -3- SUBUNIT: COMPOSED OF TWO SUBUNITS: Alpha (CATALYTIC) AND BETA.
 CC -4- SUBCELLULAR LOCATION: Integral membrane protein.
 CC -5- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (E1-E2 ATPASES). SUBFAMILY IIC.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch> or send an email to license@sib-sib.ch).
 CC
 DR EMBL: L11569; AAA40848.1; ..
 DR HSSP: P04191; IEUL.

```

DR InterPro: IPR001757; ATPase_E1_E2.
DR InterPro: IPR004014; Cation_ATPase.
DR InterPro: IPR004461; H+-K+-ATPase.
DR InterPro: IPR001454; H+ATPase.
DR Pfam: PF00122; E1_E2_ATPase_1.
DR Pfam: PF00689; Cation_ATPase_C_1.
DR Pfam: PF00690; Cation_ATPase_N_1.
DR Pfam: PF00702; Hydrolyase_1.
DR TIGRams: TIGR01106; X_K_ATPase_alp_1.
DR ProSite: PS00154; ATPase_E1_E2_1.
KW Hydrolyase; Potassium transport; Hydrogen ion transport; Transmembrane.
KW Phosphorylation; ATP-binding; Magnesium; Metal-binding
FT INIT_MET 0 0
FT DOMAIN 1 96 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 97 117 POTENTIAL.
FT DOMAIN 118 140 LUMENAL (POTENTIAL).
FT TRANSMEM 141 161 POTENTIAL.
FT DOMAIN 162 297 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 298 317 POTENTIAL.
FT DOMAIN 318 329 LUMENAL (POTENTIAL).
FT TRANSMEM 330 347 POTENTIAL.
FT DOMAIN 348 781 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 782 801 POTENTIAL.
FT DOMAIN 802 811 LUMENAL (POTENTIAL).
FT TRANSMEM 812 842 POTENTIAL.
FT DOMAIN 843 852 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 853 875 POTENTIAL.
FT DOMAIN 876 947 LUMENAL (POTENTIAL).
FT TRANSMEM 928 947 POTENTIAL.
FT DOMAIN 948 961 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 962 980 POTENTIAL.
FT DOMAIN 981 995 LUMENAL (POTENTIAL).
FT TRANSMEM 996 1016 POTENTIAL.
FT DOMAIN 1017 1033 CYTOPLASMIC (POTENTIAL).
FT MDL_RES 385 385 PHOSPHORYLATION (BY SIMILARITY).
FT MDL_RES 952 952 PHOSPHORYLATION (BY PKA) (BY SIMILARITY).
FT METAL 726 726 MAGNESIUM (BY SIMILARITY).
FT METAL 730 730 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE: 1033 AA; 113974 MW; 4525278C4E2658E8 CRC64;

Query Match 81.2%; Score 26; DP 1; Length 1033;
Best Local Similarity 80.0%; Pred. No. 4.4e-02;
Matches 4; Conservation 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 QYFN 7
11:11
Db 957 QYFN 961

RESULT 43
ALPHA_P03
ID ALPHA_P03 STANDARD; PRI: 1033 AA.
AC P19156;
DT 01-NOV-1990 (Rel. 16, Created)
DT 15-JUN-2002 (Rel. 41, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Potassium transporting ATPase alpha chain 1 (EC 3.6.3.10) (Proton
pump) (Gastric H+/K+ ATPase alpha subunit).
GN ATPA.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
OX NCBI_TaxID 9823;
UN 111
RF SEQUENCE FROM N.A.
RX MEDLINE 89061712; PubMed 2648518;
RA Maeda M., Ishizaki J., Futai M.
R1 "cDNA cloning and sequence determination of pig gastric H+-
K+ ATPase".
R1 Biochem. Biophys. Res. Commun. 157:294-298(1989).
R1 J21.
RN SEQUENCE OF 1-17.
RP MEDLINE 86275667; PubMed 4017415;
Lane L.K., Kirtley T.L., Ball W.J., Jr.:
"Structural studies on H+/K+-ATPase: determination of the
NH2-terminal amino acid sequence and immunobehavioral reactivity
with Na+/K+-ATPase."
Biochem. Biophys. Res. Commun. 138:185-192(1986).
[3]
SEQUENCE OF 1-10, AND PHOSPHORYLATION OF SER-26.
MEDLINE-97040701; PubMed-8886014;
RA Itoawa K., Kaya S., Shimada A., Imaizawa T., Maardh S., Corbin J.C.
RA Kikkawa U., Taniuchi K.:
"Ser-27, Tyr-10 and Tyr-7 in the alpha chain of pig stomach
H+/K+ ATPase as Ca2+-dependent phosphorylatable sites by
intrinsic and extrinsic protein kinases."
Biochem. Biophys. Res. Commun. 227:610-615(1996).
[4]
PHOSPHORYLATION OF TYR-6 AND TYR-9.
MEDLINE-95318126; PubMed-7797549;
RA Toiawa K., Ishiguro T., Kaya S., Shimada A., Imaizawa T., Taniuchi K.:
"Reversible phosphorylation of both Tyr7 and Tyr10 in the alpha-chain
of pig stomach H+/K+ ATPase by a membrane bound kinase and a
phosphatase."
J. Biol. Chem. 270:15475-15478(1995).
CC 1-1- FUNCTION: CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE
EXCHANGE OF H+ AND K+ IONS ACROSS THE PLASMA MEMBRANE.
CC RESPONSIBLE FOR ACID PRODUCTION IN THE STOMACH.
CC 1-1- CATALYTIC ACTIVITY: ATP + H2O + H+(in) + K+(out) ADP +
phosphate + H2O(out) + K+(in).
CC 1-1- SUBUNIT: COMPOSED OF TWO SUBUNITS: ALPHA (CATALYTIC) AND BETA.
CC 1-1- SUBCELLULAR LOCATION: Integral membrane protein.
CC 1-1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY
(E1-E2 ATPASES). SUBFAMILY 1IC.
-----
this SWISS-PROT entry is copyright, it is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation
at the European Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/amboss/
or send an email to license@isb-sib.ch).
-----
DR PDBL: M22724; AAA1004.1;
DR PIR: A31671; A31671.
DR PIR: A34238; A34238.
DR USSP: P04191; 1EML.
DR InterPro: IPR001757; ATPase_E1_E2.
DR InterPro: IPR004014; Cation_ATPase.
DR InterPro: IPR004461; H+-K+-ATPase.
DR InterPro: IPR001454; H+ATPase.
DR Pfam: PF00122; E1_E2_ATPase_1.
DR Pfam: PF00689; Cation_ATPase_C_1.
DR Pfam: PF00690; Cation_ATPase_N_1.
DR Pfam: PF00702; Hydrolyase_1.
DR TIGRams: TIGR01106; X_K_ATPase_alp_1.
DR ProSite: PS00154; ATPase_E1_E2_1.
KW Hydrolyase; Potassium transport; Hydrogen ion transport; Transmembrane;
KW Phosphorylation; ATP-binding; Magnesium; Metal-binding.
FT INIT_MET 0 0
FT DOMAIN 1 96 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 97 117 POTENTIAL.
FT DOMAIN 118 140 LUMENAL (POTENTIAL).
FT TRANSMEM 141 161 POTENTIAL.
FT DOMAIN 162 297 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 298 317 POTENTIAL.
FT DOMAIN 318 329 LUMENAL (POTENTIAL).
FT TRANSMEM 330 347 POTENTIAL.
FT DOMAIN 348 781 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 782 801 POTENTIAL.
FT DOMAIN 802 811 LUMENAL (POTENTIAL).
FT TRANSMEM 812 842 POTENTIAL.
FT DOMAIN 843 852 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 853 875 POTENTIAL.
FT DOMAIN 876 947 LUMENAL (POTENTIAL).
FT TRANSMEM 928 947 POTENTIAL.

```


Best Local Similarity: 99.0%; Pred. No. 4,4e+02;
Matches: 4; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;

QY 3 GYRN 7
11:11
Db 958 GFFRN 962

RESULT 45

ID ATHA_RABIT STANDARD; PRT: 1034 AA.
AC P27112;
DT 01-AUG-1992 (Rel. 23, Created)
DI 15-JUN-2002 (Rel. 41, Last sequence update)
DI 15-JUN-2002 (Rel. 41, Last annotation update)
DE Potassium-transporting ATPase alpha chain 1 (EC 3.6.3.10) (proton pump) (gastric H⁺/K⁺ ATPase alpha subunit).
DE pump) (gastric H⁺/K⁺ ATPase alpha subunit).
GN ATP4A.
OS Oryctolagus cuniculus (Rabbit).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eupolystegia;
CC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
CX NCBI_TaxID 9986;
RN [1]
RF SEQUENCE FROM N.A.
RC STRAIN New Zealand white;
RX MEDLINE 92256499; PubMed 1416171;
RA Bomberg K., Mercier F., Reuben M.A., Kobayashi Y., Munson K.B., Sachs G.;
RA "cDNA cloning and membrane topology of the rabbit gastric H⁺/K⁺ ATPase alpha-subunit.";
PL Biochim. Biophys. Acta 1141:59-77(1992).
CC 1- FUNCTION: CATALYZES THE HYDROLYSIS OF ATP COUPLED WITH THE EXCHANGE OF H⁺ AND K⁺ IONS ACROSS THE PLASMA MEMBRANE.
CC RESPONSIBLE FOR ACID PRODUCTION IN THE STOMACH.
CC 1- CATALYTIC ACTIVITY: ATP + H₂O -> H⁺(in) + K⁺(out) ADP + phosphate + H⁺(out) + K⁺(in).
CC 1- SUBUNIT: COMPOSED OF TWO SUBUNITS: ALPHA (CATALYTIC) AND BETA.
CC 1- SUBCELLULAR LOCATION: Integral membrane protein.
CC 1- SIMILARITY: BELONGS TO THE CATION TRANSPORT ATPASES FAMILY (F1-F2 ATPASES). SUBFAMILY 1IC.

This SWISS-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see [http://www.isb.ch/announcements/](http://www.isb.ch/announcements) or send an email to license@isb-sib.ch).

EMBL: X64694; CAA45927.1; .
PIR: S24406; S24406.
RSP: P04191; LEUL.
InterPro: IPRO01757; ATPase_E1-E2.
InterPro: IPRO04014; Cation_ATPase.
InterPro: IPRO06611; E_K_F1_F2_ATPase.
InterPro: IPRO01454; Glucanase/hydrolase.
Pfam: PF00122; E1-E2_ATPase; 1.
Pfam: PF00689; Cation_ATPase_C; 1.
Pfam: PF00690; Cation_ATPase_N; 1.
Pfam: PF00702; Hydrolase; 1.
TrGFams: TIGR01106; X_K_ATPase_atp; 1.
ProSite: PS00194; ATPase_E1-E2; 1.
Hydrolase, Potassium-transporting, H⁺-driven i.e. transport, Transmembrane;
KW Phosphorylation; ATP-binding; Magnesium; Metal-binding;
INIT-MET 0 0 BY SIMILARITY.
FT DOMAIN 1 97 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 98 118 POTENTIAL.
FT DOMAIN 119 141 LUMENAL (POTENTIAL).
FT TRANSMEM 142 162 POTENTIAL.
FT DOMAIN 163 298 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 299 318 POTENTIAL.
FT DOMAIN 319 340 LUMENAL (POTENTIAL).
FT TRANSMEM 341 348 POTENTIAL.

FT DOMAIN 349 782
FT TRANSMEM 783 902
FT DOMAIN 903 812
FT TRANSMEM 813 833
FT DOMAIN 834 853
FT TRANSMEM 854 876
FT DOMAIN 877 928
FT TRANSMEM 929 948
FT DOMAIN 949 962
FT TRANSMEM 963 981
FT DOMAIN 982 996
FT TRANSMEM 997 1017
FT DOMAIN 1018 1034
FT MOD_RES 1035 1036
FT MOD_RES 1037 1038
FT METAL 1039 1040
FT METAL 1041 1042
SO SEQUENCE 1034 AA; 114070 MB; FCD6040AR04FEA73 CR0564;
Query Match: 91.2%; Score 26; DB 1; Length 104;
Best Local Similarity: 80.0%; Pred. No. 4,4e+02;
Matches: 4; Conservative: 1; Mismatches: 0; Indels: 0; Gaps: 0;
QY 3 GYRN 7
11:11
Db 958 GFFRN 962

Search completed: April 30, 2003, 14:04:31
Job time: 31.9041 secs

GenCore version 5.1.4_P5_4578
Copyright (c) 1997 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 30, 2003, 13:21:59 ; Search time 66.1818 seconds
(without alignments)
21.797 Million Cells Updates/Sec

Title: US-09-498-556c-79
Perfect score: 32
Sequence: 1 XXCFYRN 7

Scoring table: BL/USM62
Gapop 10 0 ; Gapext 0 5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1000 summaries

Database :

SPREMBL21:*

- 1: sp.archaea:*
- 2: sp.bacteria:*
- 3: sp.fungi:*
- 4: sp.human:*
- 5: sp.invertebrate:*
- 6: sp.mammal:*
- 7: sp.mhc:*
- 8: sp.organelle:*
- 9: sp.phage:*
- 10: sp.plant:*
- 11: sp.priant:*
- 12: sp.virus:*
- 13: sp.vertebrate:*
- 14: sp.unclassified:*
- 15: sp.virus:*
- 16: sp.bacteriap:*
- 17: sp.archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	30	93.8	77	Q9K301	Q9K301 escherichia
2	30	93.8	91	Q16938	Q16938 acyclostoma
3	30	93.8	102	Q96396	Q96396 acyclostoma
4	30	93.8	110	Q9K308	Q9K308 streptococcus
5	30	93.8	134	P74345	P74345 symbiodinium
6	30	93.8	158	Q44490	Q44490 arabidopsis
7	30	93.8	172	Q9A266	Q9A266 arabidopsis
8	30	93.8	178	Q9A196	Q9A196 arabidopsis
9	30	93.8	184	Q9A196	Q9A196 arabidopsis
10	40	93.8	194	Q9K312	Q9K312 drosophila
11	40	93.8	215	Q9K312	Q9K312 drosophila
12	40	93.8	222	Q9K312	Q9K312 drosophila
13	40	93.8	230	Q9K312	Q9K312 drosophila
14	40	93.8	237	Q9K312	Q9K312 drosophila
15	40	93.8	266	Q9K312	Q9K312 drosophila
16	40	93.8	325	Q9K312	Q9K312 drosophila

17	40	93.8	329	11	Q9K309	Q9K309 mus musculus
18	40	93.8	357	5	Q9K309	Q9K309 mus musculus
19	40	93.8	361	16	Q9K309	Q9K309 mus musculus
20	40	93.8	362	16	Q9K309	Q9K309 mus musculus
21	40	93.8	379	16	Q9K309	Q9K309 mus musculus
22	40	93.8	408	5	Q9K309	Q9K309 mus musculus
23	40	93.8	415	5	Q9K309	Q9K309 mus musculus
24	40	93.8	417	5	Q9K309	Q9K309 mus musculus
25	40	93.8	455	10	Q9K309	Q9K309 mus musculus
26	40	93.8	472	3	Q9K309	Q9K309 mus musculus
27	40	93.8	475	3	Q9K309	Q9K309 mus musculus
28	40	93.8	475	11	Q9K309	Q9K309 mus musculus
29	40	93.8	481	11	Q9K309	Q9K309 mus musculus
30	40	93.8	533	11	Q9K309	Q9K309 mus musculus
31	40	93.8	554	17	Q9K309	Q9K309 mus musculus
32	40	93.8	556	2	Q9K309	Q9K309 mus musculus
33	40	93.8	600	5	Q9K309	Q9K309 mus musculus
34	40	93.8	611	10	Q9K309	Q9K309 mus musculus
35	40	93.8	650	5	Q9K309	Q9K309 mus musculus
36	40	93.8	652	8	Q9K309	Q9K309 mus musculus
37	40	93.8	656	8	Q9K309	Q9K309 mus musculus
38	40	93.8	656	8	Q9K309	Q9K309 mus musculus
39	40	93.8	698	8	Q9K309	Q9K309 mus musculus
40	40	93.8	747	5	Q9K309	Q9K309 mus musculus
41	40	93.8	776	5	Q9K309	Q9K309 mus musculus
42	40	93.8	930	11	Q9K309	Q9K309 mus musculus
43	40	93.8	930	11	Q9K309	Q9K309 mus musculus
44	40	93.8	940	4	Q9K309	Q9K309 mus musculus
45	40	93.8	1041	16	Q9K309	Q9K309 mus musculus
46	40	93.8	1048	2	Q9K309	Q9K309 mus musculus
47	40	93.8	1453	5	Q9K309	Q9K309 mus musculus
48	40	93.8	3115	5	Q9K309	Q9K309 mus musculus
49	40	93.8	36	16	Q9K309	Q9K309 mus musculus
50	40	93.8	131	2	Q9K309	Q9K309 mus musculus
51	40	93.8	136	16	Q9K309	Q9K309 mus musculus
52	40	93.8	199	3	Q9K309	Q9K309 mus musculus
53	40	93.8	211	16	Q9K309	Q9K309 mus musculus
54	40	93.8	242	17	Q9K309	Q9K309 mus musculus
55	40	93.8	244	4	Q9K309	Q9K309 mus musculus
56	40	93.8	252	9	Q9K309	Q9K309 mus musculus
57	40	93.8	256	17	Q9K309	Q9K309 mus musculus
58	40	93.8	258	5	Q9K309	Q9K309 mus musculus
59	40	93.8	260	4	Q9K309	Q9K309 mus musculus
60	40	93.8	268	2	Q9K309	Q9K309 mus musculus
61	40	93.8	275	17	Q9K309	Q9K309 mus musculus
62	40	93.8	279	16	Q9K309	Q9K309 mus musculus
63	40	93.8	284	16	Q9K309	Q9K309 mus musculus
64	40	93.8	284	16	Q9K309	Q9K309 mus musculus
65	40	93.8	305	11	Q9K309	Q9K309 mus musculus
66	40	93.8	313	2	Q9K309	Q9K309 mus musculus
67	40	93.8	313	2	Q9K309	Q9K309 mus musculus
68	40	93.8	313	2	Q9K309	Q9K309 mus musculus
69	40	93.8	319	10	Q9K309	Q9K309 mus musculus
70	40	93.8	323	2	Q9K309	Q9K309 mus musculus
71	40	93.8	323	2	Q9K309	Q9K309 mus musculus
72	40	93.8	337	2	Q9K309	Q9K309 mus musculus
73	40	93.8	340	17	Q9K309	Q9K309 mus musculus
74	40	93.8	349	17	Q9K309	Q9K309 mus musculus
75	40	93.8	359	17	Q9K309	Q9K309 mus musculus
76	40	93.8	372	5	Q9K309	Q9K309 mus musculus
77	40	93.8	379	2	Q9K309	Q9K309 mus musculus
78	40	93.8	399	10	Q9K309	Q9K309 mus musculus
79	40	93.8	425	17	Q9K309	Q9K309 mus musculus
80	40	93.8	426	16	Q9K309	Q9K309 mus musculus
81	40	93.8	456	17	Q9K309	Q9K309 mus musculus
82	40	93.8	463	16	Q9K309	Q9K309 mus musculus
83	40	93.8	463	16	Q9K309	Q9K309 mus musculus
84	40	93.8	463	16	Q9K309	Q9K309 mus musculus
85	40	93.8	463	16	Q9K309	Q9K309 mus musculus
86	40	93.8	463	16	Q9K309	Q9K309 mus musculus
87	40	93.8	463	16	Q9K309	Q9K309 mus musculus
88	40	93.8	463	16	Q9K309	Q9K309 mus musculus
89	40	93.8	463	16	Q9K309	Q9K309 mus musculus

90	27	84.4	594	10	Q88410	Q88410 arabidopsis	163	26	81.2	215	14	Q88414	Q88414 fusobacteri
91	27	84.4	596	2	Q88410	Q88410 arabidopsis	164	26	81.2	236	7	Q88418	Q88418 aplysia sal
92	27	84.4	597	1	Q88410	Q88410 arabidopsis	165	26	81.2	249	13	Q88422	Q88422 brachydanio
93	27	84.4	598	16	Q88410	Q88410 arabidopsis	166	26	81.2	249	4	Q88426	Q88426 homo sapien
94	27	84.4	599	4	Q88410	Q88410 arabidopsis	167	26	81.2	250	11	Q88430	Q88430 homo sapien
95	27	84.4	600	11	Q88410	Q88410 arabidopsis	168	26	81.2	252	14	Q88434	Q88434 arabidopsis
96	27	84.4	601	11	Q88410	Q88410 arabidopsis	169	26	81.2	253	11	Q88438	Q88438 arabidopsis
97	27	84.4	602	11	Q88410	Q88410 arabidopsis	170	26	81.2	255	4	Q88442	Q88442 candida ala
98	27	84.4	603	4	Q88410	Q88410 arabidopsis	171	26	81.2	270	4	Q88446	Q88446 homo sapien
99	27	84.4	604	4	Q88410	Q88410 arabidopsis	172	26	81.2	280	16	Q88450	Q88450 yeastia po
100	27	84.4	605	17	Q88410	Q88410 arabidopsis	173	26	81.2	281	16	Q88454	Q88454 lactococcus
101	27	84.4	606	16	Q88410	Q88410 arabidopsis	174	26	81.2	282	16	Q88458	Q88458 lactococcus
102	27	84.4	607	16	Q88410	Q88410 arabidopsis	175	26	81.2	290	4	Q88462	Q88462 lactococcus
103	27	84.4	608	11	Q88410	Q88410 arabidopsis	176	26	81.2	298	5	Q88466	Q88466 candida alb
104	27	84.4	609	11	Q88410	Q88410 arabidopsis	177	26	81.2	309	11	Q88470	Q88470 mus muscula
105	27	84.4	610	11	Q88410	Q88410 arabidopsis	178	26	81.2	322	13	Q88474	Q88474 arabidopsis
106	27	84.4	611	16	Q88410	Q88410 arabidopsis	179	26	81.2	324	2	Q88478	Q88478 thiodiphril
107	27	84.4	612	16	Q88410	Q88410 arabidopsis	180	26	81.2	324	10	Q88482	Q88482 arabidopsis
108	27	84.4	613	16	Q88410	Q88410 arabidopsis	181	26	81.2	325	10	Q88486	Q88486 arabidopsis
109	27	84.4	614	16	Q88410	Q88410 arabidopsis	182	26	81.2	342	13	Q88490	Q88490 mus muscula
110	27	84.4	615	16	Q88410	Q88410 arabidopsis	183	26	81.2	342	13	Q88494	Q88494 mus muscula
111	27	84.4	616	16	Q88410	Q88410 arabidopsis	184	26	81.2	344	5	Q88498	Q88498 clostridium
112	27	84.4	617	16	Q88410	Q88410 arabidopsis	185	26	81.2	349	14	Q88502	Q88502 maraca base
113	27	84.4	618	10	Q88410	Q88410 arabidopsis	186	26	81.2	349	14	Q88506	Q88506 streptomyce
114	27	84.4	619	10	Q88410	Q88410 arabidopsis	187	26	81.2	349	17	Q88510	Q88510 thermotace
115	27	84.4	620	5	Q88410	Q88410 arabidopsis	188	26	81.2	349	17	Q88514	Q88514 thermotace
116	27	84.4	621	5	Q88410	Q88410 arabidopsis	189	26	81.2	369	17	Q88518	Q88518 halobacteri
117	27	84.4	622	5	Q88410	Q88410 arabidopsis	190	26	81.2	377	17	Q88522	Q88522 streptomyce
118	27	84.4	623	5	Q88410	Q88410 arabidopsis	191	26	81.2	383	10	Q88526	Q88526 arabidopsis
119	27	84.4	624	16	Q88410	Q88410 arabidopsis	192	26	81.2	393	17	Q88530	Q88530 halobacteri
120	27	84.4	625	16	Q88410	Q88410 arabidopsis	193	26	81.2	426	11	Q88534	Q88534 mus muscula
121	27	84.4	626	16	Q88410	Q88410 arabidopsis	194	26	81.2	437	14	Q88538	Q88538 yeastia po
122	27	84.4	627	16	Q88410	Q88410 arabidopsis	195	26	81.2	437	17	Q88542	Q88542 yeastia po
123	27	84.4	628	16	Q88410	Q88410 arabidopsis	196	26	81.2	437	17	Q88546	Q88546 yeastia po
124	27	84.4	629	16	Q88410	Q88410 arabidopsis	197	26	81.2	437	17	Q88550	Q88550 yeastia po
125	27	84.4	630	16	Q88410	Q88410 arabidopsis	198	26	81.2	437	17	Q88554	Q88554 yeastia po
126	27	84.4	631	16	Q88410	Q88410 arabidopsis	199	26	81.2	437	17	Q88558	Q88558 yeastia po
127	27	84.4	632	16	Q88410	Q88410 arabidopsis	200	26	81.2	437	17	Q88562	Q88562 yeastia po
128	27	84.4	633	16	Q88410	Q88410 arabidopsis	201	26	81.2	437	17	Q88566	Q88566 yeastia po
129	27	84.4	634	16	Q88410	Q88410 arabidopsis	202	26	81.2	437	17	Q88570	Q88570 yeastia po
130	27	84.4	635	16	Q88410	Q88410 arabidopsis	203	26	81.2	437	17	Q88574	Q88574 yeastia po
131	27	84.4	636	16	Q88410	Q88410 arabidopsis	204	26	81.2	437	17	Q88578	Q88578 yeastia po
132	27	84.4	637	16	Q88410	Q88410 arabidopsis	205	26	81.2	437	17	Q88582	Q88582 yeastia po
133	27	84.4	638	16	Q88410	Q88410 arabidopsis	206	26	81.2	437	17	Q88586	Q88586 yeastia po
134	27	84.4	639	16	Q88410	Q88410 arabidopsis	207	26	81.2	437	17	Q88590	Q88590 yeastia po
135	27	84.4	640	16	Q88410	Q88410 arabidopsis	208	26	81.2	437	17	Q88594	Q88594 yeastia po
136	27	84.4	641	16	Q88410	Q88410 arabidopsis	209	26	81.2	437	17	Q88598	Q88598 yeastia po
137	27	84.4	642	16	Q88410	Q88410 arabidopsis	210	26	81.2	437	17	Q88602	Q88602 yeastia po
138	27	84.4	643	16	Q88410	Q88410 arabidopsis	211	26	81.2	437	17	Q88606	Q88606 yeastia po
139	27	84.4	644	16	Q88410	Q88410 arabidopsis	212	26	81.2	437	17	Q88610	Q88610 yeastia po
140	27	84.4	645	16	Q88410	Q88410 arabidopsis	213	26	81.2	437	17	Q88614	Q88614 yeastia po
141	27	84.4	646	16	Q88410	Q88410 arabidopsis	214	26	81.2	437	17	Q88618	Q88618 yeastia po
142	27	84.4	647	16	Q88410	Q88410 arabidopsis	215	26	81.2	437	17	Q88622	Q88622 yeastia po
143	27	84.4	648	16	Q88410	Q88410 arabidopsis	216	26	81.2	437	17	Q88626	Q88626 yeastia po
144	27	84.4	649	16	Q88410	Q88410 arabidopsis	217	26	81.2	437	17	Q88630	Q88630 yeastia po
145	27	84.4	650	16	Q88410	Q88410 arabidopsis	218	26	81.2	437	17	Q88634	Q88634 yeastia po
146	27	84.4	651	16	Q88410	Q88410 arabidopsis	219	26	81.2	437	17	Q88638	Q88638 yeastia po
147	27	84.4	652	16	Q88410	Q88410 arabidopsis	220	26	81.2	437	17	Q88642	Q88642 yeastia po
148	27	84.4	653	16	Q88410	Q88410 arabidopsis	221	26	81.2	437	17	Q88646	Q88646 yeastia po
149	27	84.4	654	16	Q88410	Q88410 arabidopsis	222	26	81.2	437	17	Q88650	Q88650 yeastia po
150	27	84.4	655	16	Q88410	Q88410 arabidopsis	223	26	81.2	437	17	Q88654	Q88654 yeastia po
151	27	84.4	656	16	Q88410	Q88410 arabidopsis	224	26	81.2	437	17	Q88658	Q88658 yeastia po
152	27	84.4	657	16	Q88410	Q88410 arabidopsis	225	26	81.2	437	17	Q88662	Q88662 yeastia po
153	27	84.4	658	16	Q88410	Q88410 arabidopsis	226	26	81.2	437	17	Q88666	Q88666 yeastia po
154	27	84.4	659	16	Q88410	Q88410 arabidopsis	227	26	81.2	437	17	Q88670	Q88670 yeastia po
155	27	84.4	660	16	Q88410	Q88410 arabidopsis	228	26	81.2	437	17	Q88674	Q88674 yeastia po
156	27	84.4	661	16	Q88410	Q88410 arabidopsis	229	26	81.2	437	17	Q88678	Q88678 yeastia po
157	27	84.4	662	16	Q88410	Q88410 arabidopsis	230	26	81.2	437	17	Q88682	Q88682 yeastia po
158	27	84.4	663	16	Q88410	Q88410 arabidopsis	231	26	81.2	437	17	Q88686	Q88686 yeastia po
159	27	84.4	664	16	Q88410	Q88410 arabidopsis	232	26	81.2	437	17	Q88690	Q88690 yeastia po
160	27	84.4	665	16	Q88410	Q88410 arabidopsis	233	26	81.2	437	17	Q88694	Q88694 yeastia po
161	27	84.4	666	16	Q88410	Q88410 arabidopsis	234	26	81.2	437	17	Q88698	Q88698 yeastia po
162	27	84.4	667	16	Q88410	Q88410 arabidopsis	235	26	81.2	437	17	Q88702	Q88702 yeastia po

482	25	78.1	498	16	Q8X0V3	Q8X0V3 ralistonia s	455	25	78.1	689	10	Q8W411	Q8W411 oryza sativ
483	25	78.1	499	16	Q8H0H2	Q8H0H2 rhizobium l	456	25	78.1	689	5	Q87258	Q87258 plasmidum
484	25	78.1	502	5	Q8X484	Q8X484 caecorhabdi	457	25	78.1	701	14	Q83367	Q83367 mycloa tell
485	25	78.1	504	5	Q80740	Q80740 ceratitiss e	458	25	78.1	701	5	Q8R044	Q8R044 caecorhabdi
486	25	78.1	505	8	Q83087	Q83087 spiranthes	459	25	78.1	703	5	Q8S087	Q8S087 caecorhabdi
487	25	78.1	506	4	Q80625	Q80625 homo sapien	460	25	78.1	710	10	Q81879	Q81879 arabidopsis
488	25	78.1	506	10	Q80624	Q80624 arabidopsis	461	25	78.1	729	10	Q80625	Q80625 myobacteri
489	25	78.1	514	4	Q80WV7	Q80WV7 homo sapien	462	25	78.1	735	10	Q80001	Q80001 zea mays
490	25	78.1	515	10	Q80K84	Q80K84 arabidopsis	463	25	78.1	746	14	Q80V16	Q80V16 myobacteri
491	25	78.1	522	12	Q80444	Q80444 mekela vira	464	25	78.1	747	10	Q80M24	Q80M24 arabidopsis
492	25	78.1	522	12	Q80444	Q80444 mekela vira	465	25	78.1	747	8	Q80H76	Q80H76 torostia ra
493	25	78.1	523	5	Q80201	Q80201 caecorhabdi	466	25	78.1	754	4	Q80H76	Q80H76 torostia ra
494	25	78.1	524	10	Q80W59	Q80W59 arabidopsis	467	25	78.1	779	14	Q80V19	Q80V19 listeria mo
495	25	78.1	524	10	Q80W12	Q80W12 arabidopsis	468	25	78.1	801	17	Q81180	Q81180 methanosa
496	25	78.1	525	6	Q80444	Q80444 homo sapien	469	25	78.1	802	4	Q81237	Q81237 homo sapien
497	25	78.1	525	10	Q80746	Q80746 arabidopsis	470	25	78.1	902	14	Q80V28	Q80V28 arabidopsis
498	25	78.1	526	10	Q80594	Q80594 arabidopsis	471	25	78.1	902	14	Q80V28	Q80V28 arabidopsis
499	25	78.1	527	14	Q80761	Q80761 escherichia	472	25	78.1	917	16	Q80V28	Q80V28 arabidopsis
500	25	78.1	533	3	Q80199	Q80199 pleurotus o	473	25	78.1	924	10	Q81776	Q81776 arabidopsis
501	25	78.1	534	3	Q80881	Q80881 schizosacch	474	25	78.1	861	4	Q81080	Q81080 plebia amo
502	25	78.1	534	3	Q80881	Q80881 schizosacch	475	25	78.1	866	5	Q80881	Q80881 schizosacch
503	25	78.1	534	3	Q80881	Q80881 schizosacch	476	25	78.1	866	5	Q80881	Q80881 schizosacch
504	25	78.1	534	3	Q80881	Q80881 schizosacch	477	25	78.1	873	10	Q80881	Q80881 schizosacch
505	25	78.1	534	3	Q80881	Q80881 schizosacch	478	25	78.1	873	10	Q80881	Q80881 schizosacch
506	25	78.1	534	3	Q80881	Q80881 schizosacch	479	25	78.1	873	10	Q80881	Q80881 schizosacch
507	25	78.1	534	3	Q80881	Q80881 schizosacch	480	25	78.1	873	10	Q80881	Q80881 schizosacch
508	25	78.1	534	3	Q80881	Q80881 schizosacch	481	25	78.1	873	10	Q80881	Q80881 schizosacch
509	25	78.1	534	3	Q80881	Q80881 schizosacch	482	25	78.1	873	10	Q80881	Q80881 schizosacch
510	25	78.1	534	3	Q80881	Q80881 schizosacch	483	25	78.1	873	10	Q80881	Q80881 schizosacch
511	25	78.1	534	3	Q80881	Q80881 schizosacch	484	25	78.1	873	10	Q80881	Q80881 schizosacch
512	25	78.1	534	3	Q80881	Q80881 schizosacch	485	25	78.1	873	10	Q80881	Q80881 schizosacch
513	25	78.1	534	3	Q80881	Q80881 schizosacch	486	25	78.1	873	10	Q80881	Q80881 schizosacch
514	25	78.1	534	3	Q80881	Q80881 schizosacch	487	25	78.1	873	10	Q80881	Q80881 schizosacch
515	25	78.1	534	3	Q80881	Q80881 schizosacch	488	25	78.1	873	10	Q80881	Q80881 schizosacch
516	25	78.1	534	3	Q80881	Q80881 schizosacch	489	25	78.1	873	10	Q80881	Q80881 schizosacch
517	25	78.1	534	3	Q80881	Q80881 schizosacch	490	25	78.1	873	10	Q80881	Q80881 schizosacch
518	25	78.1	534	3	Q80881	Q80881 schizosacch	491	25	78.1	873	10	Q80881	Q80881 schizosacch
519	25	78.1	534	3	Q80881	Q80881 schizosacch	492	25	78.1	873	10	Q80881	Q80881 schizosacch
520	25	78.1	534	3	Q80881	Q80881 schizosacch	493	25	78.1	873	10	Q80881	Q80881 schizosacch
521	25	78.1	534	3	Q80881	Q80881 schizosacch	494	25	78.1	873	10	Q80881	Q80881 schizosacch
522	25	78.1	534	3	Q80881	Q80881 schizosacch	495	25	78.1	873	10	Q80881	Q80881 schizosacch
523	25	78.1	534	3	Q80881	Q80881 schizosacch	496	25	78.1	873	10	Q80881	Q80881 schizosacch
524	25	78.1	534	3	Q80881	Q80881 schizosacch	497	25	78.1	873	10	Q80881	Q80881 schizosacch
525	25	78.1	534	3	Q80881	Q80881 schizosacch	498	25	78.1	873	10	Q80881	Q80881 schizosacch
526	25	78.1	534	3	Q80881	Q80881 schizosacch	499	25	78.1	873	10	Q80881	Q80881 schizosacch
527	25	78.1	534	3	Q80881	Q80881 schizosacch	500	25	78.1	873	10	Q80881	Q80881 schizosacch
528	25	78.1	534	3	Q80881	Q80881 schizosacch	501	25	78.1	873	10	Q80881	Q80881 schizosacch
529	25	78.1	534	3	Q80881	Q80881 schizosacch	502	25	78.1	873	10	Q80881	Q80881 schizosacch
530	25	78.1	534	3	Q80881	Q80881 schizosacch	503	25	78.1	873	10	Q80881	Q80881 schizosacch
531	25	78.1	534	3	Q80881	Q80881 schizosacch	504	25	78.1	873	10	Q80881	Q80881 schizosacch
532	25	78.1	534	3	Q80881	Q80881 schizosacch	505	25	78.1	873	10	Q80881	Q80881 schizosacch
533	25	78.1	534	3	Q80881	Q80881 schizosacch	506	25	78.1	873	10	Q80881	Q80881 schizosacch
534	25	78.1	534	3	Q80881	Q80881 schizosacch	507	25	78.1	873	10	Q80881	Q80881 schizosacch
535	25	78.1	534	3	Q80881	Q80881 schizosacch	508	25	78.1	873	10	Q80881	Q80881 schizosacch
536	25	78.1	534	3	Q80881	Q80881 schizosacch	509	25	78.1	873	10	Q80881	Q80881 schizosacch
537	25	78.1	534	3	Q80881	Q80881 schizosacch	510	25	78.1	873	10	Q80881	Q80881 schizosacch
538	25	78.1	534	3	Q80881	Q80881 schizosacch	511	25	78.1	873	10	Q80881	Q80881 schizosacch
539	25	78.1	534	3	Q80881	Q80881 schizosacch	512	25	78.1	873	10	Q80881	Q80881 schizosacch
540	25	78.1	534	3	Q80881	Q80881 schizosacch	513	25	78.1	873	10	Q80881	Q80881 schizosacch
541	25	78.1	534	3	Q80881	Q80881 schizosacch	514	25	78.1	873	10	Q80881	Q80881 schizosacch
542	25	78.1	534	3	Q80881	Q80881 schizosacch	515	25	78.1	873	10	Q80881	Q80881 schizosacch
543	25	78.1	534	3	Q80881	Q80881 schizosacch	516	25	78.1	873	10	Q80881	Q80881 schizosacch
544	25	78.1	534	3	Q80881	Q80881 schizosacch	517	25	78.1	873	10	Q80881	Q80881 schizosacch
545	25	78.1	534	3	Q80881	Q80881 schizosacch	518	25	78.1	873	10	Q80881	Q80881 schizosacch
546	25	78.1	534	3	Q80881	Q80881 schizosacch	519	25	78.1	873	10	Q80881	Q80881 schizosacch
547	25	78.1	534	3	Q80881	Q80881 schizosacch	520	25	78.1	873	10	Q80881	Q80881 schizosacch
548	25	78.1	534	3	Q80881	Q80881 schizosacch	521	25	78.1	873	10	Q80881	Q80881 schizosacch
549	25	78.1	534	3	Q80881	Q80881 schizosacch	522	25	78.1	873	10	Q80881	Q80881 schizosacch
550	25	78.1	534	3	Q80881	Q80881 schizosacch	523	25	78.1	873	10	Q80881	Q80881 schizosacch
551	25	78.1	534	3	Q80881	Q80881 schizosacch	524	25	78.1	873	10	Q80881	Q80881 schizosacch
552	25	78.1	534	3	Q80881	Q80881 schizosacch	525	25	78.1	873	10	Q80881	Q80881 schizosacch
553	25	78.1	534	3	Q80881	Q80881 schizosacch	526	25	78.1	873	10	Q80881	Q80881 schizosacch
554	25	78.1	534	3	Q80881	Q80881 schizosacch	527	25	78.1	873	10	Q80881	Q80881 schizosacch
555	25	78.1	534	3	Q80881	Q80881 schizosacch	528	25	78.1	873	10	Q80881	Q80881 schizosacch
556	25	78.1	534	3	Q80881	Q80881 schizosacch	529	25	78.1	873	10	Q80881	Q80881 schizosacch
557	25	78.1	534	3	Q80881	Q80881 schizosacch	530	25	78.1	873	10	Q80881	Q80881 schizosacch
558	25	78.1	534	3	Q80881	Q80881 schizosacch	531	25	78.1	873	10	Q80881	Q80881 schizosacch
559	25	78.1	534	3	Q80881	Q80881 schizosacch	532	25	78.1	873	10	Q80881	Q80881 schizosacch
560	25	78.1	534	3	Q80881	Q80881 schizosacch	533	25	78.1	873	10	Q80881	Q80881 schizosacch
561	25	78.1	534	3	Q80881	Q80881 schizosacch	534	25	78.1	873	10	Q80881	Q80881 schizosacch
562	25	78.1	534	3	Q80881	Q80881 schizosacch	535	25	78.1	873	10	Q80881	Q80881 schizosacch
563	25	78.1	534	3	Q80881	Q80881 schizosacch	536	25	78.1	873	10	Q80881	Q80881 schizosacch
564	25	78.1	534	3	Q80881	Q80881 schizosacch	537	25	78.1	873	10	Q80881	Q80881 schizosacch
565	25	78.1	534	3	Q80881	Q80881 schizosacch	538	25	78.1	873	10	Q80881	Q80881 schizosacch
566	25	78.1	534	3	Q80881	Q80881 schizosacch	539	25	78.1	873	10	Q80881	Q80881 schizosacch
567	25	78.1	534	3	Q80881	Q80881 schizosacch	540	25	78.1	873	10	Q80881	Q80881 schizosacch
568	25	78.1	534	3	Q80881	Q80881 schizosacch	541	25	78.1	873	10	Q80881	Q80881 schizosacch
569	25	78.1	534	3	Q80881	Q80881 schizosacch	542	25	78.1	873	10	Q80881	Q80881 schizosacch
570	25	78.1	534	3	Q80881	Q80881 schizosacch	543	25	78.1	873	10	Q80881	Q80881 schizosacch
571	25	78.1	534	3	Q80881	Q80881 schizosacch	544	25	78.1	873	10	Q80881	Q80881 schizosacch
572	25	78.1	534										

528	25	78.1	1233	16	Q0132	strepptococcus	601	24	75.0	100	16	Q0092	Q0092 rhizobium m
529	25	78.1	1294	5	Q07361	flammediat	602	24	75.0	104	3	Q0097	Q0097 baculovirus
530	25	78.1	1336	5	Q01216	monobactam	603	24	75.0	104	3	Q0097	Q0097 baculovirus
531	25	78.1	1511	5	Q00905	drosocephala	604	24	75.0	104	3	Q01692	Q01692 saccharomyce
532	25	78.1	1522	3	Q00109	actinobacilli	605	24	75.0	105	15	Q00766	Q00766 ctenophorus
533	25	78.1	1525	3	Q00690	kinetoplast	606	24	75.0	105	15	Q00766	Q00766 human immun
534	25	78.1	1529	16	Q00767	gaxara ralisolalis	607	24	75.0	107	5	Q00766	Q00766 arabidopsis sp
535	25	78.1	1646	5	Q00085	quedas drosocephala	608	24	75.0	107	5	Q00766	Q00766 stylus blm
536	25	78.1	1905	2	Q00102	actinobacilli	609	24	75.0	107	5	Q00766	Q00766 sulfolobus
537	25	78.1	2035	2	Q00013	actinobacilli	610	24	75.0	107	5	Q00766	Q00766 sulfolobus
538	25	78.1	2039	16	Q00007	actinobacilli	611	24	75.0	107	5	Q00766	Q00766 sulfolobus
539	25	78.1	2161	12	Q00101	actinobacilli	612	24	75.0	107	5	Q00766	Q00766 sulfolobus
540	25	78.1	2164	12	Q00102	actinobacilli	613	24	75.0	107	5	Q00766	Q00766 sulfolobus
541	25	78.1	3695	4	Q00008	actinobacilli	614	24	75.0	107	5	Q00766	Q00766 sulfolobus
542	25	78.1	6077	12	Q00105	white spot	615	24	75.0	107	5	Q00766	Q00766 sulfolobus
543	25	78.1	6077	12	Q00105	white spot	616	24	75.0	107	5	Q00766	Q00766 sulfolobus
544	25	78.1	6077	12	Q00105	white spot	617	24	75.0	107	5	Q00766	Q00766 sulfolobus
545	25	78.1	6077	12	Q00105	white spot	618	24	75.0	107	5	Q00766	Q00766 sulfolobus
546	25	78.1	6077	12	Q00105	white spot	619	24	75.0	107	5	Q00766	Q00766 sulfolobus
547	24	75.0	6077	12	Q00105	white spot	620	24	75.0	107	5	Q00766	Q00766 sulfolobus
548	24	75.0	6077	12	Q00105	white spot	621	24	75.0	107	5	Q00766	Q00766 sulfolobus
549	24	75.0	6077	12	Q00105	white spot	622	24	75.0	107	5	Q00766	Q00766 sulfolobus
550	24	75.0	6077	12	Q00105	white spot	623	24	75.0	107	5	Q00766	Q00766 sulfolobus
551	24	75.0	6077	12	Q00105	white spot	624	24	75.0	107	5	Q00766	Q00766 sulfolobus
552	24	75.0	6077	12	Q00105	white spot	625	24	75.0	107	5	Q00766	Q00766 sulfolobus
553	24	75.0	6077	12	Q00105	white spot	626	24	75.0	107	5	Q00766	Q00766 sulfolobus
554	24	75.0	6077	12	Q00105	white spot	627	24	75.0	107	5	Q00766	Q00766 sulfolobus
555	24	75.0	6077	12	Q00105	white spot	628	24	75.0	107	5	Q00766	Q00766 sulfolobus
556	24	75.0	6077	12	Q00105	white spot	629	24	75.0	107	5	Q00766	Q00766 sulfolobus
557	24	75.0	6077	12	Q00105	white spot	630	24	75.0	107	5	Q00766	Q00766 sulfolobus
558	24	75.0	6077	12	Q00105	white spot	631	24	75.0	107	5	Q00766	Q00766 sulfolobus
559	24	75.0	6077	12	Q00105	white spot	632	24	75.0	107	5	Q00766	Q00766 sulfolobus
560	24	75.0	6077	12	Q00105	white spot	633	24	75.0	107	5	Q00766	Q00766 sulfolobus
561	24	75.0	6077	12	Q00105	white spot	634	24	75.0	107	5	Q00766	Q00766 sulfolobus
562	24	75.0	6077	12	Q00105	white spot	635	24	75.0	107	5	Q00766	Q00766 sulfolobus
563	24	75.0	6077	12	Q00105	white spot	636	24	75.0	107	5	Q00766	Q00766 sulfolobus
564	24	75.0	6077	12	Q00105	white spot	637	24	75.0	107	5	Q00766	Q00766 sulfolobus
565	24	75.0	6077	12	Q00105	white spot	638	24	75.0	107	5	Q00766	Q00766 sulfolobus
566	24	75.0	6077	12	Q00105	white spot	639	24	75.0	107	5	Q00766	Q00766 sulfolobus
567	24	75.0	6077	12	Q00105	white spot	640	24	75.0	107	5	Q00766	Q00766 sulfolobus
568	24	75.0	6077	12	Q00105	white spot	641	24	75.0	107	5	Q00766	Q00766 sulfolobus
569	24	75.0	6077	12	Q00105	white spot	642	24	75.0	107	5	Q00766	Q00766 sulfolobus
570	24	75.0	6077	12	Q00105	white spot	643	24	75.0	107	5	Q00766	Q00766 sulfolobus
571	24	75.0	6077	12	Q00105	white spot	644	24	75.0	107	5	Q00766	Q00766 sulfolobus
572	24	75.0	6077	12	Q00105	white spot	645	24	75.0	107	5	Q00766	Q00766 sulfolobus
573	24	75.0	6077	12	Q00105	white spot	646	24	75.0	107	5	Q00766	Q00766 sulfolobus
574	24	75.0	6077	12	Q00105	white spot	647	24	75.0	107	5	Q00766	Q00766 sulfolobus
575	24	75.0	6077	12	Q00105	white spot	648	24	75.0	107	5	Q00766	Q00766 sulfolobus
576	24	75.0	6077	12	Q00105	white spot	649	24	75.0	107	5	Q00766	Q00766 sulfolobus
577	24	75.0	6077	12	Q00105	white spot	650	24	75.0	107	5	Q00766	Q00766 sulfolobus
578	24	75.0	6077	12	Q00105	white spot	651	24	75.0	107	5	Q00766	Q00766 sulfolobus
579	24	75.0	6077	12	Q00105	white spot	652	24	75.0	107	5	Q00766	Q00766 sulfolobus
580	24	75.0	6077	12	Q00105	white spot	653	24	75.0	107	5	Q00766	Q00766 sulfolobus
581	24	75.0	6077	12	Q00105	white spot	654	24	75.0	107	5	Q00766	Q00766 sulfolobus
582	24	75.0	6077	12	Q00105	white spot	655	24	75.0	107	5	Q00766	Q00766 sulfolobus
583	24	75.0	6077	12	Q00105	white spot	656	24	75.0	107	5	Q00766	Q00766 sulfolobus
584	24	75.0	6077	12	Q00105	white spot	657	24	75.0	107	5	Q00766	Q00766 sulfolobus
585	24	75.0	6077	12	Q00105	white spot	658	24	75.0	107	5	Q00766	Q00766 sulfolobus
586	24	75.0	6077	12	Q00105	white spot	659	24	75.0	107	5	Q00766	Q00766 sulfolobus
587	24	75.0	6077	12	Q00105	white spot	660	24	75.0	107	5	Q00766	Q00766 sulfolobus
588	24	75.0	6077	12	Q00105	white spot	661	24	75.0	107	5	Q00766	Q00766 sulfolobus
589	24	75.0	6077	12	Q00105	white spot	662	24	75.0	107	5	Q00766	Q00766 sulfolobus
590	24	75.0	6077	12	Q00105	white spot	663	24	75.0	107	5	Q00766	Q00766 sulfolobus
591	24	75.0	6077	12	Q00105	white spot	664	24	75.0	107	5	Q00766	Q00766 sulfolobus
592	24	75.0	6077	12	Q00105	white spot	665	24	75.0	107	5	Q00766	Q00766 sulfolobus
593	24	75.0	6077	12	Q00105	white spot	666	24	75.0	107	5	Q00766	Q00766 sulfolobus
594	24	75.0	6077	12	Q00105	white spot	667	24	75.0	107	5	Q00766	Q00766 sulfolobus
595	24	75.0	6077	12	Q00105	white spot	668	24	75.0	107	5	Q00766	Q00766 sulfolobus
596	24	75.0	6077	12	Q00105	white spot	669	24	75.0	107	5	Q00766	Q00766 sulfolobus
597	24	75.0	6077	12	Q00105	white spot	670	24	75.0	107	5	Q00766	Q00766 sulfolobus
598	24	75.0	6077	12	Q00105	white spot	671	24	75.0	107	5	Q00766	Q00766 sulfolobus
599	24	75.0	6077	12	Q00105	white spot	672	24	75.0	107	5	Q00766	Q00766 sulfolobus
600	24	75.0	6077	12	Q00105	white spot	673	24	75.0	107	5	Q00766	Q00766 sulfolobus

[illegible]

Q8455	mus musculus	224	75.0	224	11	Q8455
Q8456	metabact	224	75.0	224	12	Q8456
Q8457	pacibacill	224	75.0	224	13	Q8457
Q8458	eschertibia	224	75.0	224	14	Q8458
Q8459	eschertibia	224	75.0	224	15	Q8459
Q8460	san marcel	224	75.0	224	16	Q8460
Q8461	bacillus ha	224	75.0	224	17	Q8461
Q8462	gerstina pe	224	75.0	224	18	Q8462
Q8463	psudomonas	224	75.0	224	19	Q8463
Q8464	psudomonas	224	75.0	224	20	Q8464
Q8465	psudomonas	224	75.0	224	21	Q8465
Q8466	psudomonas	224	75.0	224	22	Q8466
Q8467	psudomonas	224	75.0	224	23	Q8467
Q8468	psudomonas	224	75.0	224	24	Q8468
Q8469	psudomonas	224	75.0	224	25	Q8469
Q8470	psudomonas	224	75.0	224	26	Q8470
Q8471	psudomonas	224	75.0	224	27	Q8471
Q8472	psudomonas	224	75.0	224	28	Q8472
Q8473	psudomonas	224	75.0	224	29	Q8473
Q8474	psudomonas	224	75.0	224	30	Q8474
Q8475	psudomonas	224	75.0	224	31	Q8475
Q8476	psudomonas	224	75.0	224	32	Q8476
Q8477	psudomonas	224	75.0	224	33	Q8477
Q8478	psudomonas	224	75.0	224	34	Q8478
Q8479	psudomonas	224	75.0	224	35	Q8479
Q8480	psudomonas	224	75.0	224	36	Q8480
Q8481	psudomonas	224	75.0	224	37	Q8481
Q8482	psudomonas	224	75.0	224	38	Q8482
Q8483	psudomonas	224	75.0	224	39	Q8483
Q8484	psudomonas	224	75.0	224	40	Q8484
Q8485	psudomonas	224	75.0	224	41	Q8485
Q8486	psudomonas	224	75.0	224	42	Q8486
Q8487	psudomonas	224	75.0	224	43	Q8487
Q8488	psudomonas	224	75.0	224	44	Q8488
Q8489	psudomonas	224	75.0	224	45	Q8489
Q8490	psudomonas	224	75.0	224	46	Q8490
Q8491	psudomonas	224	75.0	224	47	Q8491
Q8492	psudomonas	224	75.0	224	48	Q8492
Q8493	psudomonas	224	75.0	224	49	Q8493
Q8494	psudomonas	224	75.0	224	50	Q8494
Q8495	psudomonas	224	75.0	224	51	Q8495
Q8496	psudomonas	224	75.0	224	52	Q8496
Q8497	psudomonas	224	75.0	224	53	Q8497
Q8498	psudomonas	224	75.0	224	54	Q8498
Q8499	psudomonas	224	75.0	224	55	Q8499
Q8500	psudomonas	224	75.0	224	56	Q8500
Q8501	psudomonas	224	75.0	224	57	Q8501
Q8502	psudomonas	224	75.0	224	58	Q8502
Q8503	psudomonas	224	75.0	224	59	Q8503
Q8504	psudomonas	224	75.0	224	60	Q8504
Q8505	psudomonas	224	75.0	224	61	Q8505
Q8506	psudomonas	224	75.0	224	62	Q8506
Q8507	psudomonas	224	75.0	224	63	Q8507
Q8508	psudomonas	224	75.0	224	64	Q8508
Q8509	psudomonas	224	75.0	224	65	Q8509
Q8510	psudomonas	224	75.0	224	66	Q8510
Q8511	psudomonas	224	75.0	224	67	Q8511
Q8512	psudomonas	224	75.0	224	68	Q8512
Q8513	psudomonas	224	75.0	224	69	Q8513
Q8514	psudomonas	224	75.0	224	70	Q8514
Q8515	psudomonas	224	75.0	224	71	Q8515
Q8516	psudomonas	224	75.0	224	72	Q8516

FL Submitted: 07/11/2001 to the EMBL/GenBank/TrEMBL databases.

DB EMBL: AB397110; AAK81743.1; ...

DB InterPro: IPR000561; PIP-1160.

DB InterPro: IPR000561; PIP-1160.

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

DB Pfam: PF01826, TH1.1

```

Ephraida; Insectophila; Pro-ephila.
OX NCBI_TaxID=7227;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN CAMION S.
RC
RE
EX MELLINE 9924776, PubMed 9821974;
FA Refs N.E., Vaidyan R., Gaskell T., Cohen P.T.W.:
RT "Characterisation of a novel Insectophila melanogaster testis specific
RI ppi inhibitor related to mammalian inhibitor-2: identification of the
RL site of interaction with ppi";
RM FEBS Lett. 438:131-140(1998).
RP EMBL: AJ006467; CAA97278.1;
RI Flybase: FBam025821; 1 U. A + L.
RT VARIANT 21 21 D + G.
RI VARIANT 184 184
SQ SEQUENCE 184 AA; 25908 MW; 16971691271A762 C6664;
Query Match 94.8%; Score 30; DB %; Length 184;
Best Local Similarity 100.0%; Pred. No. 72;
Match %; Characteristic %; Magnitude %; Index %; Gaps

```

QY	3 QYRN 7				
DB	41 QYRN 45				
RESULT 10					
DD	Q9VGJ2	PRELIMINARY:	PR1	184 AA.	
AC	Q9VGJ2:				
DT	01-MAY-2000 (TFMB:rel. 15, Created)				
DT	01-MAY-2000 (TFMB:rel. 15, Last sequence update)				
DT	01-MAR-2001 (TFMB:rel. 16, Last annotation update)				
DE	1-T protein.				
GN	CG14719.				
OS	Drosophila melanogaster (Fruit fly).				
OC	Eukaryota, Metazoa, Arthropoda, Insecta, Hexapoda, Insecta:				
OC	Pterygota, Neoptera, Endopterygota, Diptera, Brachycera, Muscomorpha:				
OC	Ephydroidea, Drosophilidae, Drosophila.				
OX	NCBI_TaxID=7227;				
EN	[1]				
RP	SEQUENCE FROM N.A.				
CC	STRAIN=BERKLEY;				

[illegible]


```

ID 191 GFYRN 195
      |||||
RESULT 14
Q9HIV4
AC Q9HIV4 PRELIMINARY: PRI: 247 AA.
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DI 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
GN Vag1457c.
OS Halobacterium sp. (strain NRC-1).
OC Archaea; Euryarchaeota; Halobacteriia; Halobacteriales;
OC Halobacteriaceae; Halobacterium
OX NCBI_TaxID:64091;
RN [1]
RX MEDLINE:20504483; PubMed 11015050;
RA Ng W.V., Kennedy S.P., Mahairas G.G., Benquist R., Pan M.,
RA Shukla H.B., Lasky S.F., Ralston J., Hartman V., Struelens
RA Swartzell S., Weir D., Hall J., Dahl T.A., Weltri R., Goo Y.A.,
RA Leithausen B., Keller K., Cruz R., Danson M.J., Hough D.W.,
RA Maddocks J.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,
RA Isonbarger T.A., Cook R.F., Pohlschroder M., Spudis J.L., Jung K.-H.,
RA Alam M., Freitas I., How S., Daniels C.J., Dennis P.P., Giner A.D.,
RA Ehardt H., Lowe J.M., Lind P., Piley M., Reed L., DasSarma S.,
RA Proc. Natl. Acad. Sci. U.S.A. 97:12176-12191(2000)
DI EMBL: AE005061; AAC19763.1;
DI InterPro: IPR000182; GCM5acetyltransf.
DI Pfam: PF00583; Acetyltransf. 1
KW Complete proteome.
SQ SEQUENCE 247 AA: 25295 MW: 248321FE9-1HE29F CMC64;
      |||||
Query Match 93.8%; Score 30; DB 17; Length 237;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 4 GFYRN 7
      |||||
ID 191 GFYRN 195
      |||||
RESULT 15
Q8Z119
AC Q8Z119 PRELIMINARY: PRI: 266 AA.
DI 01-MAR-2002 (TREMBLrel. 20, Created)
DI 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DI 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical protein PAE3474.
GN PAE3474.
OS Pyrobaculum aerophilum.
OC Archaea; Euryarchaeota; Thermoprotei; Thermoproteales;
OC Thermoproteaceae; Pyrobaculum.
OX NCBI_TaxID:14773;
RN [1]
RX MEDLINE:11742869; PubMed 127722;
RA Fitz Gibbon S.L., Ladner H., Kim D.-J., Stotter K.O., Simon M.L.,
RA Miller J.H.;
RA Proc. Natl. Acad. Sci. U.S.A. 99:994-999(2002).
DI EMBL: AE009934; AAC14944.1;
DI InterPro: IPR000687; R101LNG
DI Pfam: PF01163; R101; 1
DI SMART: SM00090; R101; 1
DI PROSITE: PS00109; PF07FIN_KINASE_TYP; UNKNNWN_1

```

```

KW Hypothetical proteins: Complete proteome.
SQ SEQUENCE 266 AA: 46564 MW: A-24985A8a22B4Z-7664;
      |||||
Query Match 93.8%; Score 40; DB 17; Length 266;
Best Local Similarity 100.0%; Pred. No. 100;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 4 GFYRN 7
      |||||
ID 126 GFYRN 140
      |||||
RESULT 16
Q9HKK3
AC Q9HKK3 PRELIMINARY: PRI: 325 AA.
DI 01-JUN-2001 (TREMBLrel. 17, Created)
DI 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DI 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Sex lethal protein SXL2.
OS Lucilia cuprina (Greenbottle fly) (Diptera: Tephritidae).
OC Pterygota; Neoptera; Endopterygota; Diptera; Tephritidae;
OC Cecidomyiidae; Tephritidae; Lucilia.
OX NCBI_TaxID:7475;
RN [1]
RX SEQUENCE FROM N.A.
RA Hayward D.J., Rowley A.J., Atkinson P.W.;
RA "The Sex-lethal homolog of Lucilia cuprina."
DI EMBL: AF234184; AAC20026.1;
DI BSS: P19339; ISXL.
DI InterPro: IPR002443; Hsd_SXL_RNA.
DI Pfam: PF00076; rim; 2.
DI PRINTS: PR00661; HDSXL_RNA.
DI SMART: SM03460; RRM; 2.
DI PROSITE: PS00102; EPM; 2.
DI PROSITE: PS00310; RRM_RNP_1; UNKNNWN_1.
SQ SEQUENCE 325 AA: 35736 MW: 34642FB79C695214 C8664;
      |||||
Query Match 93.8%; Score 40; DB 5; Length 325;
Best Local Similarity 100.0%; Pred. No. 1;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.
QY 4 GFYRN 7
      |||||
ID 313 GFYRN 417
      |||||
RESULT 17
Q9H8R9
AC Q9H8R9 PRELIMINARY: PRI: 329 AA.
DI 01-JUN-2001 (TREMBLrel. 17, Created)
DI 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DI 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Tryptophanyl tRNA synthetase.
GN WARS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Gradata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Scurionathia; Muridae; Murinae; Mus
OX NCBI_TaxID:10090;
RN [1]
RX SEQUENCE FROM N.A.
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Akabawa T., Hara A., Fukunishi Y., Kame H., Adachi J., Fukuda S.,
RA Akabawa T., Itoh M., Kishi K., Kishimoto A., Kishimoto A.,
RA Saito T., Okazaki Y., Gotoh T., Itoh H., Kasukawa T., Saito K.,
RA Kadota K., Matsuda H.A., Ashburner M., Gattolusi L., Gattolusi L.,
RA Fleischmann W., Gattolusi L., Gattolusi L., Kim P., Kochwa H.,

```



```

RESULT 20
Q9P819 PRELIMINARY: PRT: 362 AA.
ID Q9P819
AC Q9P819
DT 01-06-2000 (TREMBLrel. 15, Created)
DT 01-06-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Phosphoserine aminotransferase.
GN XP2326.
OS Xylella fastidiosa.
OC Bacteria; Proteobacteria, gamma subdivision, Xanthomonas group.
OC Xylella
OC NCBI_TaxID=23371
KN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 9A5C;
RX MEDLINE 20365717; PubMed 10910471;
RA Simpson A.J.G., Reinach F.C., Arruda P., Abreu F.A., Acencio M.,
RA Alvarado P., Alves L.M.C., Araya J.E., Baia G.S., Baptista C.S.,
RA Barros M.H., Bonavetti E.D., Bordin S., Bove J.M., Briones M.R.S.,
RA Bueco M.R.P., Camargo A.A., Camargo L.R.A., Carraro D.M., Carter H.,
RA Couto N.B., Colombo C., Costa F.F., Costa M.C.R., Costa-Neto C.M.,
RA Coutinho J.L., Cristofani M., Dias-Neto E., Pereira C., El-Berry B.,
RA Facchini A.P., Ferreira A.J.S., Ferreira V.C.A., Ferro J.A.,
RA Fraga J.S., Franca S.C., Franco M.C., Frohme M., Furian L.R.,
RA Gartner M., Goldman G.H., Goldman M.H.S., Gomes S.L., Gruber A.,
RA Ho P.J., Holsel J.D., Junqueira M.H., Kemper E.L., Kitajima J.P.,
RA Krieger J.E., Kuramae E.F., Lalart F., Lambais M.R., Leite L.C.C.,
RA Lemos E.G.M., Lemos M.V.F., Lopes S.A., Lopes C.R., Machado J.A.,
RA Machado M.A., Madeira H.M.F.N., Madeira H.M.F., Marino C.L.,
RA Marques M.V., Martins E.A.L., Martins E.M.F., Matsukuma A.Y.,
RA Menck C.F.M., Miranda E.C., Miyaki C.Y., Monteiro-Vitorello C.B.,
RA Moon B.H., Nadi M.A., Nascimento A.L.T.G., Netto L.R.S.,
RA Niani A., Jr., Nobrega F.G., Nunes L.P., Oliveira M.A.,
RA de Oliveira M.C., de Oliveira R.C., Palmieri D.A., Paris A.,
RA Peixoto B.R., Pereira G.A.G., Pereira H.A.T., Pasquero J.R.,
RA Quaggio R.R., Roberto P.G., Rodrigues V., de Rosa A.T.M.,
RA da Silva V.E., Jr., de Sa R.G., Santoli R.V., Sawasaki H.E.,
RA da Silva A.C.R., da Silva A.M., da Silva F.F., Silva W.A., Jr.,
RA da Silva V.F., Silvestri M.F., Silvestri W., de Souza A.A.,
RA de Souza A.P., Torresi M.P., Truffi P., Tsai S.M., Tsubako M.B.,
RA Vallada H., Van Sluys M.A., Verjovski-Almeida S., Vettore A.L.,
RA Zaki M.A., Zatz M., Zeldin J., Zetubal J.C.
RT "The genome sequence of the plant pathogen Xylella fastidiosa";
RL Nature 406:151-159(2000).
DR EMBL: AF040434; AAF85125.1;
DR BSSP: P24721; BGJN.
DR InterPro: IPR000192; AminoTransIV.
DR Plan: PF09266; aminoTransI_5; 1.
DR Problem: P0001544; Pser_aminotransf; 1.
KW Complete proteome.
SQ SEQUENCE 362 AA; 6915 MW; 10E451A7A627A4 C99264;

Query Match 93.88; Score 40; DB 16; Length 362;
Best Local Similarity 100.00; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 284 GYRN 285
|||||
RESULT 21
Q9Y020 PRELIMINARY: PRT: 378 AA.
ID Q9Y020
AC Q9Y020
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Probable phosphoserine aminotransferase (PSAT) protein
DE (EC 2.6.1.52).
GN SERC OR RSC0903 OR R504512.

```

```

OS Kalstonia solanacearum (Pseudomonas solanacearum)
OC Bacteria; Proteobacteria; beta subdivision; Kalstonia group.
OC Kalstonia
OC NCBI_TaxID 305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-GM11000;
RX MEDLINE-21681879; PubMed 11823852;
RA Salendykat M., Gelin S., Artigache F., Garry J., Marchet S.,
RA Ariat M., Billault A., Brotier P., Camus J.F., Carlotto L.,
FA Chonglet M., Chetoui N., Claude-Robard P., Dumas S., Demange N.,
PA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schlex T.,
PA Squier P., Thebault P., Whalen M., Wincker P., Woy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Kalstonia solanacearum";
RL Nature 415:457-502(2002).
DR EMBL: AL046061; CAP14605.1; 1.
DR InterPro: IPR00192; AminoTransIV.
DR Plan: PF09266; aminoTransI_5; 1.
DR Problem: P0001544; Pser_aminotransf; 1.
KW Transferrase; AminoTransferase; Complete proteome.
SQ SEQUENCE 378 AA; 41869 MW; 14CA5695098F97B C9664;

Query Match 93.88; Score 40; DB 16; Length 378;
Best Local Similarity 100.00; Pred. No. 1.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 300 GYRN 304
|||||
RESULT 22
ID 001482 PRELIMINARY: PRT: 408 AA.
AC 001482;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Hypothetical 46.2 kDa protein.
GN C06A5.9.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhadittida; Rhadittoidae.
OC Rhadittidae; Polidornidae; Caenorhabditis.
OC NCBI_TaxID 6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN BRISTOL N2;
RX MEDLINE 99066613; PubMed 9851916;
RA None;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology. The C. elegans Sequencing Consortium";
RL Science 282:2012-2018(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN BRISTOL N2;
RA Davidson S., Wohldmann P.;
RT "The sequence of C. elegans cosmid C06A5.9";
RL Submitted (APR-1997) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterston R.;
RT "Direct Submission";
EL 2001.1.1 (31.1.01); in the EMBL/Genbank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 KING-TYPE ZINC FINGER.
DS EMBL_097193; AAF52442.1;
DR InterPro: IPR018411; Znf_Fing.
DR Plan: PF000097; ZF_C4HC4; 1.
DR SMART: SM00184; ZINC; 1.
DR PROSITE: PS00519; ZF_RING_1; 1.
DR Hypothetical protein; Zinc finger.
KW

```


DR InterPro: IPR000738: WHEP-TFS
 DR Pfam: PF00579: tRNA-synt_1b: 1.
 DR Pfam: PF00458: WHEP-TFS: 1.
 DR PRINTS: PF01239: TPNASYNTHPP.
 DR TIGRFAMs: TIGR00233: tfs: 1.
 DR PROSITE: PS00178: AA:TPNA_LIGASE_I: 1.
 DR PROSITE: PS00762: WHEP-TFS: 1.
 SC PROSITE: PS00762: WHEP-TFS: 1

Query Match 93.8% Score 30; DP 11; Length 481.
 Best Local Similarity 100.0% Prod. No. 1 96-00.
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
 |||||
 DB 250 GFYRN 254

RESULT 29
 Q99J58
 ID Q99J58 PRELIMINARY: PRT; 481 AA.
 AC Q99J58
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Trp synthase; tRNA synthetase.
 GN WARS
 GS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MAMMARY TOWP WAP-TAC MODEL 5 MONTHS OLD;
 RA Strassberg P.;
 EL Submitted (FEB 2001) to the EMBL/GenBank/DDBJ databases
 DP EMBL: BC003450; AAH03450.1; 5;
 MD: MGI:104630; WARS.
 DR InterPro: IPR002365: tRNA-synt_1b.
 DR InterPro: IPR001412: tRNA-synt_1.
 DR InterPro: IPR002306: TRP_tRNA_synt_1b.
 DR InterPro: IPR000738: WHEP-TFS.
 DR Pfam: PF00579: tRNA-synt_1b: 1.
 DR Pfam: PF00458: WHEP-TFS: 1.
 DR PRINTS: PR01039: TPNASYNTHPP
 DR TIGRFAMs: TIGR00233: tfs: 1
 DR PROSITE: PS00178: AA:TPNA_LIGASE_I: 1
 DR PROSITE: PS00762: WHEP-TFS: 1.
 KW Amidoglutamyl-tRNA synthetase
 SQ SEQUENCE 481 AA; 54325 MW; A754E1EDD58CELEF3 CRC64.

Query Match 93.8% Score 30; DB 11; Length 481.
 Best Local Similarity 100.0% Prod. No. 1 96-00.
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
 |||||
 DB 250 GFYRN 254

RESULT 30
 Q91X80
 ID Q91X80 PRELIMINARY: PRT; 523 AA.
 AC Q91X80
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE 0 day neonatal skin cDNA, ERK1 full-length cDNA library.
 DE clone:463340207, full insert sequence.
 GN TYR.
 GS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN: C57BL/6J; TISSUE: SKIN;
 RA Adachi T., Carninci P., Fukuda S., Fukunishi Y., Furuno M.,
 RA Hara A., Hayatsu M., Hiramoto K., Hirakawa T., Hori F.,
 RA Iwatsuki K., Ishii Y., Itoh H., Iwata M., Kato H., Kawai M., Kojima Y.,
 RA Kondo H., Kondo M., Koyu S., Kurihara S., Matsuyama T., Miyazaki A.,
 RA Mizuno Y., Muraoka Y., Murakami K., Ohno H., Okazaki Y., Okido T.,
 RA Oshida S., Saito H., Saito F., Saito T., Sakai Y., Sato H., Suzuki D.,
 RA Shibata K., Shibata Y., Shikawa A., Shiraki T., Sodabe Y.,
 RA Suzuki H., Tawami M., Tagawa A., Takahashi F., Tanaka T., Tojima Y.,
 RA Itoya T., Yamamura T., Yasunishi A., Yoshida K., Yoshino M.,
 RA Muramatsu M., Hayashizaki Y.;
 RA GenBank: U00289; (307,289 bp); (1995) GenBank/EMBL/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=SKIN;
 MDLINE=21895660; PubMed=11217851;
 RA EKEN FANTOM Consortium;
 RT Functional annotation of a full length mouse cDNA collection.";
 RL Nature 409:685-690(2001).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN: C57BL/6J; TISSUE: SKIN;
 MDLINE=99279953; PubMed=1049636;
 RA Carninci P., Hayashizaki Y.;
 RT High efficiency full length cDNA cloning.";
 RL Meth. Enzymol. 303:19-44(1999).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=SKIN;
 MDLINE=20499474; PubMed=11942159;
 RA Carninci P., Shibata Y., Hayatsu M., Sugahara Y., Shibata K., Itoh M.,
 RA Itoya T., Ishii Y., Murakami M., Hayashizaki Y.;
 RT "Normalization and subtraction of cDNA libraries for rapid discovery of new genes.";
 RL Genome Res. 10:1617-1626(2000).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN: C57BL/6J; TISSUE: SKIN;
 MDLINE=20530913; PubMed=11076861;
 RA Shibata K., Itoh M., Aizawa K., Sugawara S., Sasaki N., Carninci P.,
 RA Kondo H., Akiyama T., Nishi K., Kitsuai T., Tashiro H., Itoh M.,
 RA Sano H., Ishii Y., Nakamura S., Hatanaka M., Nishino T., Harada A.,
 RA Yamamoto K., Matsumoto H., Sakaguchi S., Ikegami T., Kashikawa K.,
 RA Fujisake S., Inoue K., Tojima Y., Iizawa M., Ohara E., Watabiki M.,
 RA Tanaka Y., Tsukikawa T., Goto F., Tanaka T., Hatanaka S., Kawai J.,
 RA Oshida Y., Matsuda S., M. Inoue Y., Fira A., Hayashizaki Y.;
 RT "RIKEN integrated sequence analysis (RISA) system: a format
 RT sequence pipeline with 384 multicapillary sequencer.";
 RL Genome Res. 10:1617-1626(2000).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN: C57BL/6J; TISSUE: SKIN;
 MD: MGI:104630; WARS
 DR InterPro: IPR002365: tRNA-synt_1b.
 DR InterPro: IPR002306: TRP_tRNA_synt_1b.
 DR InterPro: IPR002227: Tyrosinase.
 DR Pfam: PF00264: tyrosinase: 1.
 DR PROSITE: PS00022: ESK_1: UNKN-WN_1.
 DR PROSITE: PS01248: LAMININ_TYR_EGF: UNKN-WN_1.
 DR PROSITE: PS00497: TYRGIN_NAGLE_1: UNKN-WN_1.
 DR PROSITE: PS00498: TYRGIN_NAGLE_2: UNKN-WN_1.
 SQ SEQUENCE 533 AA; 60606 MW; A6C109A973B05D6A CRC64;

Query Match 93.8% Score 30; DB 11; Length 533
 Best Local Similarity 100.0% Prod. No. 216-00;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GFYRN 7
 |||||
 DB 459 GFYRN 462

```

RESULT 41
QBZL2
ID QBZL2 PRELIMINARY: PRI: 554 AA.
AC QBZL2
DT 01-MAR-2002 (TREMREL: 20, Created)
DT 01-MAR-2002 (TREMREL: 20, Last sequence update)
DT 01-JUN-2002 (TREMREL: 21, Last annotation update)
DE Helicase, probable.
DN PAE0208.
OS Pyrobaculum aerophilum.
OC Archaea: Euryarchaeota: Thermoproteales:
OC Thermoproteaceae: Pyrobaculum.
GX NCBI_TaxID:13773;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN 182 / ATCC 3796 / 600 7622.
EX PubMed:11792669;
SA Fitch-Baker S.L., Baker H., Kim H.-J., Stetter K.O., Simon M.I.,
SA Miller J.H.:
SA "Genome sequences of the hyperthermophilic euryarchaeon Pyrobaculum
SA aerophilum."
SA Proc. Natl. Acad. Sci. U.S.A. 99:984-987(2002).
DR EMBL: AF009756; AAL26271.1;
DR InterPro: IPR001410; DEAD.
DR InterPro: IPR001650; Helicase_C.
DR Pfam: PF00270; DEAD_1.
DR Pfam: PF00271; Helicase_C; 1.
DR SMART: SM00487; DEAD_1.
DR SMART: SM00490; Helicase_C; 1.
DR Complete Proteome.
KW Complete Proteome.
SQ SEQUENCE 554 AA: 64761 MW: 99697575.1181140 CRG54.

Query Match 93.8%, Score 30; DB 17; Length 554;
Best Local Similarity 100.0%, Pred. No. 2,4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 49 GYRN 54

RESULT 42
QBZL2
ID QBZL2 PRELIMINARY: PRI: 596 AA.
AC QBZL2
DT 01-NOV-1998 (TREMREL: 08, Created)
DT 01-NOV-1998 (TREMREL: 08, Last sequence update)
DT 01-MAR-2002 (TREMREL: 20, Last annotation update)
DE Uptake hydrolase.
DN B0001.
OS Rhodospirillum rubrum.
OC Bacteria: Proteobacteria: alpha subdivision: Rhodospirillum rubrum.
OC Rhodospirillum rubrum.
GX NCBI_TaxID:1063;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN RV;
SA Franchi E., Iosi C., Redini E., Pedroni F.;
SA Submitted (HAF 5556) to the EMBL/GenBank/CCDB databases.
DR EMBL: Y14197; CAA74567.1;
DR BSSD: P12944; PRV.
DR InterPro: IPR001501; Ni_HDL.
DR Pfam: PF00474; NiFeSe_Hases; 1.
DR PROSITE: PS00567; NiFe_HASE_1; 1.
DR PROSITE: PS00568; NiFe_HASE_2; 1.
SQ SEQUENCE 596 AA: 66255 MW: 64641676.108660 CRG54.

Query Match 93.8%, Score 30; DB 22; Length 596;
Best Local Similarity 100.0%, Pred. No. 2,4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7

```

```

DB 283 GYRN 287

RESULT 43
QBZL2
ID QBZL2 PRELIMINARY: PRI: 638 AA.
AC QBZL2
DT 01-OCT-2000 (TREMREL: 15, Created)
DT 01-OCT-2000 (TREMREL: 15, Last sequence update)
DT 01-JUN-2001 (TREMREL: 17, Last annotation update)
DE Netrin.
GX NCBI_TaxID:7719;
RN [1]
RP SEQUENCE FROM N.A.
RC Takamura K.;
SA "Expression patterns of ascidian netrin homologues."
SA Eur. J. Cell Biol. 159:1-10(2000).
DR EMBL: AB033352; BAA94303.1;
DR InterPro: IPR000561; EGF-like.
DR InterPro: IPR002049; Laminin_EGF.
DR InterPro: IPR001886; Lamin.
DR InterPro: IPR001134; Netrin_C.
DR Pfam: PF00053; Laminin_EGF; 2.
DR Pfam: PF00055; Laminin_Nterm; 1.
DR Pfam: PF01759; NTR; 1.
DR ProDom: PD002082; Lamin; 1.
DR SMART: SM00130; EGF_Lam; 2.
DR SMART: SM00136; Lamin; 1.
DR PROSITE: PS00022; EGF_1; UNPKNWN_1.
DR PROSITE: PS01246; LAMININ_TYPE_EGF; UNKNWN_1.
SQ SEQUENCE 600 AA: 68112 MW: 22753124.170268 CRG54.

Query Match 93.8%, Score 30; DB 5; Length 600;
Best Local Similarity 100.0%, Pred. No. 2,4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 438 GYRN 442

RESULT 44
QBZL2
ID QBZL2 PRELIMINARY: PRI: 611 AA.
AC QBZL2
DT 01-OCT-2000 (TREMREL: 15, Created)
DT 01-OCT-2000 (TREMREL: 15, Last sequence update)
DT 01-MAR-2002 (TREMREL: 20, Last annotation update)
DE Tyrosine phosphatase like protein (putative tyrosine
DE phosphatase).
GX NCBI_TaxID:4702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN COLOMBIA;
SA Sato S., Nakamura Y., Kasako T., Kato T., Asanizu E., Tabata S.;
SA Submitted (ABF 556) to the EMBL/GenBank/CCDB databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN COLOMBIA;
EX MEDLINE 20277480; PubMed 10819429;
SA Nakamura Y.;
SA "Structural analysis of Arabidopsis thaliana chromosome 4. I. Sequence
SA features of the regions of 4,564,864 bp covered by sixty F1 and F2"

```



```

RT clones."
RL DNA Res. 7:131-135(2000)
RN [3]
RP SEQUENCE FROM N.A.
RA Yamada K., Banh J., Chang C.H., Chang E., Dale J.M., Goldsmith A.D.,
  Lee J.M., Onodera C.S., Quach H.L., Tang C., Toriumi M., Wu H.C.,
  Yamamura Y., Yu G., Yu S., Bowser J., Carninci P., Chen H., Cheuk R.,
  Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
  Kawai J., Kim C., Lam B., Lin J., Meyers M.C., Miranda M.,
  Narasaka M., Nguyen M., Palm C.F., Sakurai T., Salton M., Seki M.,
  Shinn P., Smithwick A., Srinivasan K., Davis F.W., Ecker J.P.,
  Theodoris A.;
PT "Full length cDNA of gene At3g19420 (GI:15240479)."
RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB025624; BAB02466.1;
DR EMBL: AY000442; AA149799.1;
DR InterPro: IP000340; PS_phosphatase
DR InterPro: IP000187; TVR_phosphatase
DR SMART: SM00012; PTFC_DSPEC; 1.
DR PROSITE: PS00393; TVR_PHOSPHATASE_1; 1.
DR PROSITE: PS50056; TVR_PHOSPHATASE_2; 1.
KW Hydrolase.
SQ SEQUENCE 611 AA; 66430 MW; CB4FB3CFE0C6C577 CRC64;

Query Match 93.8%; Score 30; DR 5; Length 650;
Best Local Similarity 100.0%; Pred. No. 2.7e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3 GYRN 7
DB 183 GYRN 187

RESULT 35
QYNT28 PRELIMINARY; PRI: 650 AA.
AC Q9NL28
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DI 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Netrin.
GN CI-NET1A.
OS Clona intestinalis.
OC Eukaryota; Metazoa; Chordata; Vertebrata; Ascidiacea; Enteropneusta.
OC Phlebobranchia; Cloniidae; Clona.
OX NCBI_TaxID=7719;
RN [1]
RP SEQUENCE FROM N.A.
RA Takamura K.;
PT "Expression patterns of ascidian netrin homologues."
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases
DR EMBL: AB033331; BA054302.1;
DR HSSP: P02468; 1KIO.
DR InterPro: IP000561; FGF-like.
DR InterPro: IP002049; Lamin_EGF.
DR InterPro: IP001886; Lamin.
DR InterPro: IP001134; Netrin_C.
DR Pfam: PF00053; Laminin_EGF_3.
DR Pfam: PF00055; Laminin_Nterm; 1.
DR Pfam: PF01759; RTR; 1.
DR PRINTS: PR00011; EGF_LAMININ
DR ProDom: PD002082; Lamin; 1.
DR SMART: SM00180; EGF_Lam; 3.
DR SMART: SM00136; Lamin; 1.
DR PROSITE: PS00022; EGF_L1_EKHCN_1.
DR PROSITE: PS01248; LAMININ_EGF_EGF_LIKE_N_1.
SQ SEQUENCE 450 AA; 73807 MW; F520C163A16F2C CRC64;

Query Match 93.8%; Score 30; DR 5; Length 650;
Best Local Similarity 100.0%; Pred. No. 2.7e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3 GYRN 7
DB 183 GYRN 187

RESULT 36
QYNT28 PRELIMINARY; PRI: 650 AA.
AC Q9NL28
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH dehydrogenase (Fragment).
GN NDHF.
OS Cryptantha flavoculata.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Asterales; easterids 1; easterids 1; Solanales; Hydrophyllales; Phacelia.
OX NCBI_TaxID=79334;
RN [1]
RP SEQUENCE FROM N.A.
RA Ferguson D.M.;
PT "Phylogenetic analysis and characterization of Hydrophyllales based on
  ndhf sequence data."
RL Syst. Bot. 03:0-0(1998).
CC 1. GATAGATGTCATGTCCTT. NADH + FLAST-QUINONE NAD(+) + FLAST-QUINOL.
DR EMBL: AF047803; AA22410.1;
DR InterPro: IP001750; oxidored_q1.
DR InterPro: IP002128; oxidored_q1_C.
DR InterPro: IP001516; oxidored_q1_N.
DR Pfam: PF00361; oxidored_q1; 1.
DR Pfam: PF01010; oxidored_q1_C_1.
DR Pfam: PF00662; oxidored_q1_N; 1.
KW Chloroplast; NAD; oxidoreductase; Plastocyanone.
PT NON_TER
FT NON_TER 692 692
SQ SEQUENCE 692 AA; 78525 MW; 02172226A17B3AC CRC64;

Query Match 94.8%; Score 30; DR 5; Length 692;
Best Local Similarity 100.0%; Pred. No. 2.7e-02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0.

QY 3 GYRN 7
DB 329 GYRN 333

RESULT 37
QYNT28 PRELIMINARY; PRI: 696 AA.
AC Q9NT28
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH dehydrogenase (Fragment).
GN NDHF.
OS Phacelia rotundifolia.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
  Asterales; easterids 1; Solanales; Hydrophyllales; Phacelia.
OX NCBI_TaxID=79395;
RN [1]
RP SEQUENCE FROM N.A.
RA Ferguson D.M.;
PT "Phylogenetic analysis and characterization of Hydrophyllales based on
  ndhf sequence data."
RL Syst. Bot. 03:0-0(1998).
CC 1. GATAGATGTCATGTCCTT. NADH + FLAST-QUINONE NAD(+) + FLAST-QUINOL.
DR EMBL: AF047779; AA22406.1;
DR InterPro: IP001750; oxidored_q1.
DR InterPro: IP002128; oxidored_q1_C.

```

```

DR InterPro: IP0001516; oxidored_q1_N.
DR Pfam: PF00361; oxidored_q1_C; 1.
DR Pfam: PF001010; oxidored_q1_N; 1.
DR Pfam: PF00662; oxidored_q1_N; 1.
KW Chloroplast; NAD; oxidoreductase; Plastopquinone.
FT NON_TER 1
FT NON_TER 696
SQ SEQUENCE 696 AA; 78638 MW; 2305644488210869 CRC64;

Query Match
Best Local Similarity 93.8%; Score 30; DB 8; Length 696;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 329 GYRN 333

RESULT 38
QY1W6
ID QY1W6 PRELIMINARY; PKI; 696 AA.
AC QY1W6;
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH dehydrogenase (Fragment).
GN NDRF.
OS Phacelia patuliflora.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta.
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Hydrophyllaceae; Phacelia.
OX NCBI_TaxID=79393;
RN 11
RP SEQUENCE FROM N.A.
RA Ferguson D.M.;
RT "Phylogenetic analysis and circumscription of Hydrophyllaceae based on ndhF sequence data."
RL Syst. Bot. 0:0-0(1998).
CC 1 CATALYTIC ACTIVITY: NADH + PLASTOQUINONE -> NAD(+) + PLASTOQUINOL.
DR EMBL: AF047791; A022398.1;
DR InterPro: IP0001750; oxidored_q1.
DR InterPro: IP0002128; oxidored_q1_C.
DR InterPro: IP0001516; oxidored_q1_N.
DR Pfam: PF00361; oxidored_q1_C; 1.
DR Pfam: PF001010; oxidored_q1_C; 1.
DR Pfam: PF00662; oxidored_q1_N; 1.
KW Chloroplast; NAD; oxidoreductase; Plastopquinone.
FT NON_TER 1
FT NON_TER 696
SQ SEQUENCE 696 AA; 78723 MW; 6006088722477271 CRC64;

Query Match
Best Local Similarity 93.8%; Score 30; DB 8; Length 696;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 329 GYRN 333

RESULT 39
QY1U4
ID QY1U4 PRELIMINARY; PKI; 698 AA.
AC QY1U4;
DI 01-MAY-2000 (TrEMBLrel. 13, Created)
DI 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE NADH dehydrogenase (Fragment).
GN NDRF.
OS Cordia nodosa.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta.

```

```

ST: Streptophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; euasterids I; Invertillales; Ranunculaceae;
OC Cordia.
OX NCBI_TaxID=79432;
RN 11
RP SEQUENCE FROM N.A.
RA Ferguson D.M.;
RT "Phylogenetic analysis and circumscription of Hydrophyllaceae based on ndhF sequence data."
RL Syst. Bot. 0:0-0(1998).
CC 1 CATALYTIC ACTIVITY: NADH + PLASTOQUINONE -> NAD(+) + PLASTOQUINOL.
DR EMBL: AF047839; A022415.1;
DR InterPro: IP0001750; oxidored_q1.
DR InterPro: IP0002128; oxidored_q1_C.
DR InterPro: IP0001516; oxidored_q1_N.
DR Pfam: PF00361; oxidored_q1_C; 1.
DR Pfam: PF001010; oxidored_q1_C; 1.
DR Pfam: PF00662; oxidored_q1_N; 1.
KW Chloroplast; NAD; oxidoreductase; Plastopquinone.
FT NON_TER 1
FT NON_TER 698
SQ SEQUENCE 698 AA; 79203 MW; 182391888788278 CRC64;

Query Match
Best Local Similarity 93.8%; Score 30; DB 8; Length 698;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 GYRN 7
DB 329 GYRN 333

RESULT 40
Q20046
ID Q20046 PRELIMINARY; PKI; 747 AA.
AC Q20046;
DI 01-NOV-1996 (TrEMBLrel. 01, Created)
DI 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DI 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE F3522.4 protein.
GN F3522.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditidae.
OC Rhabditidae; Pelodoriinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN 11
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA Willison P., Almsworth P., Anderson K., Kaynes C., Parks M.,
RA Bedford J., Burton J., Connell M., Guppy T., Gayer J., Galsbol A.,
RA Gardner M., Dear S., Du Z., Durbin R., Favetto A., Fulton L.,
RA Gartner A., Green P., Hawkins P., Hillier L., Hjer M., Johnston L.,
RA Jones M., Kershak J., Kingston J., Laister N., Latreille P.,
RA Lichting J., Lloyd C., McMurray A., Mortimore R., O'Callaghan M.,
RA Parsons J., Perry C., Riken L., Roopra A., Saunders D., Shewchen R.,
RA Smailon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Winkstock L., Wilkinson S., Wright J., Wohlman P.,
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368: 12-38(1994).
RN 12
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA Connell M.;
RT "The sequence of C. elegans cosmid F3522."
DE F3522.4 protein.
GN F3522.4.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditidae.
OX NCBI_TaxID=6239;
RN 13
RP SEQUENCE FROM N.A.
RA STRAIN-BRISTOL N2;
RA Waterston R.;
RA "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.

```


GenCore version 5.1.4_p5_4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 30, 2002, 13:21:52 ; Search time 23.555 Seconds
(without alignments)
22,641 Million cell updates/sec

Title: us-09-498-556c-357

Perfect score: 11

Sequence: 1 LXX 4

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 14350520 residues

Total number of hits satisfying chosen parameters: 929470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 1000 summaries

Database :

A_Genoseq_101002:*

1:	/SID22/seqdata/genoseq/101002/seqs/AA000001.LAI	•
2:	/SID22/seqdata/genoseq/101002/seqs/AA000002.LAI	•
3:	/SID22/seqdata/genoseq/101002/seqs/AA000003.LAI	•
4:	/SID22/seqdata/genoseq/101002/seqs/AA000004.LAI	•
5:	/SID22/seqdata/genoseq/101002/seqs/AA000005.LAI	•
6:	/SID22/seqdata/genoseq/101002/seqs/AA000006.LAI	•
7:	/SID22/seqdata/genoseq/101002/seqs/AA000007.LAI	•
8:	/SID22/seqdata/genoseq/101002/seqs/AA000008.LAI	•
9:	/SID22/seqdata/genoseq/101002/seqs/AA000009.LAI	•
10:	/SID22/seqdata/genoseq/101002/seqs/AA000010.LAI	•
11:	/SID22/seqdata/genoseq/101002/seqs/AA000011.LAI	•
12:	/SID22/seqdata/genoseq/101002/seqs/AA000012.LAI	•
13:	/SID22/seqdata/genoseq/101002/seqs/AA000013.LAI	•
14:	/SID22/seqdata/genoseq/101002/seqs/AA000014.LAI	•
15:	/SID22/seqdata/genoseq/101002/seqs/AA000015.LAI	•
16:	/SID22/seqdata/genoseq/101002/seqs/AA000016.LAI	•
17:	/SID22/seqdata/genoseq/101002/seqs/AA000017.LAI	•
18:	/SID22/seqdata/genoseq/101002/seqs/AA000018.LAI	•
19:	/SID22/seqdata/genoseq/101002/seqs/AA000019.LAI	•
20:	/SID22/seqdata/genoseq/101002/seqs/AA000020.LAI	•
21:	/SID22/seqdata/genoseq/101002/seqs/AA000021.LAI	•
22:	/SID22/seqdata/genoseq/101002/seqs/AA000022.LAI	•
23:	/SID22/seqdata/genoseq/101002/seqs/AA000023.LAI	•

Pred No is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	9	81.8	3	AA084192	Peptide comprising
2	9	81.8	4	AA048182	Conantokin peptide
3	9	81.8	4	AA048182	Conantokin peptide
4	9	81.8	4	AA079319	Conantokin peptide
5	9	81.8	4	AA024457	Amino acid sequence
6	9	81.8	4	AA024457	Peptide N glycosylation
7	9	81.8	4	AA024457	System divergent
8	9	81.8	4	AA024457	C terminal sequence
9	9	81.8	4	AA051957	PSA antibody prep
10	9	81.8	5	AA03446	PSA antibody prep
					Accessory moiety d

11,	9	81.8	5	15	AA048099	Sequence of protein
12	9	81.8	5	15	AA050135	ovine growth hormone
13	9	81.8	5	15	AA050135	ovine growth hormone
14	9	81.8	5	15	AA050134	ovine growth hormone
15	9	81.8	5	16	AA077433	Human apolipoprotein
16	9	81.8	5	17	AA006695	Cyclic pentapeptide
17	9	81.8	5	17	AA006696	Cyclic pentapeptide
18	9	81.8	5	17	AA006697	Cyclic pentapeptide
19	9	81.8	5	17	AA006698	Cyclic pentapeptide
20	9	81.8	5	18	AA037417	Subtilisin N25711
21	9	81.8	5	21	AA051458	Mammalian haemolysin
22	9	81.8	5	22	AA011109	AAV VPA derived from
23	9	81.8	5	22	AA011109	Tryptic peptide #1
24	9	81.8	5	22	AA011144	Chemotryptic peptide
25	9	81.8	5	22	AA051461	MAIP substrate #1
26	9	81.8	5	23	AA051952	PSA antibody prep
27	9	81.8	5	23	AA051955	PSA antibody prep
28	9	81.8	6	15	AA048098	Phytase derived from
29	9	81.8	6	15	AA050141	ovine growth hormone
30	9	81.8	6	15	AA050142	ovine growth hormone
31	9	81.8	6	15	AA050143	ovine growth hormone
32	9	81.8	6	15	AA057411	dsRNA dependent kinase
33	9	81.8	6	17	AA006511	Hydratoma A102 HB
34	9	81.8	6	18	AA074092	4-methylcholanthrene
35	9	81.8	6	19	AA034665	complement and skin
36	9	81.8	6	18	AA07424	mammalian haemolysin
37	9	81.8	6	18	AA024572	Peptide immunoreactive
38	9	81.8	6	19	AA076724	pancreatic polypeptide
39	9	81.8	6	19	AA076725	pancreatic polypeptide
40	9	81.8	6	19	AA076726	pancreatic polypeptide
41	9	81.8	6	19	AA076727	pancreatic polypeptide
42	9	81.8	6	19	AA076728	pancreatic polypeptide
43	9	81.8	6	19	AA076729	pancreatic polypeptide
44	9	81.8	6	19	AA076730	pancreatic polypeptide
45	9	81.8	6	19	AA076731	pancreatic polypeptide
46	9	81.8	6	19	AA076732	pancreatic polypeptide
47	9	81.8	6	19	AA076733	pancreatic polypeptide
48	9	81.8	6	19	AA076734	pancreatic polypeptide
49	9	81.8	6	19	AA076735	pancreatic polypeptide
50	9	81.8	6	19	AA076736	pancreatic polypeptide
51	9	81.8	6	19	AA076737	pancreatic polypeptide
52	9	81.8	6	19	AA076738	pancreatic polypeptide
53	9	81.8	6	19	AA076739	pancreatic polypeptide
54	9	81.8	6	19	AA076740	pancreatic polypeptide
55	9	81.8	6	19	AA076741	pancreatic polypeptide
56	9	81.8	6	19	AA076742	pancreatic polypeptide
57	9	81.8	6	19	AA076743	pancreatic polypeptide
58	9	81.8	6	19	AA076744	pancreatic polypeptide
59	9	81.8	6	19	AA076745	pancreatic polypeptide
60	9	81.8	6	19	AA076746	pancreatic polypeptide
61	9	81.8	6	19	AA076747	pancreatic polypeptide
62	9	81.8	6	19	AA076748	pancreatic polypeptide
63	9	81.8	6	19	AA076749	pancreatic polypeptide
64	9	81.8	6	19	AA076750	pancreatic polypeptide
65	9	81.8	6	19	AA076751	pancreatic polypeptide
66	9	81.8	6	19	AA076752	pancreatic polypeptide
67	9	81.8	6	19	AA076753	pancreatic polypeptide
68	9	81.8	6	19	AA076754	pancreatic polypeptide
69	9	81.8	6	19	AA076755	pancreatic polypeptide
70	9	81.8	6	19	AA076756	pancreatic polypeptide
71	9	81.8	6	19	AA076757	pancreatic polypeptide
72	9	81.8	6	19	AA076758	pancreatic polypeptide
73	9	81.8	6	19	AA076759	pancreatic polypeptide
74	9	81.8	6	19	AA076760	pancreatic polypeptide
75	9	81.8	6	19	AA076761	pancreatic polypeptide
76	9	81.8	6	19	AA076762	pancreatic polypeptide
77	9	81.8	6	19	AA076763	pancreatic polypeptide
78	9	81.8	6	19	AA076764	pancreatic polypeptide
79	9	81.8	6	19	AA076765	pancreatic polypeptide
80	9	81.8	6	19	AA076766	pancreatic polypeptide
81	9	81.8	6	19	AA076767	pancreatic polypeptide
82	9	81.8	6	19	AA076768	pancreatic polypeptide
83	9	81.8	6	19	AA076769	pancreatic polypeptide
84	9	81.8	6	19	AA076770	pancreatic polypeptide

[illegible]

522	7	23	ABP48129	zinc finger protein	555	7	23	ABP48551	zinc finger protein
523	9	81.8	ABP48130	zinc finger protein	556	9	81.8	ABP48552	zinc finger protein
524	7	23	ABP48131	zinc finger protein	557	7	23	ABP48553	zinc finger protein
525	9	81.8	ABP48132	zinc finger protein	558	9	81.8	ABP48554	zinc finger protein
526	7	23	ABP48133	zinc finger protein	559	7	23	ABP48555	zinc finger protein
527	9	81.8	ABP48134	zinc finger protein	560	9	81.8	ABP48556	zinc finger protein
528	7	23	ABP48135	zinc finger protein	561	7	23	ABP48557	zinc finger protein
529	9	81.8	ABP48136	zinc finger protein	562	9	81.8	ABP48558	zinc finger protein
530	7	23	ABP48137	zinc finger protein	563	7	23	ABP48559	zinc finger protein
531	9	81.8	ABP48138	zinc finger protein	564	9	81.8	ABP48560	zinc finger protein
532	7	23	ABP48139	zinc finger protein	565	7	23	ABP48561	zinc finger protein
533	9	81.8	ABP48140	zinc finger protein	566	9	81.8	ABP48562	zinc finger protein
534	7	23	ABP48141	zinc finger protein	567	7	23	ABP48563	zinc finger protein
535	9	81.8	ABP48142	zinc finger protein	568	9	81.8	ABP48564	zinc finger protein
536	7	23	ABP48143	zinc finger protein	569	7	23	ABP48565	zinc finger protein
537	9	81.8	ABP48144	zinc finger protein	570	9	81.8	ABP48566	zinc finger protein
538	7	23	ABP48145	zinc finger protein	571	7	23	ABP48567	zinc finger protein
539	9	81.8	ABP48146	zinc finger protein	572	9	81.8	ABP48568	zinc finger protein
540	7	23	ABP48147	zinc finger protein	573	7	23	ABP48569	zinc finger protein
541	9	81.8	ABP48148	zinc finger protein	574	9	81.8	ABP48570	zinc finger protein
542	7	23	ABP48149	zinc finger protein	575	7	23	ABP48571	zinc finger protein
543	9	81.8	ABP48150	zinc finger protein	576	9	81.8	ABP48572	zinc finger protein
544	7	23	ABP48151	zinc finger protein	577	7	23	ABP48573	zinc finger protein
545	9	81.8	ABP48152	zinc finger protein	578	9	81.8	ABP48574	zinc finger protein
546	7	23	ABP48153	zinc finger protein	579	7	23	ABP48575	zinc finger protein
547	9	81.8	ABP48154	zinc finger protein	580	9	81.8	ABP48576	zinc finger protein
548	7	23	ABP48155	zinc finger protein	581	7	23	ABP48577	zinc finger protein
549	9	81.8	ABP48156	zinc finger protein	582	9	81.8	ABP48578	zinc finger protein
550	7	23	ABP48157	zinc finger protein	583	7	23	ABP48579	zinc finger protein
551	9	81.8	ABP48158	zinc finger protein	584	9	81.8	ABP48580	zinc finger protein
552	7	23	ABP48159	zinc finger protein	585	7	23	ABP48581	zinc finger protein
553	9	81.8	ABP48160	zinc finger protein	586	9	81.8	ABP48582	zinc finger protein
554	7	23	ABP48161	zinc finger protein	587	7	23	ABP48583	zinc finger protein
555	9	81.8	ABP48162	zinc finger protein	588	9	81.8	ABP48584	zinc finger protein
556	7	23	ABP48163	zinc finger protein	589	7	23	ABP48585	zinc finger protein
557	9	81.8	ABP48164	zinc finger protein	590	9	81.8	ABP48586	zinc finger protein
558	7	23	ABP48165	zinc finger protein	591	7	23	ABP48587	zinc finger protein
559	9	81.8	ABP48166	zinc finger protein	592	9	81.8	ABP48588	zinc finger protein
560	7	23	ABP48167	zinc finger protein	593	7	23	ABP48589	zinc finger protein
561	9	81.8	ABP48168	zinc finger protein	594	9	81.8	ABP48590	zinc finger protein
562	7	23	ABP48169	zinc finger protein					
563	9	81.8	ABP48170	zinc finger protein					
564	7	23	ABP48171	zinc finger protein					
565	9	81.8	ABP48172	zinc finger protein					
566	7	23	ABP48173	zinc finger protein					
567	9	81.8	ABP48174	zinc finger protein					
568	7	23	ABP48175	zinc finger protein					
569	9	81.8	ABP48176	zinc finger protein					
570	7	23	ABP48177	zinc finger protein					
571	9	81.8	ABP48178	zinc finger protein					
572	7	23	ABP48179	zinc finger protein					
573	9	81.8	ABP48180	zinc finger protein					
574	7	23	ABP48181	zinc finger protein					
575	9	81.8	ABP48182	zinc finger protein					
576	7	23	ABP48183	zinc finger protein					
577	9	81.8	ABP48184	zinc finger protein					
578	7	23	ABP48185	zinc finger protein					
579	9	81.8	ABP48186	zinc finger protein					
580	7	23	ABP48187	zinc finger protein					
581	9	81.8	ABP48188	zinc finger protein					
582	7	23	ABP48189	zinc finger protein					
583	9	81.8	ABP48190	zinc finger protein					
584	7	23	ABP48191	zinc finger protein					
585	9	81.8	ABP48192	zinc finger protein					
586	7	23	ABP48193	zinc finger protein					
587	9	81.8	ABP48194	zinc finger protein					
588	7	23	ABP48195	zinc finger protein					
589	9	81.8	ABP48196	zinc finger protein					
590	7	23	ABP48197	zinc finger protein					
591	9	81.8	ABP48198	zinc finger protein					
592	7	23	ABP48199	zinc finger protein					
593	9	81.8	ABP48200	zinc finger protein					
594	7	23	ABP48201	zinc finger protein					

960 9 81.8 7 23 ARP49998
 961 9 81.8 7 23 ARP49999
 962 9 81.8 7 23 ARP49100
 963 9 81.8 7 23 ARP49102
 964 9 81.8 7 23 ARP49104
 965 9 81.8 7 23 ARP49105
 966 9 81.8 7 23 ARP49108
 967 9 81.8 7 23 ARP49109
 968 9 81.8 7 23 ARP49110
 969 9 81.8 7 23 ARP49111
 970 9 81.8 7 23 ARP49116
 971 9 81.8 7 23 ARP49122
 972 9 81.8 7 23 ARP49124
 973 9 81.8 7 23 ARP49125
 974 9 81.8 7 23 ARP49127
 975 9 81.8 7 23 ARP49128
 976 9 81.8 7 23 ARP49130
 977 9 81.8 7 23 ARP49131
 978 9 81.8 7 23 ARP49133
 979 9 81.8 7 23 ARP49136
 980 9 81.8 7 23 ARP49137
 981 9 81.8 7 23 ARP49138
 982 9 81.8 7 23 ARP49140
 983 9 81.8 7 23 ARP49142
 984 9 81.8 7 23 ARP49144
 985 9 81.8 7 23 ARP49146
 986 9 81.8 7 23 ARP49147
 987 9 81.8 7 23 ARP49148
 988 9 81.8 7 23 ARP49149
 989 9 81.8 7 23 ARP49150
 990 9 81.8 7 23 ARP49152
 991 9 81.8 7 23 ARP49153
 992 9 81.8 7 23 ARP49155
 993 9 81.8 7 23 ARP49156
 994 9 81.8 7 23 ARP49157
 995 9 81.8 7 23 ARP49159
 996 9 81.8 7 23 ARP49161
 997 9 81.8 7 23 ARP49162
 998 9 81.8 7 23 ARP49163
 999 9 81.8 7 23 ARP49169
 1000 9 81.8 7 23 ABA47816

ALIGNMENTS

RESULT 1
 AAW4194
 ID AAW4194 standard; peptide: 4 AA.

XX AAW4194;
 XX 25 MAR 1994 (first entry)
 DE Peptide comprising a proteinase site.

XX Protease site; bone morphogenetic fusion protein; bone binding site;
 KW bone morphogenetic protein; transforming growth factor beta;
 KW active fragment; wound healing; bone growth.

XX Unidentified.

XX W 09055147 AL.
 XX 10 DEC 1998.

XX 02 JUN 1998; 98W0-US11189.

XX 03 JUN 1997; 97US-0868452.

XX (HALL/) HALL F I
 PA (HALL/) HALL B.
 PA (HALL/) HALL M E.

PA (SHR/) SHRKS E C.
 PA (WILL/) WILL L.
 XX Hall F I, Hall B, Simi ME, Shors E I, Will L;
 XX WFL, 1999 050875/05.
 XX New bone morphogenetic fusion proteins - comprising a purified fusion
 PT tag and a bone morphogenetic active fragment, used for enhancing
 PT wound healing or bone growth
 XX Claim 8, Page 34; 64pp; English.
 XX The present peptide represents a proteinase site used in the creation
 CC of the bone morphogenetic fusion proteins of the invention. The bone
 CC morphogenetic fusion protein may contain some or all of the following
 CC elements: a purification tag, a proteinase site, an ECM/bone binding
 CC site, a second proteinase site, and a bone morphogenetic protein
 CC active fragment. The fusion proteins of the invention also includes
 CC proteins that have transforming growth factor beta active fragments
 CC instead of bone morphogenetic protein active fragments. The bone
 CC morphogenetic fusion proteins can be used for enhancing wound healing
 CC or bone growth.
 XX Sequence 4 AA;
 SQ Query Match 81.8%; Score 9; ID 20; Length 4;
 Best Local Similarity 66.7%; Pos. No. 7,2000;
 Matches 2; Conserved Pos. 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 EXR 3
 DB 1 LTR 3

RESULT 2
 AAW48182
 ID AAW48182 standard; peptide: 4 AA.

XX AAW48182;
 XX 03 JUN 1998 (first entry)

XX Comantokin peptide derivative.
 DE Comantokin; predatory cone snail; treatment; neurological disorder;
 KW psychiatric disorder; antipsychotic; neuroprotective; analgesic.

KW HIV infection; ophthalmic indication; memory; learning defect;
 KW cognitive defect.

XX Synthetic.

XX Key Localization/Quantifiers
 XX Modified-site 4
 XX Z-score "gamma-carboxyglutamic acid"

XX W09803541 AL.

XX 29 JAN 1998.

XX 21 JUL 1997; 97W0-US12618.

XX 22 JUL 1996; 96US-0684742.

XX (COGN-) CORNETIX INC.

XX (UTAH) UNIV UTAH RES FOUND.

XX Abosadie FC, Colledge C, Cruz LJ, Hillyard DR, Jimenez E;

XX Layer RI, Mescher RI, Oliveira RM, Fivier JE, Shen GS;

XX Walker C, Zhou L;

XX WFL, 1998 120604/11.

PI New conantokin peptide(s) useful for treating neurologic or
 PI psychiatric disorders, or the management of pain
 XX
 PS Claim 15: Page 98; 125pp. English.
 XX
 CC The present sequence is a conantokin peptide derivative, which can
 CC be used to treat neurologic and psychiatric disorders, e.g. as an
 CC anticonvulsant, neuroprotective or analgesic agent. Neurologic and
 CC psychiatric disorders include epilepsy, convulsions, pain, stroke
 CC injury (associated with conditions of hypoxia, anoxia or ischemia,
 CC which typically follow stroke, cerebrovascular accident, brain or
 CC spinal cord trauma, myocardial infarct, physical trauma, drowning,
 CC suffocation, perinatal asphyxia or hypoglycemic events),
 CC neurodegeneration (associated with Alzheimer's disease, senile
 CC dementia, Amyotrophic Lateral Sclerosis, Multiple Sclerosis,
 CC Parkinson's disease, Huntington's disease, Lewy's Syndrome,
 CC Kretschmer's disease, schizophrenia, AIDS dementia, multi-infarct
 CC dementia, Binswanger dementia and neuronal damage associated with
 CC uncontrolled seizures), chemical toxicity (such as addiction, and
 CC morphine, opiate, opioid and barbiturate tolerance), pain (acute,
 CC chronic, migraine), anxiety, major depression, manic-depressive
 CC illness, obsessive compulsive disorder, schizophrenia and mood
 CC disorders (such as bipolar disorder, unipolar depression, dysthymia
 CC and seasonal affective disorder) and dementia (concurrent disorder),
 CC sleep disorder, muscle relaxation and urinary incontinence. The
 CC peptide can also be used to treat HIV infection, ophthalmic
 CC indication and memory, learning or cognitive defects.
 XX
 SQ Sequence 4 AA:
 Query Match 81.8%; Score 9; DB 19; Length 4;
 Best Local Similarity 65.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 Db 1 LAR 3
 RESULT 3
 AAW49964
 ID AAW49964 standard; peptide: 4 AA.
 AC AAW49964:
 DT 30-JUN-1998 (first entry)
 DX Conantokin peptide derivative.
 XX
 XX Conantokin, predatory cone snail, treatment, neurologic disorder,
 KW psychiatric disorder; anticonvulsant; neuroprotective; analgesic,
 KW HIV infection, ophthalmic indication, memory, learning defect,
 KW cognitive defect
 XX
 OS Synthetic.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4 /note: "gamma-carboxyglutamic acid"
 FT
 FI
 FN W09803189-A1.
 XX
 XX 29-JAN-1998.
 PD
 PF 21-JUL-1997; 97WO-US12652.
 XX
 XX 06-DEC-1996; 96US-0762377.
 PR 22-JUL-1996; 96US-0684750.
 XX
 XX (COGN-) COGNETIX INC.
 PA
 XX Layer RT, McCabe RT, Zhou L;
 PI
 XX

XX
 XX
 PI Use of conantokin peptide(s) for treating disorders involving
 PI excessive excitatory or inhibitory activity, excitatory amino acids or
 PI agonists of the N-methyl D-aspartate receptor
 XX
 PS Claim 27: Page 69; 125pp. English.
 XX
 CC The present sequence is a conantokin peptide derivative, which can
 CC be used to treat neurologic and psychiatric disorders, e.g. as an
 CC anticonvulsant, neuroprotective or analgesic agent. Neurologic and
 CC psychiatric disorders include epilepsy, convulsions, headache,
 CC injury (associated with conditions of hypoxia, anoxia or ischemia,
 CC which typically follow stroke, cerebrovascular accident, brain or
 CC spinal cord trauma, myocardial infarct, physical trauma, drowning,
 CC suffocation, perinatal asphyxia or hypoglycemic events),
 CC neurodegeneration (associated with Alzheimer's disease, senile
 CC dementia, Amyotrophic Lateral Sclerosis, Multiple Sclerosis,
 CC Parkinson's disease, Huntington's disease, Lewy's Syndrome,
 CC Kretschmer's disease, schizophrenia, AIDS dementia, multi-infarct
 CC dementia, Binswanger dementia and neuronal damage associated with
 CC uncontrolled seizures), chemical toxicity (such as addiction, and
 CC morphine, opiate, opioid and barbiturate tolerance), pain (acute,
 CC chronic, migraine), anxiety, major depression, manic-depressive
 CC illness, obsessive compulsive disorder, schizophrenia and mood
 CC disorders (such as bipolar disorder, unipolar depression, dysthymia
 CC and seasonal affective disorder) and dementia (concurrent disorder),
 CC sleep disorder, muscle relaxation and urinary incontinence. The
 CC peptide can also be used to treat HIV infection, ophthalmic
 CC indication and memory, learning or cognitive defects.
 XX
 SQ Sequence 4 AA:
 Query Match 81.8%; Score 9; DB 19; Length 4;
 Best Local Similarity 65.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 Db 1 LAR 3
 RESULT 4
 AAG79019
 ID AAG79019 standard; peptide: 4 AA.
 AC AAG79019:
 DT 10-DEC-2001 (first entry)
 DX Amino acid sequence of conantokin from *Conus* spp.
 XX
 XX Conantokin, cone snail, nerve cell excitation, RNA receptor, epilepsy;
 KW N-methyl D-aspartate receptor; pain; psychiatric disorder;
 KW neurotoxic injury; hypoxia; anoxia; ischemia; neurodegeneration;
 KW chemical toxicity; addiction; drug craving; psychiatric disorder;
 KW epilepsy; bipolar disorder; anxiety; depression; schizophrenia;
 KW mood disorder; ophthalmic disorder; neurological disorder; dystonia;
 KW sleep disorder; muscle relaxation; urinary incontinence;
 KW ophthalmic enhancement; HIV infection.
 XX
 OS Conus radiatus.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 4 /note: "gamma-carboxyglutamic acid"
 FT
 FI
 FN US6277825-B1.
 XX
 XX 21-AUG-2001.
 PD
 XX 20-JUL-1999; 99US-0457141.
 PF
 XX

XX The present invention relates to diverged delta 9 fatty acid desaturase
 CC proteins and polynucleotides encoding such proteins. The nucleic acid
 CC sequences may be used to increase the level of unsaturation in cellular
 CC lipids, including oil, in tissues when the enzyme is absent or rare.
 CC Limiting, to isolate cDNAs and genes encoding homologous proteins from
 CC the same or other plant species and to create transgenic plants in which
 CC the polypeptides are present at higher or lower levels than normal or in
 CC cell types or developmental stages in which they are not normally found,
 CC thus altering the level of mono-, poly- and unsaturated fatty acids in
 CC those cells. They are useful as probes for genetic and physical gene
 CC mapping and as markers, e.g. restriction fragment length polymorphism
 CC (RFLP) markers. The peptides can be used to immunise animals to produce
 CC antibodies specific for the peptides and proteins. The present sequence
 CC is soybean diverged delta-9 fatty acid desaturase peptide (residues
 CC 256-286).

XX Sequence 4 AA:

Query Match 91.8%, Score 9, IP 23, Length 4,

Best Local Similarity 66.7%, Pred No 7.7e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 2 LAR 4

RESULT 7

AAE14417

ID AAE14417 standard; peptide; 4 AA.

XX AAE14417;

XX 26-MAR-2002 (first entry)

XX C-terminal sequence of a delta-9 unsaturated peptide.

XX Protein quantification, protein identification, signature peptide,
 KW mass spectrometric analysis, proteolytic peptide; affinity ligand;
 KW arginine; isobaric peptide.

XX Unidentified.

XX W0200186306-A2.

XX 15-NOV-2001.

XX 04-MAY-2001; 2001WO-US14418.

XX 05-MAY-2000; 2000US-203227P.

XX 31-MAY-2000; 2000US-208184P.

XX 31-MAY-2000; 2000US-208272P.

XX (PORD) PURDUE RES FOUND.

XX (RCGN/) REIGNER F E.

XX (CHAF/) CHAKRABORTY A B.

XX (DJRM/) DORMADY S J.

XX (GENG/) G'ENG M.

XX (JHJ/) JI J.

XX (KJG/) KONGS L D.

XX (SIOW/) SIOWA C S.

XX (WANG/) WANG S.

XX (ZHAN/) ZHANG X.

XX Reigner FF, Chakraborty AB, Dormady SJ, G'eng M, Ji J, P'eng LQ;

XX Sioma CS, Wang S, Zhang X;

XX WPI: 2002-08981/012

XX Analyzing differences in protein content in protein samples, useful for
 PT identifying protein(s) in a sample or multiple proteins in a single
 PT complex mixture, by employing mass spectrometric analysis of signature

PI peptides

XX Example 9; Page 73; 106pp; English.

XX The invention relates to analysing differences in protein content among
 CC plural protein samples comprising employing mass spectrometric analysis
 CC of proteolytic peptide fragments. The method comprises
 CC fragmenting at least a first protein sample and a second protein
 CC sample to produce a first peptide pool and a second peptide pool;
 CC isotopically labelling at least a portion of the peptides in at
 CC least one of the pools so as to permit resolution of otherwise
 CC identical peptides in the first and second peptide pools by mass
 CC analysis; contacting peptides from at least a portion of both of the
 CC peptide pools with a separation matrix having affinity selected peptides
 CC comprising an affinity ligand, where the affinity matrix selects for the
 CC affinity ligand; and analysing the affinity selected peptides by mass
 CC spectrometry to determine one or more differences between the first and
 CC second samples. The method of the invention is useful for identifying one
 CC or more proteins in the sample, and is typically useful for identifying
 CC multiple proteins in a sample, sample mixtures. The method is also useful
 CC for quantifying proteins in a sample or several samples. The advantages
 CC of the novel method are that it is easier to separate peptides than
 CC proteins; native structure of the protein does not have to be maintained
 CC during the analysis; structural variants do not interfere; and
 CC putative proteins suggested from LIA database can be recognised by
 CC using a signature peptide probe. The present method permits
 CC identification of a protein in a complex sample without purifying the
 CC protein or obtaining its composite peptide signature. The present
 CC sequence is C-terminal fragment of a differentially acetylated
 CC arginine-containing peptide which is used to generate fragment ions for
 CC distinguishing isobaric peptides.

XX Sequence 4 AA:

Query Match 81.8%, Score 9, IP 23, Length 4;

Best Local Similarity 66.7%, Pred No 7.7e+05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 2 LAR 4

RESULT 8

AAM51953

ID AAM51953 standard; peptide; 4 AA.

XX AAM51953;

XX 01-FEB-2002 (first entry)

XX PSA antibody preparation immunogen peptide #5.

XX PSA: prostate-specific antigen; prostatic carcinoma; prokallikrein 2;
 KW human; antibody; immunogen.

XX Homo sapiens.

XX EEL8042646 A1.

XX 29-NOV-2001.

XX 05-JUL-2000; 2000DE-1942040.

XX 24-MAY-2000; 2000DE-1925487.

XX (ROFF) ROCHF DIAGN-SIUS GMBH.

XX WPI: 2002-04263/06.

XX Antibody comprising specificity for some truncated forms of
 PT pro prostate specific antigen, useful in immunoassays for differential
 PT diagnosis of prostatic carcinoma

```

XX PS Disclosure: Page 11; 16pp; German.
XX CC The present invention relates to an antibody specific for (-5,-6 and
XX CC or 7)-proPSA (prostate specific antigen), but with no reactivity with (-4)
XX CC or shorter forms of the protein. The antibody can be used to diagnose
XX CC prostate carcinoma and to detect human pro-kallikrein 2. The present
XX CC sequence is a peptide which forms part of a peptide-containing immunogen
XX CC described in the exemplification of the invention.
XX SQ Sequence 4 AA:
XX
XX Query Match 81.8%; Score 9; DB 24; Length 4;
XX Best Local Similarity 66.7%; Pred. No. 7.7e-05;
XX Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 LXR 4
XX 1 1
XX 2 LSR 4
XX
XX RESULT 9
XX AAM51957
XX ID AAM51957 standard; peptide; 4 AA.
XX AC AAM51957;
XX AD 01 FEB 2002 (first entry)
XX DE PSA antibody preparation immunogen peptide #9.
XX KW PSA: prostate specific antigen; prostatic carcinoma; pro-kallikrein 2;
XX KW human; antibody; immunogen.
XX QS Homo sapiens.
XX PN DB10032040-AL.
XX PD 29-NOV-2001.
XX PF 05-JUL-2000; 2000DE-1032040.
XX PR 24 MAY 2000; 2000DE-1025487.
XX QA (BOFF) ROCHE DIAGNOSTICS CMH.
XX QY 2002-04263306.
XX DB
XX PT Antibody comprising specificity for some truncated forms of
XX PT pro-prostate specific antigen, useful in immunoassays for differential
XX PT diagnosis of prostate carcinoma.
XX PS Disclosure: Page 11; 16pp; German.
XX CC The present invention relates to an antibody specific for (-5,-6 and
XX CC or 7)-proPSA (prostate specific antigen), but with no reactivity with (-4)
XX CC or shorter forms of the protein. The antibody can be used to diagnose
XX CC prostate carcinoma and to detect human pro-kallikrein 2. The present
XX CC sequence is a peptide which forms part of a peptide-containing immunogen
XX CC described in the exemplification of the invention.
XX SQ Sequence 4 AA:
XX
XX Query Match 81.8%; Score 9; DB 24; Length 4;
XX Best Local Similarity 66.7%; Pred. No. 7.7e-05;
XX Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 LXR 4
XX 1 1
XX 2 LSR 4
XX
XX RESULT 10

```

```

AAR03446
XX ID AAR03446 standard; protein; 5 AA.
XX AC AAR03446;
XX AD 02-AUG-1990 (first entry)
XX DE Accessory moiety derived from transferrin receptor.
XX KW Accessory moiety; transferrin receptor; tumour therapy.
XX QS Synthetic.
XX PN EP059447-A.
XX PD 21-MAR-1990.
XX PF 14-AUG-1989; 89EP-0250014.
XX PR 15-AUG-1988; 88US-0232337.
XX QA (NEER) NEERX CORP.
XX QY Anderson DW, Morahan AC, Abrams PG, Nichols EJ, Fitzhugh AK,
XX WPI: 1990 085154/12.
XX CC Covalently linked complex for tumour treatment comprises
XX CC treating with protein, cytotoxic agent and chelated moiety.
XX PS Claim 13; Page 22; 24pp; English.
XX CC the sequence is one of several possible accessory moieties which can be
XX CC attached to the C-terminus of an anchoring moiety which in turn is
XX CC linked to a targeting protein and a cytotoxic agent. When the anchoring
XX CC peptide intercalates into the target cell plasma membrane the accessory
XX CC moiety is translocated across the membrane and protrudes into the
XX CC cytoplasm. It can then be phosphorylated by cellular kinases at neutral
XX CC pH. This irreversibly anchors the complex to the membrane and may
XX CC enhance the translocation into the cytoplasm. The complex is useful for
XX CC treatment and diagnosis of tumours.
XX CC See also AAR03435-60.
XX SQ Sequence 5 AA:
XX
XX Query Match 81.8%; Score 9; DB 11; Length 5;
XX Best Local Similarity 66.7%; Pred. No. 7.7e-05;
XX Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 LXR 4
XX 1 1
XX 3 LSR 5
XX
XX RESULT 11
XX AAR48999
XX ID AAR48999 standard; Protein; 5 AA.
XX AC AAR48999;
XX AD 02-SEP-1994 (first entry)
XX DE Sequence of portion of wild type murine erythropoietin receptor
XX DE (rEPOR).
XX KW Erythropoietin receptor; EPOR; ss.
XX QS Mus musculus.
XX QY Key Location/Qualifiers
XX PF Misc-difference 3
XX FT Note *cys in rEPOR*
XX

```


PN US9292654 A.
 XX
 PD 08-MAR-1994.
 XX
 PF 13-DEC-1960: 900S-0526923.
 XX
 PR 13-DEC-1990: 900S-0526923.
 XX
 PA (WHEE) WHITEHEAD INST BIOMEDICAL RES.
 XX
 PI Lodish H, Longmore GD, Yoshimura A;
 XX
 XX WPI: 1994-082236/10.
 DR N-PSDR: AAR48666.
 XX
 PT Mutant erythropoietin (EPO) receptor gene - hypersensitive to
 PT EPO, useful in assay for identifying compounds, mimicking EPO
 PT action
 XX
 PS Disclosure; Flu 10; 13pp; English.
 XX
 CC cEPOR is wild-type EPO. cEPOR is a constitutive form. It contains
 CC a point mutation (4 transition from C to T at nucleotide 484) which
 CC causes one substitution (Arg to Cys) in the extracellular domain of
 CC EPO. At position 125 of the predicted N-terminus. The Arg to Cys point
 CC mutation in cEPOR is sufficient to induce factor-independent
 CC growth.
 XX
 SQ Sequence 5 AA:
 Query Match 81.8%; Score 9; DB 15; Length 5;
 Best local Similarity 66.7%; Prod. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 1 LAR 3
 XX
 RESULT 12
 AAR50115
 ID AAR50115 standard; peptide: 5 AA.
 AC AAR50115;
 XX
 DI 23-SEP-1994 (first entry)
 XX
 DE Ovine growth hormone residues 92-96.
 XX
 KW Bovine; ovine; porcine; growth hormone; BHI; OGH; pGH; antigen;
 FW growth hormone activity; potentiate; enhance; increase.
 XX
 OS Bos taurus.
 OS Ovis aries.
 OS Sus scrofa.
 XX
 PN W09405697-A.
 XX
 PD 17-MAR-1994.
 XX
 PF 07-SEP-1993: 93WO-GB01887.
 XX
 PR 07-SEP-1992: 92GB-0018907.
 PR 09-AUG-1993: 93GB-0016508.
 XX
 PA (ASRI) AGRIC & FOOD RES COUNCIL.
 PA (HANN) HANNAH RES INST.
 XX
 PI Beattie J, Holder AT;
 XX
 XX WPI: 1994-101122/12.
 XX
 CC New antigenic molecules derived from growth hormone - and derived

PT antibodies, used to stimulate the activity of growth hormone
 XX
 XX Claim 4; Page 7; 64pp; English.
 XX
 CC This peptide corresponds to residues 92-96 of bovine, ovine and
 CC porcine growth hormone. The peptide is rendered antigenic and is
 CC then capable of stimulating the production of antibodies which,
 CC when in the appropriate formulation, potentiate the effect of
 CC growth hormone.
 XX
 SQ Sequence 5 AA:
 Query Match 81.8%; Score 9; DB 15; Length 5;
 Best local Similarity 66.7%; Prod. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 2 LXR 4
 XX
 RESULT 13
 AAR50116
 ID AAR50116 standard; peptide: 5 AA.
 AC AAR50116;
 XX
 DI 23-SEP-1994 (first entry)
 XX
 DE Ovine growth hormone residues 93-97.
 XX
 KW Bovine; ovine; porcine; growth hormone; BHI; OGH; pGH; antigen;
 FW growth hormone activity; potentiate; enhance; increase.
 XX
 OS Bos taurus.
 OS Ovis aries.
 OS Sus scrofa.
 XX
 PN W09405697-A.
 XX
 PD 17-MAR-1994.
 XX
 PF 07-SEP-1993: 93WO-GB01887.
 XX
 PR 07-SEP-1992: 92GB-0018907.
 PR 09-AUG-1993: 93GB-0016508.
 XX
 PA (ASRI) AGRIC & FOOD RES COUNCIL.
 PA (HANN) HANNAH RES INST.
 XX
 PI Beattie J, Holder AT;
 XX
 XX WPI: 1994-101122/12.
 XX
 CC New antigenic molecules derived from growth hormone - and derived
 CC antibodies, used to stimulate the activity of growth hormone
 XX
 XX Claim 4; Page 7; 64pp; English.
 XX
 CC This peptide corresponds to residues 93-97 of bovine, ovine and
 CC porcine growth hormone. The peptide is rendered antigenic and is
 CC then capable of stimulating the production of antibodies which,
 CC when in the appropriate formulation, potentiate the effect of
 CC growth hormone.
 XX
 SQ Sequence 5 AA:
 Query Match 81.8%; Score 9; DB 15; Length 5;
 Best local Similarity 66.7%; Prod. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 DB 1 LAR 3

PF 15-FEB-1995; 95JP-0026674.
 XX
 PR 15-FEB-1995; 95JP-0026674.
 XX (BIOC-) BIOCOSMOS YG
 XX
 XX WPI: 1996-425431/44;
 XX

PF New cyclic pentapeptide: exhibits thrombolytic and
 PT anti-arteriosclerosis activity
 XX
 XX Disclosure: Page 8: 9pp; Japanese.
 XX

XX The invention relates to new cyclic pentapeptides of formula
 CC cyclo(A-B-C-D-E) in which A is Val, Leu, Phe, Lys, Arg, Glu, Gln or
 CC Ser; B is Leu, Val, Phe, Lys, Arg, His, Glu, Glu, Ala or Ser; C is Leu,
 CC Val, Ile, Phe, Lys, Arg, Glu, Glu, Ala or Ser; D is Phe, Val, Leu, Tyr,
 CC Lys, Arg, His, Glu, Glu, Ala or Ser; and E is Arg, Val, Leu, Phe, Lys,
 CC His, Glu, Asn, Ala or Ser. The amino acids may be in D- or L-form.
 CC The peptides have thrombolytic activity and anti-arteriosclerotic
 CC activity.
 CC The present sequence is a specific example of the new peptides.
 XX
 XX Sequence 5 AA;

Query Match 81.8%; Score 9; DB 17; Length 5;
 Post-local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 3
 DB 3 LAR 5

RESULT 17
 AAW09696
 ID AAW09696 standard; peptide; 5 AA.
 AC
 AC AAW09696;

DI 23-MAY-1997 (first entry)

XX Cyclic pentapeptide having thrombolytic activity.

XX Thrombolysis, arteriosclerosis; cyclic.

XX Synthetic.

XX Key location/qualifiers

FT Modified-site 1 /note= "this residue forms part of a cyclic
 FT peptide, being condensed with the amino acid
 FT at position 5. It is not an N-terminal site"

FT Modified-site 5 /note= "this residue forms part of a cyclic
 FT peptide, being condensed with the amino acid
 FT at position 1. It is not a C-terminal site"

FT Misc-difference 1 /note= "D-form residue"

FT Misc-difference 3 /note= "D-form residue"

FT Misc-difference 5 /note= "D-form residue"

XX JP08217794-A

XX 27-AUG-1996.

XX 15-FEB-1995; 95JP-0026674.

XX 15-FEB-1995; 95JP-0026674.

XX (BIOC-) BIOCOSMOS YG.

XX WPI: 1996-425431/44.

XX New cyclic pentapeptide: exhibits thrombolytic and
 PT anti-arteriosclerosis activity
 XX
 XX Disclosure: Page 8: 9pp; Japanese.
 XX

XX the invention relates to new cyclic pentapeptides of formula
 CC cyclo(A-B-C-D-E) in which A is Val, Leu, Phe, Lys, Arg, Glu, Gln or
 CC Ser; B is Leu, Val, Phe, Lys, Arg, His, Glu, Glu, Ala or Ser; C is Leu,
 CC Val, Ile, Phe, Lys, Arg, Glu, Glu, Ala or Ser; D is Phe, Val, Leu, Tyr,
 CC Lys, Arg, His, Glu, Glu, Ala or Ser; and E is Arg, Val, Leu, Phe, Lys,
 CC His, Glu, Asn, Ala or Ser. The amino acids may be in D- or L-form.
 CC The peptides have thrombolytic activity and anti-arteriosclerotic
 CC activity.
 CC The present sequence is a specific example of the new peptides.
 XX
 XX Sequence 5 AA;

Query Match 81.8%; Score 9; DB 17; Length 5;
 Post-local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 LXR 3
 DB 3 LSR 5

RESULT 18
 AAW00251
 ID AAW00251 standard; peptide; 5 AA.
 AC
 AC AAW00251;

DI 16-DEC-1996 (first entry)

XX Subtilisin N62D/G166D substrate peptide.

XX Subtilisin BPN'. Protease, enzyme engineering; protein engineering;
 XX Bacillus amyloliquefaciens, mutagenesis, substrate specificity;
 XX Phase display.

XX Synthetic.

XX W:9627671-A1.

XX 12-SEP-1996.

XX 27-FEB-1996; 96WI-0802861.

XX 19-JUN-1996; 96US-0504265.

XX 03-MAR-1995; 95US-0398028.

XX (GUTH) GUNTER-H INC.

XX Ballinger MD, Wells JA;

XX WPI: 1996-425431/42.

XX Subtilisin variants for cleaving substrates containing basic residues -
 PT allow effective cleavage of fused proteins with basic linker
 PT sequences

XX Example 4, Page 27; 93pp; English.

XX A phase display system was used to select 5 residue substrate
 CC linkers for cleavage by subtilisin BPN' 9627671-A1 derivative mutant
 CC (AAW00247). The library was subjected to 9 rounds of selection, and
 CC clones that were increasingly sensitive or resistant to cleavage
 CC were selected. Of 21 clones in the sensitive pool, 4 were monobasic
 CC (AAW00249) and 19 dibasic (AAW00249-5). The substrate given in
 CC AAW00251 was selected once from the pool of 21. Of 10 substrates

CC selected from the resistant pool (AAW00254-63); 7 contained no basic
 CC sites, 2 were monobasic and 1 was dibasic. The N620/G1660 double mutant
 CC specifically cleaves protein substrates contg. basic amino acid
 XX residues at positions P1 and P2.

XX Sequence 5 AA;

Query Match 81.8%; Score 9; DB 17; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 1 LXR 3

RESULT 19

AAW00252

ID AAW00252 standard; peptide; 5 AA;

XX AAW00252;

XX 16-DEC-1996 (first entry)

XX Subtilisin B20/G1660 substrate peptide.

KW Subtilisin BPN'; protease; enzyme engineering; protein engineering;
 KW Bacillus amyloliquefaciens; mutagenesis; substrate specificity;
 KW phase display.

XX Synthetic.

XX W96-276/1-A1.

XX 12 SEP-1996.

XX 27-FEB-1996; 96W0-0502861.

PR 19-JUL-1995; 95US 0504265.

PR 03-MAR-1995; 95US-0398028.

XX (GTEH) GENENTECH INC.

PI Ballinger MD, Wells JA;

XX WPI: 1996-425431/42.

PI Subtilisin variants for cleaving substrates contg. basic residues -
 PT allow effective cleavage of fusion proteins with basic linker
 PI sequences

XX Example 4: Page 27; 84pp; English.

CC A phage display system was used to screen 5-residue substrate
 CC linkers for cleavage by subtilisin BPN' B20/G1660 double mutant
 CC (AAW00247). The library was subjected to 9 rounds of selection, and
 CC clones that were increasingly sensitive to cleavage by the enzyme
 CC were selected. Of 21 clones in the sensitive pool, 3 were monobasic
 CC (AAW00248) and 18 dibasic (AAW00249-53). The substrate given in
 CC AAW00252 was selected once from the pool of 21. Of 10 substrates
 CC selected from the resistant pool (AAW00254-63), 7 contained no basic
 CC sites, 2 were monobasic and 1 was dibasic. The N620/G1660 double mutant
 CC specifically cleaves protein substrates contg. basic amino acid
 CC residues at positions P1 and P2.

XX Sequence 5 AA;

Query Match 81.8%; Score 9; DB 17; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 1 LXR 3

DB 2 LXR 4

RESULT 20

AAW37417

ID AAW37417 standard; peptide; 5 AA;

XX AAW37417;

XX 10 MAR-1996 (first entry)

XX Mammalian haemoglobin tryptic peptide C-terminal sequence.

KW Mammalian haemoglobin; tryptic peptide; bovine; porcine; equine;
 KW immune enhancer; microbial psoriasis; blood contracting; food;
 KW powdered milk; cow; pig; horse.

XX Bos taurus.

XX Equus caballus.

XX Sus scrofa.

XX Synthetic.

XX JPO9262094 A.

XX 07-OCT-1997.

XX 27 MAR-1996; 96JP 0072797.

XX 27 MAR-1996; 96JP-0072797.

XX (FIOH-) ITO HAM KK.

XX WPI: 1997-544157/50.

XX New mammalian haemoglobin tryptic peptide(s) - useful as immune
 XX enhancers and to prevent microbial psoriasis

XX claim 1; Page 1; 7pp; Japanese.

CC The present sequence represents a C-terminal peptide used in low
 CC mammalian haemoglobin tryptic peptides, consisting of 5-12 amino
 CC acids. The peptides can be produced from bovine, swine or equine
 CC haemoglobin by hydrolysis with an enzyme (e.g. trypsin) and subsequent
 CC purification. They can also be produced by chemical synthesis. The
 CC peptides correspond to the partial amino acid sequence with length of
 CC the beta-chain of bovine, swine or equine haemoglobin and have
 CC blood-contracting and immune enhancing activities. They may be used
 CC in prevention of microbiological psoriasis or as immune enhancers,
 CC functional foods or powdered milk for infants.

XX Sequence 5 AA;

Query Match 81.8%; Score 9; DB 18; Length 5;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

DB 1 LXR 5

RESULT 21

AAW51458

ID AAW51458 standard; peptide; 5 AA;

XX AAW51458;

XX 11 MAY-2000 (first entry)

XX AAV VP4 derived peptide fragment #13.

XX VP4; structural protein; capsid; tropism; diagnosis; gene therapy.

OS Adeno associated virus.
 PN W09967393-A2.
 XX
 PD 26-DEC-1999.
 XX
 PS 21-JUN-1999; 99WO-EP04288.
 XX
 PF 19-JUN-1999; 99EP-1927457.
 PR
 XX (MEDICI) MEDIGENE AG
 PA
 PI Hallick M, Ried M, DeLage G, Girard A,
 XX WPI: 2000-59055/66.
 XX
 PS Structure proteins of adeno-associated virus with at least one mutation
 PT have increased infectiveness -
 XX
 PS Claim 15; Page 31; 43pp; German.
 XX
 CC This invention describes novel structural proteins of adeno associated
 CC virus (AAV) especially AAV-capsids with at least one mutation and which
 CC have an increased infectiveness. The structural proteins are used to
 CC alter the tropism of AAV, to transform cells, for diagnosis and for
 CC effectivity studies for gene therapy and/or for genomic targeting.
 CC AAV51446-V51457 represent AAV derived peptides used to illustrate the
 CC method of the invention.
 XX
 SQ Sequence 5 AA:
 Query Match 91.9%; Score 9; ID 23; Length 5;
 Best local similarity 66.7%; Prod No 776-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 J I
 Db 3 LSR 5
 RESULT 22
 AAE11109
 ID AAE11109 standard; peptide: 5 AA.
 XX
 AC AAE11109;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Tryptic peptide #11 of phAR fusion protein.
 XX
 KW Phenylalanine hydroxylase; PAH; pHA; 4a-carbinolamine dehydratase; phbB;
 KW aromatic aminotransferase; phbC; milk protein; animal protein; casein;
 KW proteinaceous food product; albumin; whey protein; phenylketonuria;
 KW PKU; inherited metabolic disorder; impaired brain function; nootropic;
 KW cell therapy; tryptic peptide.
 XX
 OS Unidentified.
 XX
 PN W0200169822-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 14-MAR-2001; 2001WO-DK00172.
 XX
 PR 14-MAR-2000; 2000US-0525116.
 XX
 XX (NIIA) NIIAH APS.
 XX
 XX Johnson M, Ravn P, Madsen SM, Vrang A, Israelson B, Brodmose L;
 PI Arnan J, Jensen SH, Gjetting T, Nielsen E;
 XX WPI: 2001-59055/66.
 XX
 PT Novel recombinant cells comprising a nucleic acid encoding a gene

PT Novel recombinant cells comprising a nucleic acid encoding a gene
 PT product having phenylalanine hydroxylase activity; that is derived from
 PT a prokaryotic organism, is useful for treating phenylketonuria in
 PT mammals -
 XX
 PS Example 8; Page 47; 91pp; English.
 XX
 CC The patent discloses novel cells comprising a nucleic acid encoding
 CC a gene product having phenylalanine hydroxylase (PAH) activity such
 CC as phenylalanine hydroxylase (pHA), 4a-carbinolamine dehydratase
 CC (phbB) and aromatic aminotransferase (phbC), which are derived
 CC from a prokaryotic organism, the patent also relates to fusion
 CC proteins comprising a protein subunit and/or stabilising the
 CC PAH activity in addition to PAH activity; the cells are useful
 CC for producing PAH; the sequences of the insertion are also useful
 CC for preparing a proteinaceous food product (animal protein such
 CC as a milk protein derived from casein, whey protein or a whey protein)
 CC having reduced content of phenylalanine. The method involves contacting
 CC the food product starting material with the cells or fusion proteins
 CC such that at least part of the phenylalanine content of the starting
 CC material is converted into compounds that do not cause phenylketonuria
 CC (PKU) by the enzymatically active product. PAH enzyme is useful for
 CC manufacturing a medicament for treating PKU, which is an inherited
 CC metabolic disorder resulting in an accumulation in the body of
 CC a phenylalanine and derivatives that can cause impaired brain
 CC function. The present sequence is tryptic peptide of phbB fusion
 CC protein.
 XX
 SQ Sequence 5 AA:
 Query Match 91.9%; Score 9; ID 22; Length 5;
 Best local similarity 66.7%; Prod No 776-05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 J I
 Db 3 LSR 5
 RESULT 23
 AAE11144
 ID AAE11144 standard; peptide: 5 AA.
 XX
 AC AAE11144;
 XX
 DT 18-DEC-2001 (first entry)
 XX
 DE Chymotryptic peptide #14 of phAR fusion protein.
 XX
 KW Phenylalanine hydroxylase; PAH; pHA; 4a-carbinolamine dehydratase; phbB;
 KW aromatic aminotransferase; phbC; milk protein; animal protein; casein;
 KW proteinaceous food product; albumin; whey protein; phenylketonuria;
 KW PKU; inherited metabolic disorder; impaired brain function; nootropic;
 KW cell therapy; chymotryptic peptide.
 XX
 OS Unidentified.
 XX
 PN W0200169822-A2.
 XX
 PD 20-SEP-2001.
 XX
 PF 14-MAR-2001; 2001WO-DK00172.
 XX
 PR 14-MAR-2000; 2000US-0525116.
 XX
 XX (NIIA) NIIAH APS.
 XX
 XX Johnson M, Ravn P, Madsen SM, Vrang A, Israelson B, Brodmose L;
 PI Arnan J, Jensen SH, Gjetting T, Nielsen E;
 XX WPI: 2001-59055/66.
 XX
 PT Novel recombinant cells comprising a nucleic acid encoding a gene

PI product having phenylalanine hydroxylase activity, that is derived from
 PT a prokaryotic organism, is useful for treating phenylketonuria in
 XX mammals

PS Example A: Page 46: 91pp: English

XX the patent discloses novel cells comprising a nucleic acid encoding
 CC a gene product having phenylalanine hydroxylase (PAH) activity such
 CC as phenylalanine hydroxylase (pH4), 4a carbinolamine dehydratase
 CC (p4hd) and aromatic aminotransferase (p4hc), which are derived
 CC from a prokaryotic organism. The patent also relates to fusion
 CC proteins comprising a protein enhancer and/or stabilising the
 CC PAH activity in addition to PAH activity. The cells are useful
 CC for producing PAH. The sequences of the invention are also useful
 CC for preparing a proteinaceous food product (animal protein such
 CC as a milk protein derived from casein, globulin or a whey protein)
 CC having reduced content of phenylalanine. The method involves activating
 CC the food product starting material with the cells or fusion proteins
 CC such that at least part of the phenylalanine content of the starting
 CC material is converted into compounds that do not cause phenylketonuria
 CC (PKU) by the enzymatically active product. PAH enzyme is useful for
 CC manufacturing a medicament for treating PKU, which is an inherited
 CC metabolic disorder resulting in an accumulation in the body of
 CC L-phenylalanine and metabolites that can cause retarded brain
 CC function. The present sequence is chymotryptic peptide of p4hAB fusion
 CC protein.

XX Sequence 5 AA;

Query Match 81.99; Score 9; DB 22; Length 5;
 Best Local Similarity 66.79; Pred. No. 7.7e-05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 4
 | |
 DB 1 LXR 4

RES011 24

AAE05461
 ID AAE05461 standard; peptide: 5 AA.

XX AAE05461;

XX 24-SEP-2001 (first entry)

XX MASP substrate #4.

XX Mannan binding protein-associated serine protease; MASP substrate;
 KW complement activation; C-activation; microbial infection;
 KW cytoequilibrium; CMV; hepatitis virus; human immunodeficiency virus;
 KW HIV; organ transplant rejection; tissue injury; autoimmune disease;
 KW rheumatoid arthritis; systemic lupus erythematosus; SLE; measles,
 KW inflammatory response; Alzheimer's disease; anaphylatoxin.

XX Synthesis.

XX Key location/Qualifiers

XX Modified-site 1

XX Note "N-terminal acetyl"

XX Modified-site 5

XX Note: "Conjugated to para-nitroaniline (pNA)"

XX US624544 B1.

XX 22-MAY-2001.

XX 08-FEB-1999; 990S 0246500.

XX 08-FEB-1999; 990S-0246500.

XX (SCK1) SCHIPPS RES INST.

XX

PI Huq11 PE;

XX WPI: 2001-450022/48.

XX Method for determining in vivo levels of activated mannan binding
 PT protein-associated serine protease enzyme, and new peptide derivatives

XX Claim 47, Column 59, 9pp: English.

XX The invention relates to assays for monitoring in vivo levels of
 CC activated mannan-binding protein-associated serine protease (MASP-1 and
 CC MASP-2) activity. The assay comprises contacting a sample of blood or
 CC plasma comprising a metal ion chelator with a substrate of tosyl-L-
 CC K-peptide Y, wherein the peptide comprises at least 4 residues from the
 CC C-terminus of an anaphylatoxin selected from C3a, C4a and C5a; R is a
 CC peptide backbone protected at N-terminus by a Y and Y is any group
 CC cleavable from the substrate by MASP and comprises a labelled tag. The
 CC substrate of the invention is also useful for monitoring in vitro and
 CC in vivo complement activation (C-activation) by classical alternative
 CC or lectin pathways. The assays of MASP activity can be used for
 CC detecting or monitoring a condition associated with complement
 CC activation; the conditions include microbial infections
 CC caused by particularly cytomegalovirus (CMV), hepatitis virus and
 CC human immunodeficiency virus (HIV), organ transplant rejection, tissue
 CC injury, autoimmune diseases (e.g. rheumatoid arthritis, systemic lupus
 CC erythematosus (SLE)) and inflammatory responses (e.g. in Alzheimer's
 CC disease and bacterial diseases). The assay of MASP is also useful for
 CC assessing the toxicity or injury of therapeutic treatments or screening
 CC test compounds as agents for treatment of viral diseases, parasitic
 CC infections, tissue injury, organ transplant rejection, autoimmune
 CC diseases or inflammatory responses. The present sequence is a
 CC mannan-binding protein-associated serine protease (MASP) substrate.

XX Sequence 5 AA;

Query Match 81.88; Score 9; DB 22; Length 5;
 Best Local Similarity 66.79; Pred. No. 7.7e-05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 | |
 DB 3 LXR 5

RES011 25

AAE01952
 ID AAE01952 standard; peptide: 5 AA.

XX AAE01952;

XX 01-FEB-2002 (first entry)

XX PSA antibody preparation immunogen peptide #4.

XX PSA; prostate-specific antigen; prostatic carcinoma; pro kallikrein 2;
 KW human; antibody; immunogen.

XX Homo sapiens.

XX DE10042040-A1.

XX 29-NOV-2001.

XX 05-JUL-2000; 2000DE-1042040.

XX 24-MAY-2000; 2000DE-1925467.

XX (HOPF) ROCHE DIAGNOSTICS GmbH.

XX WPI: 2002 042634/06.

PT Antibody comprising specificity for some truncated forms of

PI pro-prostate specific antigen, useful in immunoassays for differential
 PI diagnosis of prostatic carcinoma
 XX
 PS Disclosure; Page 10; 16pp; German.
 XX
 CC The present invention relates to an antibody specific for (-5,-6 and
 CC -7)-proPSA (prostate-specific antigen), but with no reactivity with (-4)
 CC or shorter forms of the protein. The antibody can be used to diagnose
 CC prostatic carcinoma and to detect human pro-kallikrein 2. The present
 CC sequence is a peptide which forms part of a peptide-containing immunogen
 CC described in the exemplification of the invention.

XX Sequence 5 AA;

Query Match 81.8%; Score 9; DB 23; Length 5;

Best Local Similarity 66.7%; Pred. No. 7.7e-05;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

Db 3 LSR 5

RESULT 26

AAM51956

ID AAM51956 standard; peptide; 5 AA

XX

AC AAM51956;

XX

DI 01-FEB-2002 (first entry)

XX

DE PSA antibody preparation immunogen; peptide #2.

XX

KW PSA, prostate specific antigen; prostatic carcinoma; pro-kallikrein 2;

XX

KW human; antibody; immunogen.

XX

OS Homo sapiens.

XX

FN DE10032040-A1.

XX

PD 29-NOV-2001.

XX

PF 05-JUL-2000; 2000EE 1032049.

XX

PP 24-MAY-2000; 2000PE 1025387

XX

PA (HOFF) POCHÉ DIAGNOSTICS GMRH

XX

DP WPI: 2000-042632/06

XX

PI Antibody comprising specificity for PSA, prostatic carcinoma of

XX

PT pro prostate specific antigen, useful in immunoassays for differential

XX

PT diagnosis of prostatic carcinoma

XX

PS Disclosure; Page 11; 16pp; German.

XX

XX

CC The present invention relates to an antibody specific for (-5,-6 and

XX

CC -7)-proPSA (prostate-specific antigen), but with no reactivity with (-4)

XX

CC or shorter forms of the protein. The antibody can be used to diagnose

XX

CC prostatic carcinoma and to detect human pro-kallikrein 2. The present

XX

CC sequence is a peptide which forms part of a peptide-containing immunogen

XX

CC described in the exemplification of the invention.

XX

SQ Sequence 5 AA;

Query Match

Best Local Similarity 81.8%; Score 9; DB 23; Length 5;

Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

Db 2 LSR 4

RESULT 27

AAR46808

ID AAR46808 standard; Protein; 6 AA.

XX

AC AAR46808;

XX

DI 19-AUG-1994 (first entry)

XX

DE Phytase derived peptide 794(9 phy).

XX

KW ph 2, 5; acid phosphatase; Trichoderma; Aspergillus; phytic acid;

XX

KW phytate diesterase; phytic acid; Aspergillus; phytic acid;

XX

OS Synthetic.

XX

PN W09403612-A.

XX

PD 17-FEB-1994.

XX

PF 30-JUL-1993; 93WO-FI00410.

XX

PP 31-JUL-1992; 92US-0924724.

XX

XX (AIK3-) ALK3 L1D.

XX

PI Cantrell M. Fagerstrom KB. Miettinen-Oinonen ASK;

XX

PI Rockwell TR. Turunen MK;

XX

XX WPI: 1993-053709/08.

XX

XX Comensal, secreted phytate degraded enzymes, obtained by expression

XX

PT of their genes in Trichoderma, used partic. for producing animal

XX

PT feed composit.

XX

PS Example 4, Page 43, 142pp; English.

XX

XX

CC The sequences given in AAR46794-824 are peptides derived from the

XX

CC phytase protein. The phytase protein may be used in the composition

XX

CC of the invention. The RNA encoding the phytase protein may be

XX

CC introduced into a Trichoderma host which then expresses it and the

XX

CC protein is collected from the culture medium. By using Trichoderma as

XX

CC a host for Aspergillus phytase, a feeding enzyme such as this, a

XX

CC totally different enzyme composition compared to that derived from

XX

CC Aspergillus results. The enzyme composition can be used for removal

XX

CC of phytic acid or inositol hexaphosphoric acid from raw material,

XX

CC particularly plant material. The composition is used in feed

XX

CC compositions for animals. By using Trichoderma as a source of a

XX

CC composition containing phytate degrading enzymes some difficult

XX

CC downstream processing problems, e.g. filtration, that occur with

XX

CC similar Aspergillus compositions are avoided and yields are improved.

XX

SQ Sequence 6 AA;

Query Match

Best Local Similarity 81.8%; Score 9; DB 19; Length 6;

Matches 2; Conservative 0; Mismatches 1; Indels 0;

QY 1 LXR 3

Db 4 LTR 6

RESULT 28

AAR50141

ID AAR50141 standard; peptide; 6 AA.

XX

AC AAR50141;

XX

DI 24-SEP-1994 (first entry)

XX

SQ Sequence 6 AA:
 Query Match 81.8%; Score 9; DB 15; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 3
 Db 1 LSR 3
 RESULT 31
 AAR55741
 ID AAR55741 standard; peptide; 6 AA.
 AC AAR55741;
 XX
 DI 16-NOV-1994 (first entry)
 DE dsRNA-dependent kinase inhibitor.
 KW dsRNA dependent kinase inhibitor; fatty acyl-peptide; conjugate;
 KW antiproliferative; tumor; psoriasis; docosahexaenoic acid; DHA;
 KW eicosapentaenoic acid; EPA; anti-tumor.
 XX
 QS Synthetic.
 XX
 FN W09412530-A.
 XX
 PD 06-JUN-1994
 XX
 PF 29-NOV-1993; 93WO-H000065
 XX
 PR 30-NOV-1992; 92US-0984393.
 XX
 PA (BIOS-) BIOSIGNAL KURIATO FELLESETO KFT.
 PA (SYNT-) SYNTHETIC PEPTIDES INC.
 XX
 PI Balogh A., Gachia PJ., Hodges ES., Horvath A., Keri G.;
 PI Szoderkenyi E., Vadász Z.
 XX
 PD WPI: 1994-280194/24.
 XX
 PT New fatty acyl-peptide conjugates for inhibiting cell
 PT proliferation more active than free peptide, particle, for
 PT treating tumours, virus-infected cells, psoriasis, etc.
 XX
 PS Disclosure; Fig. 1; 45pp; English.
 XX
 CC The peptides given in AAR55718 18 can each be conjugated through an
 CC amide linkage with a polyunsaturated fatty acid moiety, such as
 CC docosahexaenoic acid or eicosapentaenoic acid, to improve
 CC antiproliferative activity. The dsRNA-dependent kinase
 CC inhibitor given in AAR55741 modulates various kinases associated
 CC with cell proliferation.
 XX
 SQ Sequence 6 AA:
 Query Match 81.8%; Score 9; DB 15; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 3
 Db 3 LSR 5
 RESULT 32
 AAR90511
 ID AAR90511 standard; peptide; 6 AA.
 AC AAR90511;
 XX
 DI 03-SEP-1996 (first entry)
 DE Hybridoma ATCC HB-11884 antibody displacing peptide #9.
 AC Antibody. Displacement, cell separation system, cell surface antigen; Aa;
 XX random peptide library; complementarity determining region; CDR;
 KW antibody; Ab; peptide; CD34 cell; haematopoietic cell; tumour cell;
 KW lymphocyte; high dose therapy; immune system; chemotherapy;
 KW patient specific vaccine.
 XX
 QS Synthetic.
 XX
 FN W09534817-A1.
 XX
 PD 21-DEC-1995.
 XX
 PF 14-JUN-1995; 95WO-0807491.
 XX
 PR 14 JUN 1994. 94US 0259427.
 XX
 PA (BAXT) BAXTER INC.
 XX
 PI Al abdaly EA, Fadia EZ, Giffelton E, Gelfand SL;
 PI Kozori JA, Isner JW J;
 XX
 PD WPI: 1996-049806/05.
 XX
 PT Selecting target cells by reacting specific antibody to surface
 PT antigen - then disrupting the complex formed with peptide displacer.
 PT antigen for selecting CD34 cells for reconstitution of immune system
 PT after anticancer treatment
 XX
 PS Claim 27; Page 158; 170pp; English.
 XX
 CC AAR90503-R90511 represent antibody displacing peptides. These sequences
 CC displace the antibody produced by the hybridoma ATCC HB 11884 (9187).
 CC These sequences can be used in a method to select target cells from a
 CC heterologous cell suspension. In the suspension, there is at least one
 CC complex of a cell separation system, linked to a primary antibody (Ab)
 CC which is bound to the cell surface antigen (Aa). The complex is
 CC separated from the rest of the suspension, and contacted with a peptide
 CC (such as this sequence) that binds to the Ab, displacing it from the Aa
 CC and releasing the cell. These sequences can be identified by biopanning
 CC random peptide display libraries with the Ab, by analysis of potential
 CC antigenic parts of the cell surface antigen, or by analysis of the
 CC complementarity determining regions of the Ab. These sequences can also
 CC be used in a method for determining the number of specific cells in a
 CC reposition. The methods can be used for positive selection of CD34
 CC haematopoietic cells, and removal of undesired tumour cells or
 CC lymphocytes from the selected cells. The peptide CD34 cells are released
 CC into a can of patient after high dose therapy to reconstitute the immune
 CC system. Target cells can also be isolated to determine their
 CC chemotherapeutic susceptibility, or for the production of
 CC patient specific vaccines or antibodies. These sequences allow for the
 CC recovery of cells from solid supports, in high yield, without enzymatic
 CC cleavage. They are relatively inexpensive and safe, and leave cell
 CC surface proteins intact.
 XX
 SQ Sequence 6 AA:
 Query Match 81.8%; Score 9; DB 15; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.
 QY 1 LXR 3
 Db 1 LSR 3
 RESULT 33
 AAR74602
 ID AAR74602 standard; peptide; 6 AA.
 AC AAR74602;
 XX

AC AAB74602;
 XX
 PT 21-MAY-2001 (first entry)
 XX
 DE 3-methylcholanthrene (MCA) peptide substrate.
 XX
 KW 3-methylcholanthrene; MCA; substrate; metalloproteinase inhibitor;
 XX cancer; metastasis; arthritis.
 XX
 OS Synthetic.
 XX
 PH Key
 FT Location/Qualifiers
 FT Modified-site 1
 FT /note= "pro in N-terminally modified to
 FT 7-methoxycoumarin-4-yl-acetyl-pro"
 FT Modified-site 5
 FT /note= "Ala is N-terminally modified to
 FT 3-(2,4-dichlorophenyl)-2,2-dimethylpropyl-ala"
 FT Modified-site 6
 FT /note= "amidated"
 XX
 PN W09729824 AL.
 XX
 PD 12-JUN-1997.
 XX
 PE 05-DEC-1996; 66W0-051932#
 XX
 PR 08-DEC-1995; 95US-0569766
 XX
 PA (AG00-) AG00FON PHARM INC.
 XX
 PI Zook SE, Iannino E, Deason ME, Bender SL, Melnick MJ;
 DR WF1: 1997-442465/30
 XX
 XX New N-hydroxy benzoxaldehyde carbamate derivatives - are
 PT metalloproteinase inhibitors, useful for treating cancer, metastasis,
 PT and arthritis
 XX
 PS Example 22 Page 100, 151pp. English
 XX
 CC The present invention describes metalloproteinase inhibitors and
 CC pharmaceutical compositions containing them. Also described are methods
 CC and intermediates useful in the preparation of the metalloproteinase
 CC inhibitors. R¹ is: 3-phenyl-5-phenyl (thiazole or pyridine)
 CC carbamate derivatives are metalloproteinase (MP) inhibitors. The
 CC present sequence represents a 3-methylcholanthrene (MCA) peptide
 CC substrate which is used in the exemplification of the present invention.
 CC The metalloproteinase inhibitors are useful for treating cancer,
 CC metastasis and arthritis.
 XX
 SQ Sequence 6 AA;
 Query Match 81.8%; Score 9; DB 18; Length 6;
 Post Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 LXR 3
 DB 1 LAR 6
 RESULT 64
 AAW43665
 ID AAW43665 standard; peptide; 6 AA.
 XX
 AC AAW43665;
 XX
 DE 24 APR-1998 (first entry)
 XX
 DE Complement antagonising peptide.
 XX
 KW Bacteriophage; capsid protein; mutant; half-life; phage therapy;
 bacterial infection; antibacterial; complement antagonising peptide.
 KW
 OS Synthetic.
 XX
 PN W09739118-A1.
 XX
 PD 27-OCT-1997.
 XX
 PF 03-APR-1997; 97W0-0804714.
 XX
 PR 12 APR-1996; 96US-0641427.
 XX
 PA (EXPO-) EXPONENTIAL BIOTHERAPIES INC.
 PA (USSH) US DEPT HEALTH & HUMAN SERVICES
 XX
 PI Adhya SL, Carlton RM, Merrill CR;
 XX
 DE WF1: 1997-526157/48.
 XX
 PT Amplifying gene to extend half-life of phage in circulation - gene
 PT encodes modified capsid protein; useful for therapy of bacterial
 PT infections
 XX
 PS Example 4; Page 23; 49pp; English.
 XX
 CC This is a complement antagonising peptide. A double stranded DNA encoding
 CC this peptide was synthesised. This nucleotide sequence is fused at the 3'
 CC end of a gene encoding a phage coat surface protein. This is used in the
 CC construction of a phage that can express molecules antagonising the host
 CC defence system. This enables the phage to delay inactivation by the host
 CC defence system. This is used in the construction of a modified phage with
 CC extended half-life. The phage has a modified capsid protein, having an
 CC acidic amino acid replaced by a basic amino acid, and extended half-life
 CC (at least 15%). The modified phages are used to treat a very wide range
 CC of bacterial infections, optionally in conjunction with antibiotics, in
 CC human or veterinary medicine. The modified phages are more resistant to
 CC inactivation by the host's immune system, so are more efficient
 CC antibacterial agents than wild-type phages. Phage therapy has fewer side
 CC effects than treatment with antibiotics or other drugs. It is suitable
 CC for patients allergic to conventional therapy and is especially valuable
 CC for treating infections caused by drug resistant bacteria.
 XX
 SQ Sequence 6 AA;
 Query Match 91.0%; Score 9; DB 18; Length 6;
 Post Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 OY 1 LXR 3
 DB 1 LAR 3
 RESULT 35
 AAW37324
 ID AAW37324 standard; peptide; 6 AA.
 XX
 AC AAW37324;
 XX
 DE 10 MAR-1998 (first entry)
 XX
 DE Mammalian haemoglobin tryptic peptide leucine derived sequence.
 XX
 KW Mammalian; haemoglobin; tryptic peptide; bovine; porcine; equine;
 KW immune enhancer; microbial polysaccharide; from contracta; food;
 KW powdered milk; cow; pig; horse.
 XX
 OS Synthetic.
 OS Bos taurus.
 XX
 PN JP09262094-A.
 XX
 PD 07-OCT-1997.

XX 27-MAR-1996; 96JP-0072767
 XX 27-MAR-1996; 96JP-0072797.
 XX (ITOH-) ITO HAM KK.
 XX WPI: 1997-544157/50.
 XX
 XX New mammalian haemoglobin tryptic peptide(s) - useful as immune
 XX enhancers and to prevent microbial psoriasis
 XX
 XX Example 5; Page 4; 7pp: Japanese.
 XX
 XX The present sequence represents a bovine haemoglobin derived tryptic
 XX peptides. The peptide can be produced from bovine haemoglobin by
 XX hydrolysis with an enzyme (e.g. trypsin) and subsequent purification.
 XX It can also be produced by chemical synthesis. The peptide corresponds
 XX to the partial amino acid sequence 105th-116th of the beta-chain of
 XX bovine haemoglobin and has haem-contracting and immune enhancing
 XX activities. It may be used in prevention of microbiological psoriasis
 XX or as in immune enhancers, functional foods or powdered milk for
 XX infants.

XX Sequence 6 AA:

Query Match 81.8%; Score 9; BB 18; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0.

QY 1 LXR 3
 I I
 Db 4 LAR 6

RESULT 36

AAW26572
 ID AAW26572 standard; Peptide: 6 AA.

AC AAW26572;

PT 19-JAN-1998 (first entry)

DE Peptide immunoreactive with HuMAb L94.

XX Tumour associated antigen, melanoma, cancer, therapy, immunotherapy;
 XX diagnosis; prognosis; vaccine.

XX Synthetic.

XX W09714795-A1.

XX 24-APR-1997.

XX 19-OCT-1995; 95WO-US13331.

XX 19-OCT-1995; 95WO-US13331.

XX (WAYN-) WAYNE CANCER INST JOHN.

XX Irie RF, Kikumoto Y;

XX WPI: 1997-245112/22.

XX Antibody against polypeptide having C-terminal amino acid sequence
 XX comprising Ala-Pro, Gly-Pro or Pro-Pro - useful to purify
 XX polypeptide which can be useful in human melanoma treatment

XX Claim 3; Page 71; 87pp: English.

XX This peptide is immunoreactive with human monoclonal antibody JWC
 XX L94 that reacts to a human melanoma cell line. Claimed peptides
 XX (AAW26566-73) that are immunoreactive with L94 share a C-terminal

XX Ala-Pro sequence. They can be used in an antigen composition to
 XX elicit an immune response, particularly a cytotoxic T lymphocyte
 XX response, specifically as a polyvalent tumour cell vaccine in
 XX conjunction with a cancer whole cell vaccine therapy for human
 XX melanoma. The peptides can also be used to enhance an immune
 XX response, treat and diagnose cancer.

XX Sequence 6 AA:

Query Match 81.8%; Score 9; BB 18; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Caps 0.

QY 1 LXR 3
 I I
 Db 1 LAR 3

RESULT 37

AAW76723
 ID AAW76723 standard; Peptide: 6 AA.

XX AAW76723;

XX 13 JAN 1999 (first entry)

XX Pancreatic polypeptide C-terminal fragment for NIDDM treatment.

XX NIDDM insulin dependent diabetes mellitus; NIDDM; hepatic glucose;
 XX pancreatic polypeptide; PP; treatment; GS protein alpha subunit;
 XX inhibitor; cyclic adenosine monophosphate; cAMP; glucagon; secretion;
 XX exocrine pancreas; beta cell; pancreatic islet; hyperglycaemia;
 XX neuro-peptide Y; hyperglycaemia.

XX Homo sapiens.

XX US5830434-A.

XX 04-NOV-1998.

XX 26-FEB-1997; 97US-0306203.

XX 26-FEB-1997; 97US-0306203.

XX (UYSC) UNIV SOUTH CAROLINA MEDICAL RES FOUND.

XX Gettys T, Taylor IL;

XX WPI: 1998-609185/51.

XX Treatment of non-insulin-dependent diabetes mellitus with
 XX pancreatic polypeptide or C-terminal fragment

XX Claim 1; Column 3; 11pp: English.

XX This human pancreatic polypeptide C-terminal fragment is used in a method
 XX for treating non insulin dependent diabetes mellitus (NIDDM). The method
 XX involves administering a composition comprising pancreatic polypeptide or
 XX C-terminal pancreatic polypeptide fragment in a carrier. Screening a
 XX composition for the ability to treat NIDDM is also possible and involves
 XX determining if the composition decreases hepatic expression of the
 XX alpha subunit of a GS protein in a liver cell plasma membrane, thereby
 XX inhibiting stimulation of cyclic adenosine monophosphate (cAMP) by
 XX glucagon, determined if the composition binds the vacuolar nuclear complex
 XX and inhibits secretions of digestive enzymes by the exocrine pancreas,
 XX thereby inhibiting beta cell and pancreatic islet hypertrophy or
 XX determining if the composition binds the arcuate nucleus in the
 XX hypothalamus and potentiates the effect of leptin in reducing
 XX neuro-peptide Y synthesis, thereby enhancing insulin sensitivity and
 XX reversing the effects of neuro-peptide Y. The NIDDM treatment method
 XX decreases hepatic acids and increases insulin sensitivity without
 XX additional detrimental effects.

SQ Sequence 6 AA;

Query Match 81.8%; Score 9; DB 19; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 | |
 Db 1 LTR 3

RESULT 40

AAW67626

ID AAW76726 standard; peptide; 6 AA.

XX

AC AAW76726;

XX

DI 13-JAN-1999 (first entry)

XX

DE Pancreatic polypeptide C-terminal fragment analogue #3.

XX

KW Non-insulin dependent diabetes mellitus; NIDDM; hepatic glucose;
 KW pancreatic polypeptide; P; treatment; Gs protein alpha subunit;
 KW inhibitor; cyclic adenosine monophosphate, cAMP; glucagon secretion;
 KW exocrine pancreas; beta cell; pancreatic islet hypertrophy; insulin;
 KW neuropeptide Y; hyperglycaemia.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Misc-difference 5

FT /note= "D-form residue"

FT Modified-site 6

FT /note= "C-terminal amide group"

FT XX

PN US5830434-A.

XX

PD 03-NOV-1998.

XX

PF 26-FEB-1997; 97US-0806203.

XX

PK 26-FEB-1997; 97US-0806203.

XX

PA (UWSC-) UNIV SOUTH CAROLINA MEDICAL RES FOUND.

XX

PI Gettys T. Taylor IL;

XX

DK WPI; 1998-609185/51.

XX

PI Treatment of non-insulin-dependent diabetes mellitus - with
 pancreatic polypeptide or C-terminal fragment

XX

PS Disclosure; Column 6; 11pp; English.

XX

CC This human pancreatic polypeptide analogue C-terminal fragment is used in
 a method for treating non-insulin-dependent diabetes mellitus (NIDDM).
 The method involves administering a composition comprising pancreatic
 polypeptide or C-terminal pancreatic polypeptide fragment in a carrier.
 Screening a composition for the ability to treat NIDDM is also possible,
 and involves determining if the composition decreases hepatic expression
 of the alpha subunit of Gs protein in a liver cell plasma membrane,
 thereby inhibiting stimulation of cyclic adenosine monophosphate (cAMP)
 by glucagon. Determined if the composition binds the cyclic adenosine
 complex and inhibits secretions of alpha-glucagon, the exocrine
 pancreas, thereby inhibiting beta cell and pancreatic islet hypertrophy
 or determining if the composition binds the arcuate nucleus in the
 hypothalamus and potentiates the effect of leptin in reducing
 neuropeptide Y synthesis, thereby enhancing insulin sensitivity and
 reversing the effects of neuropeptide Y. The NIDDM treatment method
 decreases hyperglycaemia and increases insulin sensitivity without
 additional detrimental effects.

SQ Sequence 6 AA;

Query Match 81.8%; Score 9; DB 19; Length 6;
 Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 4
 | |
 Db 1 LTR 3

RESULT 41

AAW52139

ID AAW52139 standard; Peptide; 6 AA.

XX

AC AAW52139;

XX

DI 20-JUL-1998 (first entry)

XX

DE Matrix metalloproteinase MMP 9 substrate B.

XX

KW Membrane-type matrix metalloproteinase; MT-MMP; MT1-MMP;
 KW matrix metalloproteinase; MMP; matrix metalloproteinase;
 KW osteoclast inhibitor; metalloproteinase; osteoporosis;
 KW bone metastasis; metastasis; tumour; cancer; ulcer; arthritis;
 KW periodontal disease; therapy.

XX

OS Synthetic.

XX

FH Key Location/Qualifiers

FT Modified-site 1

FT /note= "Met-proline"

FT Cleavage-site 3..4

FT Modified-site 5

FT /note= "Ipa-alanine"

FT XX

PN W09804287-A1.

XX

PD 05-FEB-1998.

XX

PF 29 JUL 1997; 97WO-EP04110.

XX

PK 30-JUL-1999; 96GA-0015976.

XX

PA (CLIN-) CINT CLINICAL & BASIC RES.

XX

PI Lelaisse J. Faged NI. Molital M;

XX

DK WPI; 1998-140425/12.

XX

PI Use of inhibitors of protease(S) involved in osteoclast activity -
 useful for, e.g. treating metabolic bone disease such as
 osteoporosis

XX

PS Example 6b; Page 44; 11pp; English.

XX

CC Peptide B is a subunit of matrix metalloproteinase MMP 9. MMP 9
 is a peptidase that degrades extracellular matrix (ECM) and is
 a peptidase that degrades MMP-inhibitors (see AAW52139) are
 promising agents for use in treatment of bone metabolic disease.
 They can be used to inhibit proteolysis involved in the
 recruitment, proliferation, differentiation or migration of
 osteoclast precursor cells or in the migration, fusion, attachment,
 polarisation, removal of mineralised osseous substance or death of
 osteoclasts. The inhibitors reduce the rate of bone resorption
 and are used to treat of patient, e.g. osteoporosis and osteolytic
 bone metastases. They are also useful in, e.g. treatment of
 cancer, ulcers, arthritis and periodontal disease

XX

SQ Sequence 6 AA;

Query Match

Best Local Similarity 66.7%; Pred. No. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3
 II 1
 DB 4 LXR 6

RESULT 42
 AAW43147
 ID AAW43147 standard; peptide: 6 AA.
 AC AAW43147;
 XX
 XX 31-MAR-1998 (first entry)
 XX
 XX Peptide #26 tested for anti-melittin activity.
 DE
 XX Anti-melittin peptide; bee sting; melittin; haemolytic activity;
 KW bee venom; red blood cell; cell lysis; anti-melittin;
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 PH Modified-site 1
 FT Modified-site 6 /note- "N terminally acetylated"
 FT Modified-site 6 /note- "C-terminally amidated"
 FI
 FI US5698674 A.
 XX
 XX 16-DEC-1997.
 XX
 XX 04-MAY-1995; 95US-0434761.
 XX
 XX 18-JUN-1994; 94US-0079445.
 XX
 XX (TORK-) F-BREY FINES INST.
 XX
 XX Blondelle SE, Houghton KA, Pinilla C;
 XX WP1: 1998-051545/05
 XX
 XX Anti-melittin peptide(s) useful for treating bee stings
 XX
 XX Example 2; Column 32; 24pp; English.
 XX
 XX This peptide was tested for anti-melittin activity and showed an IC50
 CC value of greater than 250 microgram. The tested peptides peptides
 CC having anti-melittin activity with IC50 values of less than 60 microgram,
 CC which are useful for treating melittin poisoning. Melittin is the active
 CC compound in bee venom and causes cell lysis. Peptides having anti-
 CC melittin activity have one of the following formulae: Ac-IVILIZ-NH2;
 CC Ac-IVILIZ-NH2; Ac-IVILIZ-NH2; Ac-IVILIZ-NH2; Ac-IVILIZ-NH2;
 CC Ac-IVILIZ-NH2; Ac-IVILIZ-NH2; Ac-IVILIZ-NH2; Ac-IVILIZ-NH2;
 CC methylated or chlorinated D-form of natural amino acid; Z1: F or I;
 CC Z2: I or Q; Z3: W or Y and Z4: C or F.
 XX
 XX Sequence 6 AA:
 SQ

Query Match 81.8%; Score 9; DB 19; Length 6;
 Best Local Similarity 66.7%; Pred. NO. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 3
 II 1
 DB 4 LXR 6

RESULT 43
 AAY55249
 ID AAY55249 standard; peptide: 6 AA.
 XX
 XX AAY55249;
 XX
 XX 07-JAN-2000 (first entry)
 XX
 XX

XX AICC HB 11884 monoclonal antibody 9187 releasing peptide SEQ ID NO:144.
 DE
 XX
 XX Antibody releasing peptide; Ch34; hybridoma; binding; antigen;
 KW cell surface antigen; identification; haematopoietic stem cell;
 KW tumour; cancer; immune system; therapy; displacement.
 XX
 XX Synthetic.
 OS
 XX Homo sapiens.
 XX
 XX US5968753-A.
 XX
 XX 19-OCT-1999.
 XX
 XX 07-JUN-1995; 95US-0482228.
 XX
 XX 14-JUN-1994; 94US-0259427.
 XX
 XX (NEXEL-) NEXELL THERAPEUTICS INC.
 XX
 XX Guillermo R. Helgeson SL, Lewis RJ, Tseng Law J, Kohori JA;
 PI Al-Mudaly FA;
 XX
 XX WP1: 1999-590399/50.
 XX
 XX Short peptides useful for displacing antibodies from cell surface
 PT antigens.
 XX
 XX Claim 9; Column 148; 81pp; English.
 XX
 XX The present invention describes peptides of 4-17 amino acids which
 CC displace either the anti-CD34 monoclonal antibody designated 561, the
 CC anti-CD34 mouse monoclonal antibody produced by the hybridoma A10V
 CC HB-11646 (designated 9069), the anti-CD34 antibody produced by
 CC hybridoma A10V HB 11665 (9075), or the anti-human breast cancer
 CC antibody produced by hybridoma A10V HB-11884 (9187), from a cell
 CC surface antigen on a target cell. The peptides are useful for
 CC displacing antibodies bound to cell surfaces to release cells that
 CC have been positively selected by antibody-mediated binding to beads
 CC or other solid support. AAY55107 to AAY55319 represent peptides used in
 CC the exemplification of the present invention.
 XX
 XX Sequence 6 AA:
 SQ

Query Match 81.8%; Score 9; DB 20; Length 6;
 Best Local Similarity 66.7%; Pred. NO. 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0.

QY 1 LXR 3
 II 1
 DB 1 LXR 3

RESULT 44
 AAY41045
 ID AAY41045 standard; peptide: 6 AA.
 XX
 XX AAY41045;
 XX
 XX 21-DEC-1999 (first entry)
 XX
 XX Non-crosslinked protein particle peptide 84.
 DE
 XX
 XX Non-crosslinked protein particle; diagnostic; therapy; monodisperse;
 KW albumin; haemoglobin; monomer; micrometer; clearance.
 XX
 XX Synthetic.
 XX
 XX US5945033-A.
 XX
 XX 31-AUG-1999.
 XX
 XX 12-NOV-1996; 96US-0747147.
 XX
 XX

XX 14-MAR-1994; 94US 0212546.
 PR 15-JAN-1991; 91US 0641720.
 PR 13-OCT-1992; 92US-0959560.
 PR 01-JUN-1993; 93US-0069831.
 PR 12-JUN-1996; 96US-0747137.
 XX (HEMO-) HEMOSPHERE INC.
 XX Yen FCK;
 DR WPI: 1999-508153/42.
 PT Non-crosslinked protein particles for therapeutic and diagnostic use
 XX Example 22; Column 83-84; 65pp, English.
 CC This invention describes a novel aqueous suspension of non-crosslinked particles on non-crosslinked, non-denatured albumin (bovine nm) which is stable against dissolving upon dilution with an alcohol-free aqueous medium. The method involves (a) forming an aqueous solution containing albumin and hemoglobin and (b) treating the aqueous solution with an alcohol to cause the solution to become turbid. The particles are useful as agents for in vivo administration, either of their own administration or as a vehicle for other therapeutic or diagnostic agents. The method permits the formation of albumin and hemoglobin particles in the nanometer and micrometer size range, in a form closer to their natural form than the forms of the prior art. The particles therefore constitute a more closely controlled agent for in vivo administration, with greater ease of clearance from the body after their period of usefulness.
 CC AAY30952-Y31135 represent peptides used in the method of the invention.
 XX Sequence 6 AA;
 SQ
 Query Match 81.88; Score 9; DB 20; Length 6;
 Best Local Similarity 56.7%; Pred No 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 LXR 3
 Db 4 LAR 6
 RESULT 45
 AAY23392
 ID AAY23392 standard; Peptide: 6 AA.
 XX AAY23392;
 AC AAY23392;
 XX 02-SEP-1999 (first entry)
 DT V beta 6 clone found in MS patients after vaccination with TCR.
 DE
 DE
 KW Vaccine, T cell receptor, TCR, T cell, V beta 6.2/3, V beta 5/5,
 KW V beta 6.7, V beta 2, V beta 5/1, V beta 7, V beta 13; V beta 6,
 KW multiple sclerosis.
 XX Synthetic.
 OS Homo sapiens.
 OS
 FN WO9927957-A1.
 XX 10-JUN-1999.
 PD
 PF 03-DEC-1997; 97WO-US23147.
 XX 03-DEC-1997; 97WO-US23147.
 PR (IMMUN-) IMMUNE RESPONSE CORP.
 PA (KIMM-) KIMMEL CANCER CENT SIDNEY.
 XX
 PI Brostoff SW, Carlo DJ, Gold DP, Smith LR, Wilson DB;
 XX

DR WPI: 1999-404801/34.

XX T cell receptor peptide derived vaccines

XX Example 11; Page 84; 104pp; English.

CC The specification describes vaccines which comprise immunologically effective amounts of T cell receptor (TCR) peptides. The TCRs are present on the surface of T cells. The TCRs are chosen from V beta 5.2/1, V beta 6/5, V beta 6.7, V beta 2, V beta 5/1, V beta 7 or V beta 13. The V beta top peptide-based vaccines are useful for prevention or treatment of multiple sclerosis (MS). The presence of V beta 6.7 appears to be particularly associated with multiple sclerosis and can be used to determine an individual's susceptibility to multiple sclerosis. CC Vaccinating, rather than passively administering heterologous antibodies, allows the host's own immune system to mobilize and suppress auto aggressive T cells. Therefore, the suppression is persistent and may involve any and all immunological mechanisms in effecting that suppression. Such a multi-targeted response is more effective than the immunosuppressant suppression achieved by passive administration of monoclonal antibodies. T cell receptor peptide regulatory T cell clones. CC AAY30952-Y31135 represent peptides derived from the V beta 6 clones found in the cerebrospinal fluid (CSF) of MS patients after vaccination with V beta 6.

SQ Sequence 6 AA;

Query Match 81.88; Score 9; DB 20; Length 6;
 Best Local Similarity 56.7%; Pred No 7.7e+05;
 Matches 2; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LXR 3

Db 1 LAR 3

Search completed: April 30, 2003, 13:34:14

Job time : 28.5455 secs

